

GenCore version 5.1.6
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ein search, using sw model

February 20, 2004, 16:47:50 ; Search time 38.5367 Seconds
(without alignments)
4378.325 Million cell updates/sec

S-10-090-827-15

599

MAAGCLLALTITLTFQSILIG.....PDVCFNNVLEDTDCGVS 1063

LOSUM62

apop 10.0 , Gapext 0.5

107863 seqs, 158726573 residues

its satisfying chosen parameters: 1107863

ngth: 0

ngth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

s the number of results predicted by chance to have a
er than or equal to the score of the result being printed,
ved by analysis of the total score distribution.

SUMMARIES

Query	Length	DB	ID	Description
00.0	1063	22	AAU01034	Human secreted sol
00.0	1063	22	AA62258	Porcine calcium ch
00.0	1091	16	AA71011	Human neuronal cal
00.0	1091	19	AAW63145	Human calcium chan
00.0	1091	21	AA10576	Human calcium chan
00.0	1091	22	AAU01035	Human secreted sol
00.0	1091	22	AA62259	Porcine calcium ch
00.0	1091	23	AAE24789	Human calcium chan
99.9	1091	19	AAW37879	Human calcium chan

Sequence	10	5593	99.9	1091	14	AA33553
Human cal	11	5579.5	99.7	1110	19	AAW63148
Human net	12	5559.5	99.3	1086	16	AA71013
Human cal	13	5559.5	99.3	1086	19	AAW63153
Human cal	14	5559.5	99.3	1086	21	AA10587
Human cal	15	5559.5	99.3	1086	23	AAE24799
Human net	16	5542.5	99.0	1084	16	AAW71015
Human cal	17	5542.5	99.0	1084	19	AAW63155
Human cal	18	5542.5	99.0	1084	21	AA10589
Human cal	19	5542.5	99.0	1084	23	AAE24801
Pig secre	20	5532	98.8	1063	22	AAU01030
Porcine c	21	5532	98.8	1069	22	AA62254
Pig secre	22	5532	98.8	1069	22	AAU01031
Porcine c	23	5532	98.8	1069	22	AA62255
Pig secre	24	5532	98.8	1091	22	AAU01027
Porcine c	25	5532	98.8	1091	22	AA62251
Human net	26	5523	98.6	1103	16	AA71012
Human cal	27	5523	98.6	1103	19	AAW63151
Human cal	28	5523	98.6	1103	21	AA10586
Human cal	29	5523	98.6	1103	23	AAE24798
Human cal	30	5503	98.3	1079	19	AAW63154
Human cal	31	5503	98.3	1079	21	AA10588
Human cal	32	5503	98.3	1079	23	AAE24800
Human net	33	5497	98.2	1079	16	AA71014
Human sec	34	5433	97.2	1036	22	AAU01033
Porcine c	35	5443	97.2	1036	22	AA62257
Rabbit s	36	5385.5	96.2	1106	18	AAW37712
Rabbit c	37	5385.5	96.2	1106	18	AAW18389
Rabbit s	38	5385.5	96.2	1106	21	AAV7545
Pig secre	39	5380	96.1	1036	22	AAU01029
Porcine c	40	5380	96.1	1036	22	AA62253
Rabbit s	41	5364.5	95.8	1106	16	AA73056
Human sec	42	5346	95.5	1018	22	AAU01032
Porcine c	43	5346	95.5	1018	22	AA62256
Pig secre	44	5288	94.4	1018	22	AAU01028
Porcine c	45	5288	94.4	1018	22	AA62252

ALIGNMENTS

RESULT 1
AAU01034
ID AAU01034 standard; Protein; 1063 AA.
AC AAU01034;
XX
XX 04-JUL-2001 (first entry)
DT
XX
XX Human secreted soluble alpha2delta calcium channel subunit #14]
DE
XX
XX Human; secreted calcium channel alpha2delta subunit; alpha2del;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel
KW gabapentin; scintillation proximity assay; SPA; nickel flashpla
KW filter binding assay; wheat germ lectin flashplate assay.
XX
XX Homo sapiens.
OS
XX
XX WO200119870-A2.
PN
XX
XX 22-MAR-2001.
PD
XX
XX 18-SEP-2000; 2000WO-EP09137.
PF
XX
XX 16-SEP-1999; 99US-0397550.
PR
XX
XX (WARN) WARNER LAMBERT CO.
PA
XX
XX Brown JP, Bertelli F;
PI
XX
XX WPI; 2001-235262/24.
DR
XX
XX N-PSDB; AAS01425.
XX

nel alpha2delta subunits, useful in e.g. SPA assays, assays, Nickel Flashplate assays, Filter binding assays or actin Flashplate assays -

ge 137-140; 160pp; English.

sequence represents human secreted calcium channel subunit #14 which is soluble and retains the functional ics of the full length or wild type alpha2delta subunit from which it is derived. The invention relates to truncated 2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins, their affinity for radioactively labelled gabapentin. The subunit is 1 of the components of the heteromultimeric calcium channel (VCC) complexes present in neuronal and tissues including heart and skeletal muscle. Numerous as of the human calcium channel alpha2delta subunits AU01024 and AU01032-AU01038) and 5 soluble forms of the calcium channel alpha2delta subunits (AAU01027-AAU01031) are the secreted soluble alpha2delta subunit may be used in assays. Ligation proximity assay (SPA), flashplate, nickel flashplate, ng or wheat germ lectin flashplate assays to detect or binding or interaction of a ligand (e.g. gabapentin, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, xerme and/or L-Phenylalanine) of a calcium channel subunit.

1063 AA;

100.0%; Score 5599; DB 22; Length 1063;

ilarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Conservative 0;

AGCLLALTTLFQSLGIPSEBPPSAVTKSWDKMQEDLVTLAKTASGVNQLVDI 60

AGCLLALTTLFQSLGIPSEBPPSAVTKSWDKMQEDLVTLAKTASGVNQLVDI 60

KYQDLYVTPNNARQVLEIARDIEKLLSNRSLVSLAEAEKVQAHQWRDEFSN 120

KYQDLYVTPNNARQVLEIARDIEKLLSNRSLVSLAEAEKVQAHQWRDEFSN 120

VYVNAKDDLPKNSPGRQIKPVFIEDANFGRQISYQAAVHIPTDIYEGSTVL 180

VYVNAKDDLPKNSPGRQIKPVFIEDANFGRQISYQAAVHIPTDIYEGSTVL 180

LNWTSSALDVEFKKREDDPSLLMQVFGSGLTGLRTSVSEMLETLSDDDFVNVSFNSNAQD 300

WYIQGAASPKDMLTLVDVSGSVGLTLKLRITSVSEMLETLSDDDFVNVSFNSNAQD 300

CFQHLVQANVRNKKVLDVANNITAKITDYKGFSPAFQQLNINVSANCKIIML 360

CFQHLVQANVRNKKVLDVANNITAKITDYKGFSPAFQQLNINVSANCKIIML 360

DGGERAQEIPFNKNDKVRVFRFSVQGHNYERGPQWMAKCNKGYIIPSPGATR 420

DGGERAQEIPFNKNDKVRVFRFSVQGHNYERGPQWMAKCNKGYIIPSPGATR 420

TQEVLDVLRPMVLGAKQVQNTNVDLAEGLVITGLTPVFNITGQFENKTNLK 480

TQEVLDVLRPMVLGAKQVQNTNVDLAEGLVITGLTPVFNITGQFENKTNLK 480

LILGVMGVDSLEDKRLTPRFTLCPNGYYPFADIPNGVLLHPLNPKNPKSQBPVTL 540

LILGVMGVDSLEDKRLTPRFTLCPNGYYPFADIPNGVLLHPLNPKNPKSQBPVTL 540

LDAELNDIKVEIRNKMIDSGSEKTFRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600

LDAELNDIKVEIRNKMIDSGSEKTFRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600

NLPTVSFYIYKAKLEETITQARSKKGMKQSETLKPQNFEEGYTFTAPRDCNDLKI 660

601 ALVLPYTSFYIYKAKLEETITQARSKKGMKQSETLKPQNFEEGYTFTAPRDCY
661 SDNNTFELLNMFNFIIDRKTNNPNSCNADLINRVLLDAGFTNQLVQYWSKQKNI
661 SDNNTFELLNMFNFIIDRKTNNPNSCNADLINRVLLDAGFTNQLVQYWSKQKNI
721 FVVTGGITRIVYKAGENQENPETTEDSFYKESLNDNDNVVFTAPYFNKSGPG
721 FVVTGGITRIVYKAGENQENPETTEDSFYKESLNDNDNVVFTAPYFNKSGPG
781 MVSXAVIYIYQGLLKPAVVGKIDVNSWIENFTKTSIRDPFCAGPVCDCCKNSD
781 MVSXAVIYIYQGLLKPAVVGKIDVNSWIENFTKTSIRDPFCAGPVCDCCKNSD
841 LDDGGFLLMANHDDYTNQIGRFFGEIDPISLMRHLVNI SVYAFNKSVDYQSVCEP
841 LDDGGFLLMANHDDYTNQIGRFFGEIDPISLMRHLVNI SVYAFNKSVDYQSVCEP
901 GAGHSAYVPSVADILQIGWATAAANSILQOFLLSLTFFPELLRAVEMEDDDFT
901 GAGHSAYVPSVADILQIGWATAAANSILQOFLLSLTFFPELLRAVEMEDDDFT
961 SCITEQTYQYFFDNDKSKFSFVLDGNCNCSRIFFHGEKLMNTNLI FIMVESKGTCP
961 SCITEQTYQYFFDNDKSKFSFVLDGNCNCSRIFFHGEKLMNTNLI FIMVESKGTCP
1021 QAEQTSQYQYFFDNDKSKFSFVLDGNCNCSRIFFHGEKLMNTNLI FIMVESKGTCP
1021 QAEQTSQYQYFFDNDKSKFSFVLDGNCNCSRIFFHGEKLMNTNLI FIMVESKGTCP

RESULT 2

AA62258

ID AAB62258 standard; Protein; 1063 AA.

AC AAB62258;

DT 11-JUN-2001 (first entry)

Porcine calcium channel alpha2delta subunit.

Calcium channel alpha2delta subunit; alpha2delta-1; cerebral co
nervous system disorder; pain; epilepsy; anxiety; pig.

Sus scrofa.

WO200120336-A2.

22-MAR-2001.

18-SEP-2000; 2000WO-EP09136.

16-SEP-1999; 99US-0397549.

(WARN) WARNER LAMBERT CO.

Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee N

WPI; 2001-257902/26.

N-PSDB; AAF57562.

Competitive binding assay for screening ligands which bind a ce
cortical voltage-dependent calcium channel alpha2delta-1 subun
where the ligands identified are useful for treating disorders
nervous system, including pain -

Claim 8; Page 135-139; 158pp; English.

The invention relates to a new method for screening ligands wh
cerebral cortical voltage-dependent calcium channel alpha2delta
preferably alpha2delta-1 subunit. The method comprises contacti
secreted soluble recombinant alpha2delta-1 subunit with a ligand

QDLVTEPNNAQRLVEIAARDIEKLNRSKALVSLAEAKVQAAHQRDFASN 120
 QDLVTEPNNAQRLVEIAARDIEKLNRSKALVSLAEAKVQAAHQRDFASN 120
 YNAKDDLDPEKNDSEPGSQRIKPVIEDANFGROISYQHAHAVHIPTDIYEGSTIVL 180
 YNAKDDLDPEKNDSEPGSQRIKPVIEDANFGROISYQHAHAVHIPTDIYEGSTIVL 180
 WTSALDEVFKKRRBEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
 WTSALDEVFKKRRBEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
 TQGAASPKDMLILVDVSGVSLTLKLRITSVSEMLETLSDDDFVNVSFNSNAQD 300
 TQGAASPKDMLILVDVSGVSLTLKLRITSVSEMLETLSDDDFVNVSFNSNAQD 300
 QHLVQANVRNKKVLDKADANNITAKGITYDKKGFSAFQQLLNINYSRANCNKIIML 360
 QHLVQANVRNKKVLDKADANNITAKGITYDKKGFSAFQQLLNINYSRANCNKIIML 360
 XEERAQELFNKYNKDKKVRFRFSVQGNHYERGPQWMAKCNKGYIYIIPSGAIR 420
 XEERAQELFNKYNKDKKVRFRFSVQGNHYERGPQWMAKCNKGYIYIIPSGAIR 420
 JEVLDVGRPMVLGAKAKQVQNTVYLDALGLVITGTLVPFNITGQFNKINLK 480
 JEVLDVGRPMVLGAKAKQVQNTVYLDALGLVITGTLVPFNITGQFNKINLK 480
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 ILGVMGVDSLEDKRLTPFTLCPNGYGYFAIDPNGYVLLHPLNLPKNPKSQBPVTL 540
 JAELENDIKVEIRNKMIDGSGEKTFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
 JAELENDIKVEIRNKMIDGSGEKTFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
 LPTYSFYIYAKLEBETIQARSKKGMKQSETLKPDPNFESGYTFIAPRDYCNLDKI 660
 LPTYSFYIYAKLEBETIQARSKKGMKQSETLKPDPNFESGYTFIAPRDYCNLDKI 660
 NTEFLNMFNEFIDRKTNNPNSCNADLNRLVLLDAGFTNVLQVNSKQKIKGVKAR 720
 NTEFLNMFNEFIDRKTNNPNSCNADLNRLVLLDAGFTNVLQVNSKQKIKGVKAR 720
 TDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
 TDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
 KAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840
 KAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840
 QGFLLMANHDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
 QGFLLMANHDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
 HRSAYVPSVADILQIGWATAAANSILOQLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
 HRSAYVPSVADILQIGWATAAANSILOQLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
 TQTOYFFDNDKSGFVLDGNCRSRI FHGKLMNTNLI FIMVESKGTCPDTRLLI 1020
 TQTOYFFDNDKSGFVLDGNCRSRI FHGKLMNTNLI FIMVESKGTCPDTRLLI 1020
 3QTSQDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDGCGVYS 1063
 3QTSQDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDGCGVYS 1063

standard; Protein; 1091 AA.

XX AAB10576;
 XX 22-DEC-2000 (first entry)
 XX Human calcium channel alpha-2 subunit protein.
 XX Human; calcium channel; calcium channel subunit; diagnosis;
 XX Lambert Eaton Syndrome; calcium channel subunit alpha-2.
 XX Hemo sapiens.
 OS US6096514-A.
 XX 01-AUG-2000.
 XX 25-MAY-1995; 95US-0450562.
 XX 04-APR-1988; 88US-0176899.
 XX 02-FEB-1990; 90US-0482384.
 XX 08-NOV-1990; 90US-0603751.
 XX 30-NOV-1990; 90US-0620250.
 XX 15-AUG-1991; 91US-0745206.
 XX 10-APR-1992; 92US-0868354.
 XX 13-JUL-1992; 92US-0914231.
 XX 11-AUG-1993; 93US-0105536.
 XX 05-NOV-1993; 93US-0149097.
 XX 07-FEB-1994; 94US-0193078.
 XX 04-APR-1994; 94US-0223305.
 XX 11-AUG-1994; 94US-0290012.
 XX 23-SEP-1994; 94US-0311363.
 XX 28-SEP-1994; 94US-0314083.
 XX 07-NOV-1994; 94US-0336257.
 XX 13-MAR-1995; 95US-0404950.
 XX (SIBI-) SIBIA NEUROSCIENCES INC.
 XX Ellis SB, Williams MB, McCue AF, Harpold MM;
 WPI; 2000-548230/50.
 XX N-PSDB; AAA71707.
 XX Human calcium channel beta subunit polynucleotides, useful for
 XX producing recombinant eukaryotic cells and for diagnosing Lambert
 XX Syndrome
 XX Example IV, Column 135-144; 153pp; English.
 XX This invention describes a novel isolated DNA molecule (I) compo-
 XX sequence encoding a beta3-1 subunit of a human calcium channel.
 XX Nucleic acid probes comprising 14-30 contiguous nucleotides of
 XX beta.3 subunit encoding DNA are useful for isolation and cloning
 XX calcium channel subunit-encoding DNA. Recombinant eukaryotic cel-
 XX express heterologous calcium channel are useful for identifying
 XX that modulate calcium channel activity and in assays for identifi-
 XX agonists and antagonists of calcium channel activity in humans.
 XX calcium channel subunit or eukaryotic cells expressing the chan-
 XX useful for diagnosing Lambert Eaton Syndrome (LES) in a human.
 XX sequence represents the human calcium channel alpha-2 subunit w/
 XX described in the method of the invention.
 XX Sequence 1091 AA;
 XX Query Match 100.0%; Score 5599; DB 21; Length 1091;
 XX Best Local Similarity 100.0%; Pred. No. 0;
 XX Matches 1063; Conservative 0; Mismatches 0; Indels 0;
 QY 1 MAACGALLATLTLPQSLLIGSPSEPPSPSAVTIKSWDKQEDLVTLAKTAGSVI
 DB 1 MAACGALLATLTLPQSLLIGSPSEPPSPSAVTIKSWDKQEDLVTLAKTAGSVI
 QY 61 YEKYQDLVTEPNNAQRLVEIAARDIEKLNRSKALVSLAEAKVQAAHQRDFASN

YQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKVAQAAHQWREDFASN 120
 YNAKDDLDPEKNDSEPGSRIKPVFIEDANFGROIYQHAHVHIPTDIEVGGTIVL 180
 YNAKDDLDPEKNDSEPGSRIKPVFIEDANFGROIYQHAHVHIPTDIEVGGTIVL 180
 NWTSSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
 NWTSSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
 YIQGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETSDDDFVNVSFNSNAQD 300
 YIQGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETSDDDFVNVSFNSNAQD 300
 FOHLVQANVRNKVLDKAVNNITAGITDYKKGFSFAFEQLNINVSRAKCNKILML 360
 FOHLVQANVRNKVLDKAVNNITAGITDYKKGFSFAFEQLNINVSRAKCNKILML 360
 3GERAQEIEFNKYNKKKVRVFRFVSQGHNYERGPIQWMAKCNKGYIYEIPSGAIR 420
 3GERAQEIEFNKYNKKKVRVFRFVSQGHNYERGPIQWMAKCNKGYIYEIPSGAIR 420
 QEYLDVLRPMVLADGAKAQVQNTVYLDALGLVITGTLPVENITQGFENKTNLK 480
 QEYLDVLRPMVLADGAKAQVQNTVYLDALGLVITGTLPVENITQGFENKTNLK 480
 ILVGMVDVSLIEDIKRLTPRTLCPCNGYYPALDPNGVYLLHPNLQPKNPKSQEPVIL 540
 ILVGMVDVSLIEDIKRLTPRTLCPCNGYYPALDPNGVYLLHPNLQPKNPKSQEPVIL 540
 DAELENDIKVEIRNKMDIGSEKFTFLVKSQDERVIDKGNRTYTWTVPNGTIDYSL 600
 DAELENDIKVEIRNKMDIGSEKFTFLVKSQDERVIDKGNRTYTWTVPNGTIDYSL 600
 LPTSYFYIYKAKLBETITQARKSGKMKDSTLKPDPNFEESGYTFIAPRDYCNLDKI 660
 LPTSYFYIYKAKLBETITQARKSGKMKDSTLKPDPNFEESGYTFIAPRDYCNLDKI 660
 NTEFLNPFNEIDRKTNNPNSCNADLINRVLLDAGFTNVLQVNSKQKNIKGVKAR 720
 NTEFLNPFNEIDRKTNNPNSCNADLINRVLLDAGFTNVLQVNSKQKNIKGVKAR 720
 TDGGITRYPYKAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
 TDGGITRYPYKAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
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 KAVIYIYQKLLKPAVYGIKIDVNSWIENTFTKSTRPCAGPCVCKKNSDVMDCVI 840
 QGFLIMANHDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEFGAAPKQ 900
 QGFLIMANHDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEFGAAPKQ 900
 HRSAYVPSVADILQIGWATAAANSILOQFLLSLTFFPRLLAEVEMEDDDFTASLSKQ 960
 HRSAYVPSVADILQIGWATAAANSILOQFLLSLTFFPRLLAEVEMEDDDFTASLSKQ 960
 TEQTYQYFDNDKSPGVLDCGNCRIIFHGEKLMNTNLIIFWVSKGTCPCDTRLLI 1020
 TEQTYQYFDNDKSPGVLDCGNCRIIFHGEKLMNTNLIIFWVSKGTCPCDTRLLI 1020
 QTSQDPNFCDMVKQPRYKRGPDVCFDNNVLEDTYDCGGVS 1063
 QTSQDPNFCDMVKQPRYKRGPDVCFDNNVLEDTYDCGGVS 1063

indard; Protein; 1091 AA.

04-JUL-2001 (first entry)
 Human secreted soluble alpha2delta calcium channel subunit #15 p
 Human; secreted calcium channel alpha2delta subunit; alpha2delta
 alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel;
 gabapentin; scintillation proximity assay; SPA; nickel flashplat
 filter binding assay; wheat germ lectin flashplate assay.

Homo sapiens.

WO200119870-A2.

22-MAR-2001.

18-SEP-2000; 2000WO-EP09137.

16-SEP-1999; 99US-0397550.

(WARN) WARNER LAMBERT CO.

Brown JP, Bertelli F;

WPI; 2001-235262/24.

N-PSDB; AAS01426.

Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
 Flashplate assays, Nickel Flashplate assays, Filter binding ass
 Wheat Germ Lectin Flashplate assays -

Claim 30; Page 141-144; 160pp; English.

The present sequence represents human secreted calcium channel
 alpha2delta subunit #15 which is soluble and retains the funcitc
 characteristics of the full length or wild type alpha2delta subu
 (AAU01025) from which it is derived. The invention relates to tr
 alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble pr
 which retain their affinity for radioactively labelled gabapenti
 alpha2delta subunit is 1 of the components of the heteromultimer
 voltage-dependent calcium channel (VDCC) complexes present in ne
 and non-neuronal tissues including heart and skeletal muscle. N
 soluble forms of the human calcium channel alpha2delta subunits
 (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of
 porcine calcium channel alpha2delta subunits (AAU01027-AAU01031)
 described. The secreted soluble alpha2delta subunit may be used
 e.g. scintillation proximity assay (SPA), flashplate, nickel fla
 filter binding or wheat germ lectin flashplate assays to detect
 measure the binding or interaction of a ligand (e.g. gabapentin,
 L-Norleucine, L-Allo-isoleucine, L-methionine, L-Leucine, L-Iso
 L-valine, Spermine and/or L-Phenylalanine) of a calcium channel
 alpha2delta subunit.

Sequence 1091 AA;

Query Match 100.0%; Score 5599; DB 22; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1063; Conservative 0; Mismatches 0; Indels 0;

Qy 1 MAAGCLIALTLTLFQSLIGPSSEEPSPSAVTIKSWDKMQEDLVTLAKTASGV
 Db 1 MAAGCLIALTLTLFQSLIGPSSEEPSPSAVTIKSWDKMQEDLVTLAKTASGV

Qy 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKVAQAAHQWRE
 Db 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKVAQAAHQWRE

Qy 121 EVVYNAKDDLDPEKNDSEPGSRIKPVFIEDANFGROIYQHAHVHIPTDIEYC
 Db 121 EVVYNAKDDLDPEKNDSEPGSRIKPVFIEDANFGROIYQHAHVHIPTDIEYC

Qy 181 NELNWTSSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDI
 Db 181 NELNWTSSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDI

PN	WO200120336-A2.	
PP		
PD	22-MAR-2001.	
XX		
XX	18-SEP-2000; 2000WO-EP09136.	
PP		
XX		
PR	16-SEP-1999; 99US-0397549.	
XX		
PA	(WARN) WARNER LAMBERT CO.	
XX		
PI	Bertelli F, Brown JP, Dissanayake V, Suman-Chauthan N, Gee NS.	
DR	WPI; 2001-257902/26.	
DR	N-PSDB; AAF57563.	
XX		
PT	Competitive binding assay for screening ligands which bind a cere	
PT	cortical voltage-dependent calcium channel alpha2-delta-1 subunit	
PT	where the ligands identified are useful for treating disorders o	
PT	nervous system, including pain -	
XX		
PS	Claim 7; Page 139-142; 158pp; English.	
XX		
CC	The invention relates to a new method for screening ligands whic	
CC	cerebral cortical voltage-dependent calcium channel alpha2delta1	
CC	preferably alpha2delta1 subunit. The method comprises contacting	
CC	secreted soluble recombinant alphadelta-1 subunit with a ligand	
CC	interest and a labelled compound which binds the subunit, follow	
CC	measuring the level of binding of the labelled compound to alpha	
CC	subunit. The method is useful for screening ligands, preferably	
CC	biologically active products that modulate a nervous system func	
CC	which bind a cerebral cortical voltage-dependent calcium channel	
CC	alpha2delta-1 subunit. The ligands identified by the method are	
CC	for treating disorders of the nervous system, including pain, ep	
CC	and anxiety. The present sequence represents a porcine calcium c	
CC	alpha2delta subunit.	
XX		
SO	Sequence 1091 AA;	

AVEIYIOGKLLKPAVVGIKIDVNSW	IEFTKTSIRDP	CAGPVCDCRNSD	WMDCVI	840	
AVEIYIOGKLLKPAVVGIKIDVNSW	IEFTKTSIRDP	CAGPVCDCRNSD	WMDCVI	840	
AVEIYIOGKLLKPAVVGIKIDVNSW	IEFTKTSIRDP	CAGPVCDCRNSD	WMDCVI	840	
QFLLMANHDDVTNQIRFFGEIDPSL	MRHLVNSI	SVYAFNKS	YDYOSVCEPGAAPKQ	900	
QFLLMANHDDVTNQIRFFGEIDPSL	MRHLVNSI	SVYAFNKS	YDYOSVCEPGAAPKQ	900	
QFLLMANHDDVTNQIRFFGEIDPSL	MRHLVNSI	SVYAFNKS	YDYOSVCEPGAAPKQ	900	
RSAYVPSVADILIOIGWATAAAWSL	IOQELLISL	TEPRLL	LEAVEMEDDDFTASLSKQ	960	
RSAYVPSVADILIOIGWATAAAWSL	IOQELLISL	TEPRLL	LEAVEMEDDDFTASLSKQ	960	
RSAYVPSVADILIOIGWATAAAWSL	IOQELLISL	TEPRLL	LEAVEMEDDDFTASLSKQ	960	
TEQTYQFFOND	SKSFGVIL	DCGNC	RSIRFGEKLMNTNLFI	IMVYESKGTCPDCTRLILI	1020
TEQTYQFFOND	SKSFGVIL	DCGNC	RSIRFGEKLMNTNLFI	IMVYESKGTCPDCTRLILI	1020
TEQTYQFFOND	SKSFGVIL	DCGNC	RSIRFGEKLMNTNLFI	IMVYESKGTCPDCTRLILI	1020
YTSDGNPCDMWKQPRYKGP	DPVCFNNV	LEDY	TCGGVS	1063	
YTSDGNPCDMWKQPRYKGP	DPVCFNNV	LEDY	TCGGVS	1063	
YTSDGNPCDMWKQPRYKGP	DPVCFNNV	LEDY	TCGGVS	1063	

(first entry)

ium channel alpha2delta subunit.

nel alpha2delta subunit; alpha2delta-1; cerebral cortex; em disorder; pain; epilepsy; anxiety; pig.

ILGVMGVDSLEDIKRLTPRFTLLCPNGYYFAIDPNGVYLLHPNLQPKNPKSQBPVTL 540
ILGVMGVDSLEDIKRLTPRFTLLCPNGYYFAIDPNGVYLLHPNLQPKNPKSQBPVTL 540
DABLENDIKVEIRNKMIDGESGEKTFRTLKVSQDERVIDKGNRTYTWTPVNGTDYSL 600
DABLENDIKVEIRNKMIDGESGEKTFRTLKVSQDERVIDKGNRTYTWTPVNGTDYSL 600
LPTYSFYIYKAKLEETITQARSKGKMKDSETLKPDMFEESGYTFIAPROYCNDLKI 660
LPTYSFYIYKAKLEETITQARSKGKMKDSETLKPDMFEESGYTFIAPROYCNDLKI 660
NTEFLNFNFEIDRKTNNPNSCNADLNRLVLLDAGFTNELVQNYWSQKQIKGVKAR 720
NTEFLNFNFEIDRKTNNPNSCNADLNRLVLLDAGFTNELVQNYWSQKQIKGVKAR 720
TDGGITRVYPKEAGENQENPETYEDSFYKRSLNDNDNVFTAPYFNKSGPGAYESGI 780
TDGGITRVYPKEAGENQENPETYEDSFYKRSLNDNDNVFTAPYFNKSGPGAYESGI 780
KAVEIYITQKLLKPAVVGIIKDVSNSWIENFTKTSIRDPGAGPVCDCRNSDVMDCVI 840
KAVEIYITQKLLKPAVVGIIKDVSNSWIENFTKTSIRDPGAGPVCDCRNSDVMDCVI 840
GGFLLMANHDDYTNOIGRFFGEIDPSLWRHLVNI SVYAFNKSXDYQSVCEPGAAPKQ 900
GGFLLMANHDDYTNOIGRFFGEIDPSLWRHLVNI SVYAFNKSXDYQSVCEPGAAPKQ 900
HRSAYVPSVADILQI GHWATAAAMSILQOFLLSLITFFPRLLEAVEMEDDDFTASLSKQ 960
HRSAYVPSVADILQI GHWATAAAMSILQOFLLSLITFFPRLLEAVEMEDDDFTASLSKQ 960
TEQTYQYFFDNDKSGFSGLVDCGNCRSRIFPHGKLMNTNLIFITWVSKGTGCPCDTRLII 1020
TEQTYQYFFDNDKSGFSGLVDCGNCRSRIFPHGKLMNTNLIFITWVSKGTGCPCDTRLII 1020
QTSOGPNPCDMVKQPRYRKGPDPVCFDNNVLEDYTDCCGVG 1063
QTSOGPNPCDMVKQPRYRKGPDPVCFDNNVLEDYTDCCGVG 1063

Standard: Protein: 1091 AA.

(first entry)

im channel alpha 2b subunit protein.

um channel protein; therapeutic; autoimmune disease;
ambert Eaton Syndrome; alpha 2b subunit.

: 95US-0450272.

. B9WQ-TTS0140A

; 90US-0603751.

90US-0482384.

90US-0620250.
91US-0745206.

92WO-US06903.
93ITS-0705536

; 93US-0149097.

100

PR	23-SEP-1994;	94US-0311363.
PR	07-NOV-1994;	94US-0336257.
PR	15-FEB-1995;	95US-0404354.
XX	(MERI) MERCK & CO INC.	
XX	Harpold MM, Ellis SB, Williams ME, McCue AF;	
PI	WI; 2002-470318/50.	
DR	N-PSDB; AAD39959.	
DR		
XX	Eukaryotic cells expressing a functional heterologous human calc	
PT	channel and encoding nucleic acid isolated from human cerebellum	
PT	drug design and to diagnose Lambert Eaton Syndrome -	
XX	Disclosure; Column 137-144; 154pp; English.	
PS	The present invention relates to novel human calcium channel pro	
XX	and polynucleotides encoding such proteins. The invention also r	
CC	to eukaryotic cells expressing a functional heterologous human c	
CC	channel alpha 1, alpha 2, beta and gamma subunits. The eukaryoti	
CC	are useful for screening for potential calcium channel antagonis	
CC	agonists to select compounds that have potential as disease or t	
CC	c specific therapeutic agents. The subunits may be used in diagno	
CC	assays for the autoimmune disease Lambert Eaton Syndrome. The p	
CC	sequence is human calcium channel alpha 2b subunit protein.	
XX	Sequence 1091 AA;	
SQ	Query Match 100.0%; Score 5599; DB 23; Length 1091;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1063; Conservative 0; Mismatches 0; Indels 0;	
Qy	1 MAAGCLLALTLFOSLLIGPSSPPSPSVAITKSWDKQEDVLTKTASGV	
Dd	1 MAAGCLLALTLFOSLLIGPSSPPSPSVAITKSWDKQEDVLTKTASGV	
Qy	61 YEKYQDLYTVENNAQLVEIAARDIEKLINRSKALVSLAEAKVKQAQAHWRH	
Dd	61 YEKYQDLYTVENNAQLVEIAARDIEKLINRSKALVSLAEAKVKQAQAHWRH	
Qy	121 EVYYNKADDLDPKENDSEPGSQRIKPVFIEDANFGROIYSQHAAVHIPTDIYE	
Dd	121 EVYYNKADDLDPKENDSEPGSQRIKPVFIEDANFGROIYSQHAAVHIPTDIYE	
Qy	181 NELNWTLSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWDNSRTPNKDI	
Dd	181 NELNWTLSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWDNSRTPNKDI	
Qy	241 RPWIIIOGAASPKDMLILVDVSGVSGLTLKLRITSVSEMLETLSDDDDFVNVSFI	
Dd	241 RPWIIIOGAASPKDMLILVDVSGVSGLTLKLRITSVSEMLETLSDDDDFVNVSFI	
Qy	301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYNVSRNCI	
Dd	301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYNVSRNCI	
Qy	361 FTGGGERAQEIIFNKYNKDQKVFRFPVSGQHNTYERGP IQMACENKGYTYEIP	
Dd	361 FTGGGERAQEIIFNKYNKDQKVFRFPVSGQHNTYERGP IQMACENKGYTYEIP	
Qy	421 INTQEYLVDLGHPWLIVLAGDAKQOVNTNYLDLELGLVITGTLVPFNITGQFEN	
Dd	421 INTQEYLVDLGHPWLIVLAGDAKQOVNTNYLDLELGLVITGTLVPFNITGQFEN	
Qy	481 NQLILGMVGVDVLSLEDIKELTRFTFLCPNGYYFAIDPNGYYVLHPNI QPNKPKS	
Dd	481 NQLILGMVGVDVLSLEDIKELTRFTFLCPNGYYFAIDPNGYYVLHPNI QPNKPKS	
Qy	541 DFDLAELNDIKVEIRNMKMDISEGEKTFRLIVKSQDERYIDKGNRTYTTPVNM	
Dd	541 DFDLAELNDIKVEIRNMKMDISEGEKTFRLIVKSQDERYIDKGNRTYTTPVNM	

PTYSFYIKAKLEETITQARSKGKMDSETLKPDNFEESGYTFIAPRDYCNDLKI 660
 PTYSFYIKAKLEETITQARSKGKMDSETLKPDNFEESGYTFIAPRDYCNDLKI 660
 TEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
 TEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
 TGGITRVYPKEAGENWQENPETEYDSFYKRSIDNDNVYFTAPYFNKSGPGAYESGI 780
 TGGITRVYPKEAGENWQENPETEYDSFYKRSIDNDNVYFTAPYFNKSGPGAYESGI 780
 JAVEIYIQGLKLPAAVVGKIDVNSWIEFTKTSIRDPKAGPVCDCRNSDVMDCVI 840
 JAVEIYIQGLKLPAAVVGKIDVNSWIEFTKTSIRDPKAGPVCDCRNSDVMDCVI 840
 JQFLMANHDDYTNQIGRFGEIDPSLMRHLVNI SYAFNKSVDYQSVCEPGAAPKQ 900
 JQFLMANHDDYTNQIGRFGEIDPSLMRHLVNI SYAFNKSVDYQSVCEPGAAPKQ 900
 RSAYVPSVADILQIGWATAAASILQOFLLSLTPRLLEAVEMEDDDFTASLSKQ 960
 RSAYVPSVADILQIGWATAAASILQOFLLSLTPRLLEAVEMEDDDFTASLSKQ 960
 YEQTYFFDNDKSFSGVLDGCGNCSRI FHGEKLMNTNLIFIMVBSKGTCPDTRLLI 1020
 YEQTYFFDNDKSFSGVLDGCGNCSRI FHGEKLMNTNLIFIMVBSKGTCPDTRLLI 1020
 YSDGNPCDMVKQRYRKGPDVCFDNNVLEDYTDGCGVS 1063
 YSDGNPCDMVKQRYRKGPDVCFDNNVLEDYTDGCGVS 1063

idard; Protein; 1091 AA.

(first entry)

a channel a2d subunit.

tel; human; central nervous system disorder;
 i syndrome; diagnosis; therapy.

97WO-US16146.

96US-0713118.

ICAN HOME PROD CORP.

ranco R, Shuey DJ;

7325/18.
 9060.

human neuronal calcium channel subunit(s) - useful for
 and treatment of central nervous system disorders, e.g.
 n syndrome

Fig 2; 89pp; English.

tide comprises the a2d subunit of the human neuronal
 nel. cDNA clones (see AAV29059-61) encoding the a1b
 AAW37878), the a2d subunit and a b3 subunit (see AAW37880)
 olated. These have been inserted into expression

CC vectors and are stably expressed in transformed cell lines. The
 CC transformed cells show omega-conotoxin GVIA binding activity,
 CC and omega-conotoxin GVIA toxin sensitive potassium-stimulated
 CC calcium uptake, indicating that the proteins expressed by the
 CC clones are capable of forming a functioning calcium channel.
 CC Nucleic acids encoding the 3 subunits, as well as vectors, host
 CC cells and methods of isolating nucleic acids encoding related
 CC calcium channels are disclosed. Fusion proteins incorporating t
 CC subunit proteins, antibodies, and assays for identifying agents
 CC that modulate calcium channel activity are also provided. Such
 CC agents can be used to treat certain central nervous system
 CC disorders by altering calcium channel activity. Methods of
 CC diagnosing diseases associated with particular calcium channels,
 CC such as Lambert-Eaton syndrome, are disclosed.
 XX
 SQ Sequence 1091 AA;

Query Match 99.9%; Score 5595; DB 19; Length 1091;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1062; Conservative 0; Mismatches 1; Indels 0;

QY 1 MAAGCLLALTTLTQSLILIGSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVN
 Db 1 MAAGCLLALTTLTQSLILIGSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVN
 QY 61 YEKYQDLTYTVEPNNAQVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHQWRE
 Db 61 YEKYQDLTYTVEPNNAQVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHQWRE
 QY 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROI SYOHAHVHIPTDIYEG
 Db 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROI SYOHAHVHIPTDIYEG
 QY 181 NELNWTSSALDEVFKKNREEDPSILLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
 Db 181 NELNWTSSALDEVFKKNREEDPSILLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
 QY 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLTSTVSEMLETISDDDFNVASFN
 Db 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLTSTVSEMLETISDDDFNVASFN
 QY 301 VSCFQHLVQANVRNKKVLADAVNNITAKGITDYKKGFSFAFQOLLNINVSANCN
 Db 301 VSCFQHLVQANVRNKKVLADAVNNITAKGITDYKKGFSFAFQOLLNINVSANCN
 QY 361 FTDGGERAQEIFNKYNKDKKVRVFRFSVQHNRYERGP IQWMA CENKGYIYEIPS
 Db 361 FTDGGERAQEIFNKYNKDKKVRVFRFSVQHNRYERGP IQWMA CENKGYIYEIPS
 QY 421 INTQEYLDVLRPMVLADGKAKQVQWNTVYLDALGLVITGTLPVFNITGQFEN
 Db 421 INTQEYLDVLRPMVLADGKAKQVQWNTVYLDALGLVITGTLPVFNITGQFEN
 QY 481 NQLILGVMGVDVLSLEDIKRLTPRFTLCPNGYYPADIPNGYVLLHPLNLPKNPKSC
 Db 481 NQLILGVMGVDVLSLEDIKRLTPRFTLCPNGYYPADIPNGYVLLHPLNLPKNPKSC
 QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTRTLKVSQDERYIDKGNRTYTWTPVNG
 Db 541 DFLDAELENDIKVEIRNKMIDGESGKFTRTLKVSQDERYIDKGNRTYTWTPVNG
 QY 601 ALVLPYVSFYIYKAKLEETITQARSKGKMDSETLKPDNFEESGYTFIAPRDYCN
 Db 601 ALVLPYVSFYIYKAKLEETITQARSKGKMDSETLKPDNFEESGYTFIAPRDYCN
 QY 661 SDNNTEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIK
 Db 661 SDNNTEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIK
 QY 721 FVYTDGGITRVYPKEAGENWQENPETEYDSFYKRSIDNDNVYFTAPYFNKSGPGP
 Db 721 FVYTDGGITRVYPKEAGENWQENPETEYDSFYKRSIDNDNVYFTAPYFNKSGPGP

KAVEIYIQGLKLPAAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840
 |||||
 KAVEIYIQGLKLPAAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840
 |||||
 GGFLLMANHDDYTQIGRFFGEIDPDLMLRHLVNI SVYAFNKSYYQSVCEPAAAPKQ 900
 |||||
 GGFLLMANHDDYTQIGRFFGEIDPDLMLRHLVNI SVYAFNKSYYQSVCEPAAAPKQ 900
 |||||
 HRSAYVSVADILQIGWATAAANSIILOQFLLSLTFFPRLLLEAVEMEDDDFTASLSKQ 960
 |||||
 HRSAYVSVADILQIGWATAAANSIILOQFLLSLTFFPRLLLEAVEMEDDDFTASLSKQ 960
 |||||
 TEQTQYFPDNDKSGFSGVLDGNCNRSRIFHGEKLMNTNLI FIMVSKGTCPDTRLLI 1020
 |||||
 TEQTQYFPDNDKSGFSGVLDGNCNRSRIFHGEKLMNTNLI FIMVSKGTCPDTRLLI 1020
 |||||
 QTSQGNPCDMVKQPRYKGPDPVCPDNNVLEDDYTDGCGVS 1063
 |||||
 QTSQGNPCDMVKQPRYKGPDPVCPDNNVLEDDYTDGCGVS 1063
 |||||

ndard; Protein; 1091 AA.

(updated)
 (first entry)

the alpha 2 human calcium channel subunit.

um channel subunit; diagnosis; agonist; antagonist;
 n syndrome.

;

..

92WO-US06903.

91US-0745206.

92US-0868354.

INST BIOTECHNOLOGY IND ASSOC.

Ellis SB, Feldman DH, Harpold MM, McCue AF;

3936/11.
 37821.

specific human calcium channel sub-units - used for
 calcium channel agonists and antagonists and
 Lambert Eaton syndrome

Page 134-138; 150pp; English.

a human neuronal calcium channel alpha 2 subunit was
 am a human genomic DNA library probed under low and high
 conditions with a fragment of DNA encoding the rabbit
 sle calcium channel alpha 2 subunit. The fragment
 cletides having a sequence corresponding to the
 sequence between nucleotides 43 and 272 inclusive of
 skeletal muscle calcium channel alpha 2 subunit cDNA.
 s identified splice variants of the human calcium alpha
 ranscript. In particularly preferred embodiments, the
 g the alpha 2 subunit is produced by alternative
 of a primary transcript that includes DNA encoding the
 set forth in AAR3353 and the DNA of AAQ37823 inserted
 leotides 1624 and 1625 of AAQ37821.

CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 1091 AA;
 Query Match 99.9%; Score 5593; DB 14; Length 1091;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1062; Conservative 0; Mismatches 1; Indels 0;
 QY 1 MAAGC LALTLTLFQS LLIIGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGV
 DB 1 MAAGC LALTLTLFQS LLIIGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGV
 QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKQAAHQRRE
 DB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKQAAHQRRE
 QY 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROI SYQHAHVHPTDIYEC
 DB 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROI SYQHAHVHPTDIYEC
 QY 181 NELNWT SALDEVFKONREEDPSLLMQVFGSATGLARYYPAS PWVDSNRTNPKIDI
 DB 181 NELNWT SALDEVFKONREEDPSLLMQVFGSATGLARYYPAS PWVDSNRTNPKIDI
 QY 241 RPWYIQGAASPOMLILVDVSGSVSGLTLLKIRTSVSEMLETSLDDDFVNVASFI
 DB 241 RPWYIQGAASPOMLILVDVSGSVSGLTLLKIRTSVSEMLETSLDDDFVNVASFI
 QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEQQLLNVSFRANCI
 DB 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEQQLLNVSFRANCI
 QY 361 FTDGGEERAQEI FNKYNKDKKRVFRFSVQGNHYERGP IOMMACENKGYEYIEI
 DB 361 FTDGGEERAQEI FNKYNKDKKRVFRFSVQGNHYERGP IOMMACENKGYEYIEI
 QY 421 INTOEYLDVLGRPMVLADGKAKQVQNTNVYLDALGLVITGTLPVFNITQGFEEI
 DB 421 INTOEYLDVLGRPMVLADGKAKQVQNTNVYLDALGLVITGTLPVFNITQGFEEI
 QY 481 NQLILGWGVDVLSLEDIKRLTPFTLCPNGYFFAIDPNGYVLLHPNLQPKNPKSI
 DB 481 NQLILGWGVDVLSLEDIKRLTPFTLCPNGYFFAIDPNGYVLLHPNLQPKNPKSI
 QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTWTVPVNI
 DB 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTWTVPVNI
 QY 601 ALVLPYTSFYIYIKAKLBETITQARKSKGKMDSETLKPDPNFEESGYTFIAPRDY
 DB 601 ALVLPYTSFYIYIKAKLBETITQARKSKGKMDSETLKPDPNFEESGYTFIAPRDY
 QY 661 SDNNTFELNFEFIDRKTNNPCNADLINRVLLDAGFTNELYQVYWSKQKNI
 DB 661 SDNNTFELNFEFIDRKTNNPCNADLINRVLLDAGFTNELYQVYWSKQKNI
 QY 721 FVWTDGGITRVYPKEAGENWOENPETTEDSYKKSLONDNTVFTTAPYFNKSGPG
 DB 721 FVWTDGGITRVYPKEAGENWOENPETTEDSYKKSLONDNTVFTTAPYFNKSGPG
 QY 781 MVSKAVEIYIQGLKLPAAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSD
 DB 781 MVSKAVEIYIQGLKLPAAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSD
 QY 841 LDDGGFLLMANHDDYTQIGRFFGEIDPDLMLRHLVNI SVYAFNKSYYQSVCEP
 DB 841 LDDGGFLLMANHDDYTQIGRFFGEIDPDLMLRHLVNI SVYAFNKSYYQSVCEP
 QY 901 GAGHRSAYVSVADILQIGWATAAANSIILOQFLLSLTFFPRLLLEAVEMEDDDFT
 DB 901 GAGHRSAYVSVADILQIGWATAAANSIILOQFLLSLTFFPRLLLEAVEMEDDDFT
 QY 961 SCITEQTQYFPDNDKSGFSGVLDGNCNRSRIFHGEKLMNTNLI FIMVSKGTCP

|||||TQYFFNDKSFSGVLDGNCNRIFFGKLMNTLIFIVVESKGTCPDTRLLI 1020
|||||

|||||TSDGNPCDMVKQPRYKGPVCFDNNVLEDTDCGGVS 1063
|||||TSDGNPCDMVKQPRYKGPVCFDNNVLEDTDCGGVS 1063
|||||

idard; Protein; 1110 AA.

(updated)
(first entry)

n channel alpha-2 subunit.

ait; human; calcium channel; assay; detection;
tion; Lambert Eaton Syndrome; LES; diagnosis.

95US-0455543.

94US-0223305.
88US-0176899.
89WO-US01408.
90US-0482384.
90US-0603751.
90US-0620250.
91US-0745206.

A NEUROSCIENCES INC.

Ellis SB, Feldman DH, Harpold MM, McCue AF;

6192/39.
2694.

human calcium channel alpha 1B subunit protein -
recombinant production of the channel for screening of
rs, and diagnosis of Lambert Eaton Syndrome

Columns 131-138; 166pp; English.

sequence represents the alpha-2 subunit of a human calcium
cium channels are membrane-spanning, multi-subunit proteins
ontrolled entry of calcium ions into cells. This leads
ation events required for muscle contraction. The recombinant
n expressed with nucleic acids encoding the complete calcium
be used in assays for the detection and characterisation of
at modulate the channel. The DNA encoding the subunits can
very spliced when transcribed, giving more than one form of
from the same transcript, each having slightly different
In addition, the reactivity of the alpha 1 subunit with IgG
om the serum of an individual with Lambert Eaton Syndrome
used as a diagnostic for the disease.
25-MAR-2003 to correct PR field.)

110 AA;

99.7%; Score 5579.5; DB 19; Length 1110;
larity 98.2%; Pred.No.0;
Conservative 0; Mismatches 0; Indels 19; Gaps 1;

AGCLLALTTLFQSLIGSPSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVGNQLVDI 60

Db 1 MAAGCLLALTTLFQSLIGSPSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVGN
QY 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWRE
Db 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWRE
QY 121 EVVYNNAKDDLDPEKNDSEPGSQRIKVPFIEDANFGRQISYQHAHVHIPTDIYEG
Db 121 EVVYNNAKDDLDPEKNDSEPGSQRIKVPFIEDANFGRQISYQHAHVHIPTDIYEG
QY 181 NELNWTLSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
Db 181 NELNWTLSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKLIRTSVSEMLETSLDSDDDFVNVSFN
Db 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKLIRTSVSEMLETSLDSDDDFVNVSFN
QY 301 VSCFQHLVQANVRNKKVLDKADANNITAKGITYKKGFSPAFEPQLLNNYNSRANCN
Db 301 VSCFQHLVQANVRNKKVLDKADANNITAKGITYKKGFSPAFEPQLLNNYNSRANCN
QY 361 FTDGGEERAQELFNKYNKDKKVRVFEFSVGOHNYBERGPIQWMACENKGYEYIPLS
Db 361 FTDGGEERAQELFNKYNKDKKVRVFEFSVGOHNYBERGPIQWMACENKGYEYIPLS
QY 421 INTQEYLDVLGRPMVLADGKAKQVQMTNVYLDLELGLVITGTLPVFNITGQPEN
Db 421 INTQEYLDVLGRPMVLADGKAKQVQMTNVYLDLELGLVITGTLPVFNITGQPEN
QY 481 NQLILGVMGVDVLSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPLNLOPK-----
Db 481 NQLILGVMGVDVLSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPLNLOPKPIGVG
QY 531 -----NPKSOEPVTLDFDAELENDIKVEIRNMIDGESGEKTRFLVKSC
Db 541 LRKRPRNIQNPKSQEPVTLDFDAELENDIKVEIRNMIDGESGEKTRFLVKSC
QY 582 DKGNRITVTPVNGTDYSLALVLPITYSFYIKAKLETTITQARSKKGKMKDSETI
Db 601 DKGNRITVTPVNGTDYSLALVLPITYSFYIKAKLETTITQARSKKGKMKDSETI
QY 642 EESGYTFIAPRDYCNDLKISDNNTEFLNFEHIDRKTNNPSCNADLINRVLLI
Db 661 EESGYTFIAPRDYCNDLKISDNNTEFLNFEHIDRKTNNPSCNADLINRVLLI
QY 702 ELVQNYWSKOKNKGVKARFVTDGGITRVYPKEAGENWQENPETYEDSFYKRSI
Db 721 ELVQNYWSKOKNKGVKARFVTDGGITRVYPKEAGENWQENPETYEDSFYKRSI
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKJ
Db 781 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKJ
QY 822 CAGPVCCKNSDVMDCVILDDGFFLLMANHDDYTNOIGRFFGEIDPSLRHLV
Db 841 CAGPVCCKNSDVMDCVILDDGFFLLMANHDDYTNOIGRFFGEIDPSLRHLV
QY 882 FNKSYDYQSVCEPQAPKQAGHRSATVPSVADILQIGWATAAASILQOFLLS
Db 901 FNKSYDYQSVCEPQAPKQAGHRSATVPSVADILQIGWATAAASILQOFLLS
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSKFSFGLDCGNCRIFFHGEKI
Db 961 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSKFSFGLDCGNCRIFFHGEKI
QY 1002 IFIMVESKGTCPDTRLLIIQABQTSQGNPCDMVKQPRYKGPVCFDNNVLEDT
Db 1021 IFIMVESKGTCPDTRLLIIQABQTSQGNPCDMVKQPRYKGPVCFDNNVLEDT
QY 1062 VS 1063
|||

1082

ndard; Protein; 1086 AA.

(updated)
(first entry)

al calcium channel subunit alpha 2c.

nel subunit; antagonist; agonist; diagnosis;
n Syndrome.

94WO-US09230.

93US-0105536.

93US-0149097.

INST BIOTECHNOLOGY IND ASSOC.

Alleespie A, Harpold MM, Mecue AF, Williams MB;

0900/12.

4667.

human calcium channel sub-unit(s) - used for
rods. for studying calcium channels, e.g. for
onists and antagonists

Page 237-242; 285pp; English.

al alpha 2 coding sequence (AAQ84664) transcript is
ly processed in skeletal muscle, aorta, and CNS in
:orresp. to nt 1595-1942 of AAQ84664 in each of the
e alternatively spliced variant transcripts that differ
nce or absence of one to three different portions of
There are three sequences involved (see AAQ84664 FT
; FT), sequence 1, sequence 2 and sequence 3. The five
ding transcripts from the different tissues include
mbinations of the three sequences, except for one of
transcripts expressed in aorta which lacks all three
he five alpha 2 forms identified are (1) a form that
ce 3 called alpha 2a, expressed in skeletal muscle
; lacks sequence 1 called alpha 2b, expressed in CNS
; lacks sequences 1 and 2 called alpha 2c, expressed in
e that lacks sequences 1, 2 and 3 called alpha 2d,
1 aorta and (5) one that lacks sequences 1 and 3
a 2e. The DNA and AA sequences of alpha 2a - alpha 2e
h in AAQ84666-084669 and AAR71012-R71015 respectively.
25-MAR-2003 to correct FN field.)

1086 AA;

99.3%; Score 5559.5; DB 16; Length 1086;

ilarity 99.5%; Pred. No. 0;

Conservative 0; Mismatch 0; Indels 5; Gaps 1;

AGCLLTLTLFQSLIGPSSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60

AGCLLTLTLFQSLIGPSSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60

KYQDLYTEPNNAARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120

. A

Db 61 YEKYQDLYTEPNNAARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWRE
Qy 121 EVVYNAKDDLPEKNDSEPGSQRKIPVFIEDANFGRQISYQHAHVHIPTDIYEG
Db 121 EVVYNAKDDLPEKNDSEPGSQRKIPVFIEDANFGRQISYQHAHVHIPTDIYEG
Qy 181 NELNWTSAIDDEVFKNREEDPSLLMQVFGSATGLARYYPASPWVDSRTPNKIDL
Db 181 NELNWTSAIDDEVFKNREEDPSLLMQVFGSATGLARYYPASPWVDSRTPNKIDL
Qy 241 RPYIIOGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETSLDDDFVNVASFN
Db 241 RPYIIOGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETSLDDDFVNVASFN
Qy 301 VSCFQHLVQANVRNKKVLDVANNITAKGIDYKKGFSFAFEQLLNNVSRANCN
Db 301 VSCFQHLVQANVRNKKVLDVANNITAKGIDYKKGFSFAFEQLLNNVSRANCN
Qy 361 FTGGGERAQEI FNKNKDKKVRFPFVSGQHNRYERGPIQMMACENKGYTYEIP
Db 361 FTGGGERAQEI FNKNKDKKVRFPFVSGQHNRYERGPIQMMACENKGYTYEIP
Qy 421 INTOEYLDVLRPMVLADGKAKOVQNTVYLDALGLGLVITGTLFVFNITGQFEN
Db 421 INTOEYLDVLRPMVLADGKAKOVQNTVYLDALGLGLVITGTLFVFNITGQFEN
Qy 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYIFAIDPNGVYLLHPNLOPNKPKS
Db 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYIFAIDPNGVYLLHPNLOPNKPKS
Qy 541 DFLDAELENDIKVEIRNKMIDGESGKFTPLVKSQDERVIDKGNRTYTTPVNM
Db 536 DFLDAELENDIKVEIRNKMIDGESGKFTPLVKSQDERVIDKGNRTYTTPVNM
Qy 601 ALVLPYTSFYVIRAKLEETITQARSKKGKMKDSETLKPDNFEESGYTFIAPRDY
Db 596 ALVLPYTSFYVIRAKLEETITQARSKKGKMKDSETLKPDNFEESGYTFIAPRDY
Qy 661 SDNNTFLLNPFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSQKNII
Db 656 SDNNTFLLNPFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSQKNII
Qy 721 FVWTDGGITRVYPKEAGENQENPETYEDSFYKESLNDNDVFTAPYFNKSGPGI
Db 716 FVWTDGGITRVYPKEAGENQENPETYEDSFYKESLNDNDVFTAPYFNKSGPGI
Qy 781 MVSXAVELIYIQGLLKPAVVGKIDVNSWIENFTKTSIRDPFCAGPVCDCCKNSD
Db 776 MVSXAVELIYIQGLLKPAVVGKIDVNSWIENFTKTSIRDPFCAGPVCDCCKNSD
Qy 841 LDDGGFLLMANHDDYTQIGRPFGEIDPSLMRHLVNI SVAFNKSVDYQSVCEP
Db 836 LDDGGFLLMANHDDYTQIGRPFGEIDPSLMRHLVNI SVAFNKSVDYQSVCEP
Qy 901 GAGHRSVRSVADILQIGMWATAAASILQOFLLSLTFPRLLEAVEMEDDDFT
Db 896 GAGHRSVRSVADILQIGMWATAAASILQOFLLSLTFPRLLEAVEMEDDDFT
Qy 961 SCITEQIQYFFDNDKSKFSFVLDGCGNCSRI PFHGEKLMNTNLI FIMVESKGTCP
Db 956 SCITEQIQYFFDNDKSKFSFVLDGCGNCSRI PFHGEKLMNTNLI FIMVESKGTCP
Qy 1021 QAEQTSQDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063
Db 1016 QAEQTSQDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1058

RESULT 13

AAW63153

ID AAW63153 standard; Protein; 1086 AA.

XX

AC AAW63153;

XX

(updated)
(first entry)

1 channel alpha-2c subunit.

it; human; calcium channel; assay; detection;
:ion; Lambert Eaton Syndrome; LES; diagnosis.

95US-0455543.

94US-0223305.

89US-0176899.

89MO-US01408.

90US-0482384.

90US-0603751.

90US-0620250.

91US-0745206.

A NEUROSCIENCES INC.

Ellis SB, Feldman DH, Harpold WM, McCue AF;

6192/39.
2702.

human calcium channel alpha 1B subunit protein -
eombinant production of the channel for screening of
rs, and diagnosis of Lambert Eaton Syndrome

umns 293-300; 166pp; English.

sequence represents the alpha-2c subunit of a human calcium
cium channels are membrane-spanning, multi-subunit proteins
ontrolled entry of calcium ions into cells. This leads
ation events required for muscle contraction. The recombinant
n expressed with nucleic acids encoding the complete calcium
be used in assays for the detection and characterisation of
at modulate the channel. The DNA encoding the subunits can
vely spliced when transcribed, giving more than one form of
from the same transcript, each having slightly different
In addition, the reactivity of the alpha 1 subunit with IgG
om the serum of an individual with Lambert Eaton Syndrome
used as a diagnostic for the disease.

25-MAR-2003 to correct PR field.)

086 AA;

larity 99.3%; Score 5559.5; DB 19; Length 1086;

Conservative 0; Mismatches 0; Indels 5; Gaps 1;

GCLLALTLTQSLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGYNQLVDI 60
GCLLALTLTQSLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGYNQLVDI 60
CYQDLTVFPNNARQIVETAARDIEKLSNRKALVSLALEAKVQAHHQWEDFASN 120
CYQDLTVFPNNARQIVETAARDIEKLSNRKALVSLALEAKVQAHHQWEDFASN 120
YYNAKDDLDPEKNDSEPSQRKIPVIEDANFGROIYSQHAHVHPTDIYEGSTIVL 180
YYNAKDDLDPEKNDSEPSQRKIPVIEDANFGROIYSQHAHVHPTDIYEGSTIVL 180
NNTSALDEVFKKKNREEDPSLLMQVFGSATGLARYYPASFWVDNSRTPNKIDLYDVR 240
NNTSALDEVFKKKNREEDPSLLMQVFGSATGLARYYPASFWVDNSRTPNKIDLYDVR 240

241 RPWYIQGAASPKOMLILVDVSGSVGLTLKLRISVSSEMLETLSDDDFVNVSFN
241 RPWYIQGAASPKOMLILVDVSGSVGLTLKLRISVSSEMLETLSDDDFVNVSFN
301 VSCFQHLVQANVRNKKVLKADANNITAKGITYKKGFSAFAPOLLNYSRANCN
301 VSCFQHLVQANVRNKKVLKADANNITAKGITYKKGFSAFAPOLLNYSRANCN
361 FTDGGERAQEIFNKYNKKVKVRFPSVQOHNYERGPQWMAKCNKGYIYELPS
361 FTDGGERAQEIFNKYNKKVKVRFPSVQOHNYERGPQWMAKCNKGYIYELPS
421 INTQEYLDVLGRPMVLADGKAKQVQWNTVYLDALGLVITGLPVENITGQFEN
421 INTQEYLDVLGRPMVLADGKAKQVQWNTVYLDALGLVITGLPVENITGQFEN
481 NQLILGVNGVDVSLDIKRLTPRFTLCPNGYYPADIPNGVYLLHPLNPKSKQ
481 NQLILGVNGVDVSLDIKRLTPRFTLCPNGYYPADIPNGVYLLHPLNPKSKQ
541 DFLDASLENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNG
536 DFLDASLENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNG
601 ALVLPYSPYIKAKLEETITQARSKKGMKQSETLKPDNFESGYTFFIAPRDYC
596 ALVLPYSPYIKAKLEETITQARSKKGMKQSETLKPDNFESGYTFFIAPRDYC
661 SDNTEFLNFEFIDRKTNNPNSCNADLNRVLLDAGFTNELVQVWSKQKNIK
656 SDNTEFLNFEFIDRKTNNPNSCNADLNRVLLDAGFTNELVQVWSKQKNIK
721 FVYTDGGITRVYKPEAGENWQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGF
716 FVYTDGGITRVYKPEAGENWQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGF
781 MVSKEVYIYQGLKLPVAVVGIKIDVNSWIENTFTKTSIRDPGAGPVCDCKRNSDY
776 MVSKEVYIYQGLKLPVAVVGIKIDVNSWIENTFTKTSIRDPGAGPVCDCKRNSDY
841 LDGGLFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSXYDQSVCEPC
836 LDGGLFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSXYDQSVCEPC
901 GAGHSAYVPSVADIIQIGWATAAASIIQQFLLSLTPRLLLEAVEMEDDDFTI
896 GAGHSAYVPSVADIIQIGWATAAASIIQQFLLSLTPRLLLEAVEMEDDDFTI
961 SCITEQTYQYFFDNDKSKFSGLDCGNCSTRIFHGEKLMNTNLIIFIMVSKGTCPC
956 SCITEQTYQYFFDNDKSKFSGLDCGNCSTRIFHGEKLMNTNLIIFIMVSKGTCPC
1021 QABQTSQGNPNPCDMVKQPRYKGPDCFDNNVLEDYDTCGGVS 1063
1016 QABQTSQGNPNPCDMVKQPRYKGPDCFDNNVLEDYDTCGGVS 1058

RESULT 14

AAB10587 standard; Protein; 1086 AA.

AC AAB10587;

DT 22-DEC-2000 (first entry)

XX Human calcium channel alpha-2c subunit protein.

XX Human; calcium channel; calcium channel subunit; diagnosis;
XX Lambert Eaton Syndrome; calcium channel subunit alpha-2c.

XX Homo sapiens.

XX

95US-0450272.
 89WO-US01408.
 90US-0603751.
 92US-0914231.
 90US-0482384.
 90US-0620250.
 91US-0745206.
 92WO-US06903.
 93US-0105536.
 93US-0149097.
 94US-0193078.
 94US-0311363.
 94US-0336257.
 95US-0404354.
 & CO INC.
 Ellis SB, Williams ME, McCue AF;
 318/50.
 977.
 lls expressing a functional heterologous human calcium
 ncoding nucleic acid isolated from human cerebellum for
 nd to diagnose Lambert Eaton Syndrome -
 olumn 237-246; 154pp; English.
 nvention relates to novel human calcium channel proteins
 otides encoding such proteins. The invention also relates
 cells expressing a functional heterologous human calcium
 1, alpha 2, beta and gamma subunits. The eukaryotic cells
 r screening for potential calcium channel antagonists or
 elect compounds that have potential as disease or tissue-
 apetic agents. The subunits may be used in diagnostic
 e autoimmune disease Lambert Eaton Syndrome. The present
 uman calcium channel alpha 2c subunit protein.
 86 AA;
 99.3%; Score 5559.5; DB 23; Length 1086;
 arity 99.5%; Pred No. 0;
 onservative 0; Mismatches 0; Indels 5; Gaps 1;
 CLLALTTLFQSLIGPSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60
 CLLALTTLFQSLIGPSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60
 QDLYTVEPNNARQVIEIARDTEKLLSNRSKALVSLAEAEKQAAHWRDPASN 120
 QDLYTVEPNNARQVIEIARDTEKLLSNRSKALVSLAEAEKQAAHWRDPASN 120
 YNAKDDLPEKNDSEPGSRIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIYL 180
 YNAKDDLPEKNDSEPGSRIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIYL 180
 WTSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPMVDNSRTPNKIDLYDVR 240
 WTSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPMVDNSRTPNKIDLYDVR 240
 YIOGAASPKDMLILVDVSGSVGLTKLHRTSVSEMLETLSDDDFVNVSFNSNAQD 300
 YIOGAASPKDMLILVDVSGSVGLTKLHRTSVSEMLETLSDDDFVNVSFNSNAQD 300
 FOHLVQANVNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCKIIML 360
 FOHLVQANVNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCKIIML 360
 ZGERAQEI FNKYNKOKKVRVFRFSVQGHNYERGPQIOMMACENKGYIYEIPSGAIR 420
 ZGERAQEI FNKYNKOKKVRVFRFSVQGHNYERGPQIOMMACENKGYIYEIPSGAIR 420

QY 421 INTQEVLDVLRPMVLADKAKOVQWTVNVYLDALGLVITGLTPVFNITGQFENK
 DB 421 INTQEVLDVLRPMVLADKAKOVQWTVNVYLDALGLVITGLTPVFNITGQFENK
 QY 481 NQILGVMGVDVSLEDIKRLTPRFTLCPNGYYFAIDPNGVYLLHPNLQPKPKSQE
 DB 481 NQILGVMGVDVSLEDIKRLTPRFTLCPNGYYFAIDPNGVYLLHPNLQPKPKSQE
 QY 541 DFLDAELENDIKVEIRNMIDGESGKERTLVKSQDERYIDKGNRTVYTWTPVNGI
 DB 536 DFLDAELENDIKVEIRNMIDGESGKERTLVKSQDERYIDKGNRTVYTWTPVNGI
 QY 601 ALVLPYTSFYIYKAKLEETITQARSKKGKMDSETLKPDPNFEESGYTFIAPRDYCN
 DB 596 ALVLPYTSFYIYKAKLEETITQARSKKGKMDSETLKPDPNFEESGYTFIAPRDYCN
 QY 661 SDNTEFLANFNEFIDRKTNNPSCNADLNRVLLDAGFTNELVQNYWSKOKNIK
 DB 656 SDNTEFLANFNEFIDRKTNNPSCNADLNRVLLDAGFTNELVQNYWSKOKNIK
 QY 721 FVVTDDGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNVFTAPYFNKSGPGAI
 DB 716 FVVTDDGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNVFTAPYFNKSGPGAI
 QY 781 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWIEFTKTSIRDPCAGPVCDCCKRNSDVA
 DB 776 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWIEFTKTSIRDPCAGPVCDCCKRNSDVA
 QY 841 LDDGGFLIMANHDDYTNOIGRPFGEIDPSLMRHLVNSVIAFNKSYDYQSVCEPGI
 DB 836 LDDGGFLIMANHDDYTNOIGRPFGEIDPSLMRHLVNSVIAFNKSYDYQSVCEPGI
 QY 901 GAGHSAYVPSVADILQIGMWATAAANSILOQFLLSLTFPRLLLEAVEMEDDDFTAI
 DB 896 GAGHSAYVPSVADILQIGMWATAAANSILOQFLLSLTFPRLLLEAVEMEDDDFTAI
 QY 961 SCITEQTQYFFDNDKSPSGVLDGNCSCSRIIFHGEKLMNTNLIIFIMVESKGTCPCDI
 DB 956 SCITEQTQYFFDNDKSPSGVLDGNCSCSRIIFHGEKLMNTNLIIFIMVESKGTCPCDI
 QY 1021 QAEQTSDDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063
 DB 1016 QAEQTSDDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1058

Search completed: February 20, 2004, 16:55:19
 Job time : 42.5367 secs

GenCore version 5.1.6
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tein search, using sw model

February 20, 2004, 16:47:50 ; Search time 36.9054 Seconds
(without alignments)
4378.325 Million cell updates/sec

JS-10-090-827-13

3346

1 MAAGCLLALTLFQSLIG.....TNLIFIMVESKGTCPDTRL 1018

3LOSUM62

Gapop 10.0 , Gapext 0.5

1107863 seqs, 158726573 residues

uits satisfying chosen parameters: 1107863

angth: 0

angth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

A_Geneseq 19Jun03.*

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

is the number of results predicted by chance to have a
per than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

* Query	Match	Length	DB	ID	Description
100.0	1018	22	AAU01032		Human secreted sol
100.0	1018	22	AAAB62256		Porcine calcium ch
100.0	1036	22	AAU01033		Human secreted sol
100.0	1036	22	AAAB62257		Porcine calcium ch
100.0	1063	22	AAU01034		Human secreted sol
100.0	1063	22	AAAB62258		Porcine calcium ch
100.0	1091	16	AAU01035		Human secreted sol
100.0	1091	16	AAAB62259		Human secreted sol
100.0	1091	21	AAU01036		Human secreted sol
100.0	1091	21	AAAB62260		Human secreted sol

10	5346	100.0	1091	22	AAU01035	Human se
11	5346	100.0	1091	22	AAAB62259	Porcine
12	5346	100.0	1091	23	AAE24789	Human ca
13	5342	99.9	1091	19	AAU01037	Human ca
14	5340	99.9	1091	14	AAU01038	Sequence
15	5326.5	99.6	1110	19	AAU01039	Human ca
16	5306.5	99.3	1086	16	AAU01040	Human ca
17	5306.5	99.3	1086	19	AAU01041	Human ca
18	5306.5	99.3	1086	21	AAU01042	Human ca
19	5306.5	99.3	1086	23	AAU01043	Human ca
20	5289.5	98.9	1084	16	AAU01044	Human ne
21	5289.5	98.9	1084	19	AAU01045	Human ca
22	5289.5	98.9	1084	21	AAU01046	Human ca
23	5289.5	98.9	1084	23	AAU01047	Human ca
24	5288	98.9	1018	22	AAU01048	Pig secr
25	5288	98.9	1018	22	AAU01049	Porcine
26	5288	98.9	1036	22	AAU01050	Pig secr
27	5288	98.9	1036	22	AAU01051	Porcine
28	5288	98.9	1063	22	AAU01052	Pig secr
29	5288	98.9	1063	22	AAU01053	Porcine
30	5288	98.9	1069	22	AAU01054	Pig secr
31	5288	98.9	1069	22	AAU01055	Porcine
32	5288	98.9	1091	22	AAU01056	Pig secr
33	5288	98.9	1091	22	AAU01057	Porcine
34	5270	98.6	1103	16	AAU01058	Human ne
35	5270	98.6	1103	19	AAU01059	Human ca
36	5270	98.6	1103	21	AAU01060	Human ca
37	5270	98.6	1103	23	AAU01061	Human ca
38	5250	98.2	1079	19	AAU01062	Human ca
39	5250	98.2	1079	21	AAU01063	Human ca
40	5250	98.2	1079	23	AAU01064	Human ca
41	5244	98.1	1079	16	AAU01065	Human ne
42	5137.5	96.1	1106	18	AAU01066	Rabbit s
43	5137.5	96.1	1106	18	AAU01067	Rabbit s
44	5137.5	96.1	1106	21	AAU01068	Rabbit s
45	5116.5	95.7	1106	16	AAU01069	Rabbit s

ALIGNMENTS

RESULT 1
AAU01032
ID AAU01032 standard; Protein: 1018 AA.
XX
AC AAU01032;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human secreted soluble alpha2delta calcium channel subunit #12 ;
XX
KW Human; secreted calcium channel alpha2delta subunit; alpha2delt
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel
KW gabapentin; scintillation proximity assay; SPA; nickel flashpla
KW filter binding assay; wheat germ lectin flashplate assay.
XX
OS Homo sapiens.
XX
FN WO2000119870-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-EP09137.
XX
PR 16-SEP-1999; 99US-0397550.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Brown JP, Bertelli F;
XX
DR WPI; 2001-235262/24.
XX
DR N-PSDB; AAS01423.
XX

nel alpha2delta subunits, useful in e.g. SPA assays, assays, Nickel Flashplate assays, Filter binding assays or actin Flashplate assays -

ge 130-133; 160pp; English.

sequence represents human secreted calcium channel subunit #12 which is soluble and retains the functional sites of the full length or wild type alpha2delta subunit from which it is derived. The invention relates to truncated 2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins and their affinity for radioactively labelled gabapentin. The subunit is 1 of the components of the heteromultimeric calcium channel (VDC) complexes present in neuronal and non-neuronal tissues including heart and skeletal muscle. Numerous subunits of the human calcium channel alpha2delta subunits are of the human calcium channel alpha2delta subunits AU01024 and AU01032-AU01038 and 5 soluble forms of the human calcium channel alpha2delta subunits (AAU01027-AAU01031) are the secreted soluble alpha2delta subunit may be used in assays (e.g. SPA, flashplate, nickel flashplate, binding or wheat germ lectin flashplate assays to detect or binding or interaction of a ligand (e.g. gabapentin, L-Allo-Isoleucine, L-methionine, L-leucine, L-Isoleucine, L-phenylalanine) of a calcium channel subunit.

1018 AA;

100.0%; Score 5346; DB 22; Length 1018;

100.0%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGCLLALTTLFOSLLIGPSSEPPFPSPAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

AGCLLALTTLFOSLLIGPSSEPPFPSPAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QYDLTYVEPNNAQLVEIAARDIEKLNSKALVSLALEAKVQAAHQWRDPSN 120

QYDLTYVEPNNAQLVEIAARDIEKLNSKALVSLALEAKVQAAHQWRDPSN 120

AYNAKDDLDPEKNDSEPGSQRIPKVFIEDANFGROI SYOHAHVHPDIYEGSTVL 180

AYNAKDDLDPEKNDSEPGSQRIPKVFIEDANFGROI SYOHAHVHPDIYEGSTVL 180

ANWTSALDEVKKNREDDPSLLMQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240

ANWTSALDEVKKNREDDPSLLMQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240

YTIQGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETLSDDDDFVNVASFNQAQD 300

YTIQGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETLSDDDDFVNVASFNQAQD 300

FOHLYQANVRNKKVLKDAVNNITAKGITDYKGFSPAFQOLLNYSRANCKIIML 360

FOHLYQANVRNKKVLKDAVNNITAKGITDYKGFSPAFQOLLNYSRANCKIIML 360

OGGEERAQEIFNKYNKDKKVRFRFSVQGHNYERGPIONMACENKGYIPIPSIGAIR 420

OGGEERAQEIFNKYNKDKKVRFRFSVQGHNYERGPIONMACENKGYIPIPSIGAIR 420

FOEYLDVLRPMVLGAKQKQVQNTVNYLDALDELGLVITGLTFVFNITQGFENKTNLK 480

FOEYLDVLRPMVLGAKQKQVQNTVNYLDALDELGLVITGLTFVFNITQGFENKTNLK 480

LILGVMGVDSLEDIKELTFRFTLCPNGYYPADIPNGYVLLHPNLPKNSQSPVTL 540

LILGVMGVDSLEDIKELTFRFTLCPNGYYPADIPNGYVLLHPNLPKNSQSPVTL 540

LDLAELNDIKVEIRNKNMIDGESKEFTPLVKSQDERYIDKGNRTYTWTPVNGDYSL 600

LDLAELNDIKVEIRNKNMIDGESKEFTPLVKSQDERYIDKGNRTYTWTPVNGDYSL 600

VLPTYSFYIYKAKLEETITQARSKKGMKDSSETLKPDNPFESGYTFIAPRDYCN 660

601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSSETLKPDNPFESGYTFIAPRDY
661 SDNNTFELNPFNFIDRKTNNPNSCNADLNRLVLLDAGFTNVLQNTWSKQKNI
661 SDNNTFELNPFNFIDRKTNNPNSCNADLNRLVLLDAGFTNVLQNTWSKQKNI
721 FVVTGCGITRVYKPEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGI
721 FVVTGCGITRVYKPEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGI
781 MVSKAVIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPKAGPVCDCKRNSDI
781 MVSKAVIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPKAGPVCDCKRNSDI
841 LDDGCGFLMANHDDYTNOIGRPFGEIDPSLMRHLVNI SVYAFNKSXYDYQSVCEPK
841 LDDGCGFLMANHDDYTNOIGRPFGEIDPSLMRHLVNI SVYAFNKSXYDYQSVCEPK
901 GAGHRSAYVPSVADILQIGMWATAAAWSILQQFLLSLTFPRLLEAVEMEDDDFTI
901 GAGHRSAYVPSVADILQIGMWATAAAWSILQQFLLSLTFPRLLEAVEMEDDDFTI
961 SCITEQTYQYFPDNDKSPSGVLDGNCNSRIFPHGSKLMNTNLI FTWVSKGTCPCPI
961 SCITEQTYQYFPDNDKSPSGVLDGNCNSRIFPHGSKLMNTNLI FTWVSKGTCPCPI

RESULT 2

AAB62256

ID AAB62256 standard; Protein; 1018 AA.

XX AAB62256;

DT 11-JUN-2001 (first entry)

XX Porcine calcium channel alpha2delta subunit.

XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral co-

XX nervous system disorder; pain; epilepsy; anxiety; pig.

XX Sus scrofa.

XX WO200120336-A2.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EP09136.

XX 16-SEP-1999; 99US-0397549.

XX (WARN-) WARNER LAMBERT CO.

XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee N.

XX WPI; 2001-257902/26.

XX N-PSDB; AAF57560.

XX Competitive binding assay for screening ligands which bind a ce-

XX cortical voltage-dependent calcium channel alpha2delta-1 subun-

XX where the ligands identified are useful for treating disorders

XX nervous system, including pain -

XX Claim 8; Page 129-132; 150pp; English.

XX The invention relates to a new method for screening ligands wh-

XX cerebral cortical voltage-dependent calcium channel alpha2delta

XX preferably alpha2delta-1 subunit. The method comprises contacti-

XX secreted soluble recombinant alpha2delta-1 subunit with a ligam-

XX interest and a labelled compound which binds the subunit, follo-

XX measuring the level of binding of the labelled compound to alph-

XX subunit. The method is useful for screening ligands, preferably

XX biologically active products that modulate a nervous system fun-

N/A

cerebral cortical voltage-dependent calcium channel
1 subunit. The ligands identified by the method are useful
disorders of the nervous system, including pain, epilepsy
The present sequence represents a porcine calcium channel
subunit.

018 AA;

100.0%; Score 5346; DB 22; Length 1018;

Identity 100.0%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SCLLALTLTFLQSLLIGSSSEPPSPSVAITKSWDKMQEDLVTLAKTASGVNQLVDI 60

SCLLALTLTFLQSLLIGSSSEPPSPSVAITKSWDKMQEDLVTLAKTASGVNQLVDI 60

YQDLTYVEPNAROLVIAARDIEKLKSNKALVSLALEAEKVAQAAHQWREDPASN 120

YQDLTYVEPNAROLVIAARDIEKLKSNKALVSLALEAEKVAQAAHQWREDPASN 120

YNAKDLDPEKNDSEFGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180

YNAKDLDPEKNDSEFGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180

NWTSDLVDFKKNREEDPSLLQVFGSATGLARYYPASPMVDNSRTNPKIDLVDVRR 240

NWTSDLVDFKKNREEDPSLLQVFGSATGLARYYPASPMVDNSRTNPKIDLVDVRR 240

YIQAAAPKDWLILVDVSGSVGLTKLIRTSVSEMLETSDDDFVNVAFSNSNAQD 300

YIQAAAPKDWLILVDVSGSVGLTKLIRTSVSEMLETSDDDFVNVAFSNSNAQD 300

FQHLVQANVRNKKVLDXAVNNITAKGITDYKKGFSFAFEQLLNTVNSRANCKIIML 360

FQHLVQANVRNKKVLDXAVNNITAKGITDYKKGFSFAFEQLLNTVNSRANCKIIML 360

GGERAQBIFNKYNKDKKVRFRPSVQHNRYERGIOWMACENKGYIYEIPSGAIR 420

GGERAQBIFNKYNKDKKVRFRPSVQHNRYERGIOWMACENKGYIYEIPSGAIR 420

QEYLDVLRGPMVLADGAKAKQVQWNTNVYLDALDELGLVITGTLPVFNITQGFENKTNLK 480

QEYLDVLRGPMVLADGAKAKQVQWNTNVYLDALDELGLVITGTLPVFNITQGFENKTNLK 480

ILGVMGVDSVLEDKRLTPFTLCPNGYIFALDPNGVYVLLHPLNLPKNPKSQEPVTL 540

ILGVMGVDSVLEDKRLTPFTLCPNGYIFALDPNGVYVLLHPLNLPKNPKSQEPVTL 540

DAELENDIKVEIRNKMIDGSEKTFRTLKVSQDERVIDKGNRTYTPVNGTDYSL 600

DAELENDIKVEIRNKMIDGSEKTFRTLKVSQDERVIDKGNRTYTPVNGTDYSL 600

LPTYSFYIYKAKLETTIQAARKKGMKDSBTLKPDNFESGYTFIAPRYCNDLKI 660

LPTYSFYIYKAKLETTIQAARKKGMKDSBTLKPDNFESGYTFIAPRYCNDLKI 660

NTEFLNFEFIDRKTNNPNSCNADLINRVLDDAGTNELVQWNSQKIKGVKAR 720

NTEFLNFEFIDRKTNNPNSCNADLINRVLDDAGTNELVQWNSQKIKGVKAR 720

TDGQITRYPKAGEKNOENPETTEDSFYKRSNDNDNYVTPAPYFNKSGPGAYESGI 780

TDGQITRYPKAGEKNOENPETTEDSFYKRSNDNDNYVTPAPYFNKSGPGAYESGI 780

KAVBIYIYQGLKLPVAVGIKIDVNSWLENFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840

KAVBIYIYQGLKLPVAVGIKIDVNSWLENFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840

GGFLLMANHDDTYNQIGRFGFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPGAAPKQ 900

GGFLLMANHDDTYNQIGRFGFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPGAAPKQ 900

HRSAYVPSVADIQIGMWATAAANSILQQLFLLSLTFFRLLLEAVEMEDDDFTASLSKQ 960

901 GAGHSAYVPSVADIQIGMWATAAANSILQQLFLLSLTFFRLLLEAVEMEDDDFTY
961 SCITEQTQIFFDNDKSKSFSGVLDGNCNCRIFHGEKLMNTNLIFIMVESKGTCPCI
961 SCITEQTQIFFDNDKSKSFSGVLDGNCNCRIFHGEKLMNTNLIFIMVESKGTCPCI

RESULT 3

AAU01033

ID AAU01033 standard; Protein; 1036 AA.

XX AAU01033;

DT 04-JUL-2001 (first entry)

XX Human secreted soluble alpha2delta calcium channel subunit #13

XX Human; secreted calcium channel alpha2delta subunit; alpha2delta

XX alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel;

XX gabapentin; scintillation proximity assay; SPA; nickel flashplat

XX filter binding assay; wheat germ lectin flashplate assay.

XX Homo sapiens.

XX WO200119870-A2.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EP09137.

XX 16-SEP-1999; 99US-0397550.

XX (WARN) WARNER LAMBERT CO.

XX Brown JP, Bertelli F;

XX WPI; 2001-235262/24.

XX N-PSDB; AAS01424.

XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,

XX Flashplate assays, Nickel Flashplate assays, Filter binding as

XX Wheat Germ Lectin Flashplate assays -

XX Claim 31; Page 134-137; 160pp; English.

XX The present sequence represents human secreted calcium channel

XX alpha2delta subunit #13 which is soluble and retains the func

XX characteristics of the full length or wild type alpha2delta sub

XX (AAU01025) from which it is derived. The invention relates to t

XX alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble pr

XX which retain their affinity for radioactively labelled gabapenti

XX alpha2delta subunit is 1 of the components of the heteromultimer

XX voltage-dependent calcium channel (VDCC) complexes present in ne

XX and non-neuronal tissues including heart and skeletal muscle. Nu

XX soluble forms of the human calcium channel alpha2delta subunits

XX (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of

XX porcine calcium channel alpha2delta subunits (AAU01027-AAU01031)

XX described. The secreted soluble alpha2delta subunit may be used

XX e.g. scintillation proximity assay (SPA), flashplate, nickel fla

XX filter binding or wheat germ lectin flashplate assays to detect

XX measure the binding or interaction of a ligand (e.g. gabapentin,

XX L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Iso

XX L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel

XX alpha2delta subunit.

XX Sequence 1036 AA;

Query Match 100.0%; Score 5346; DB 22; Length 1036;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1018; Conservative 0; Mismatches 0; Indels 0;

QY 1 MAAGCULLALTTLTFLQSLLIGPSSEPPSPSVAITKSWDKMQEDLVTLAKTASGVN

|||||
AGCLLALTLTLFQSLILIGSPSEPPSAVTIKSWVDKMQEDLVTLAKTAGVQNLVDI 60
YQDLYTYVEPNNAQQLVEIARDEIKLLSNRSKALVSLALEAEKQVAAHQRWEDFASN 120
YQDLYTYVEPNNAQQLVEIARDEIKLLSNRSKALVSLALEAEKQVAAHQRWEDFASN 120
YNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROI SYQHAHVHIPTDIYEGSTIVL 180
YNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROI SYQHAHVHIPTDIYEGSTIVL 180
NNTSALDEVFKKREEDPSLLQVFGSATGLARYYPASVPWVDSNRTPNKIDLYDVR 240
NNTSALDEVFKKREEDPSLLQVFGSATGLARYYPASVPWVDSNRTPNKIDLYDVR 240
YIQGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLTSLDDDFVNVASFNNAQD 300
YIQGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLTSLDDDFVNVASFNNAQD 300
YQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCKIIML 360
YQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCKIIML 360
YQGEERAQELFNKYNKDKKVRPFRSVQGHNYERGP IQMACENKGYIYEIPIGAI 420
YQGEERAQELFNKYNKDKKVRPFRSVQGHNYERGP IQMACENKGYIYEIPIGAI 420
YQYLDVLRGPMVLGDKAKQVQWNTVYLDALGLVITGLPVFNITGQFNKTNLK 480
YQYLDVLRGPMVLGDKAKQVQWNTVYLDALGLVITGLPVFNITGQFNKTNLK 480
YILGVMGVDVSLDEIKRLTPRFTLCPNGYFYAIDPNGYVLLHNPLOPKPKSDEPVT 540
YILGVMGVDVSLDEIKRLTPRFTLCPNGYFYAIDPNGYVLLHNPLOPKPKSDEPVT 540
YDAELNDIKVEIRNKMIDGESSEKFTPLVKSQDERYIDKGNRTTWTTPVNGTDSL 600
YDAELNDIKVEIRNKMIDGESSEKFTPLVKSQDERYIDKGNRTTWTTPVNGTDSL 600
YLPYTFYIYKAKLETTIQAARKKGMKDSKSETLKPDPNFEESGYTPIAPRDYCNLDKI 660
YLPYTFYIYKAKLETTIQAARKKGMKDSKSETLKPDPNFEESGYTPIAPRDYCNLDKI 660
YNTFLNFEFIDRTKTPNNPSCNADLINRVLLDAGFTNELVQYWSKQNKINGVKAR 720
YNTFLNFEFIDRTKTPNNPSCNADLINRVLLDAGFTNELVQYWSKQNKINGVKAR 720
YTDGGITRVYPKEAGENWQENPETYEDSPYKRSNDNDNVFTAPYFNKSGPGAYESGI 780
YTDGGITRVYPKEAGENWQENPETYEDSPYKRSNDNDNVFTAPYFNKSGPGAYESGI 780
YKAVEIYIQKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDKRNSDVMDCVI 840
YKAVEIYIQKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDKRNSDVMDCVI 840
YQGLFLMANHDDYTNQIGRFFGEBIDPSLMRHLVNI SVYAFNKSYYQSVCEPAAPKQ 900
YQGLFLMANHDDYTNQIGRFFGEBIDPSLMRHLVNI SVYAFNKSYYQSVCEPAAPKQ 900
YHRSVAVPSVADILQIGWATAAANSILOQFLSLTFFRLLLEAVEHEDDDFTASLSQ 960
YHRSVAVPSVADILQIGWATAAANSILOQFLSLTFFRLLLEAVEHEDDDFTASLSQ 960
YTEQTYFFDNDKSGVGLDCNCSRI FHGEKLMNTNLI FIMVESKGTCPDTRL 1018
YTEQTYFFDNDKSGVGLDCNCSRI FHGEKLMNTNLI FIMVESKGTCPDTRL 1018

undard; Protein; 1036 AA.

XX 11-JUN-2001 (first entry)
XX Porcine calcium channel alpha2delta subunit.
XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral co
XX nervous system disorder; pain; epilepsy; anxiety; pig.
XX Sus-~~serofa~~
XX WO200120336-A2.
XX 22-MAR-2001.
XX 18-SEP-2000; 2000WO-EP09136.
XX 16-SEP-1999; 99US-0397549.
XX (WARN) WARNER LAMBERT CO.
XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee N;
XX WPI; 2001-257902/26.
XX N-PSDB; AAF57561.
XX Competitive binding assay for screening ligands which bind a ce:
XX cortical voltage-dependent calcium channel alpha2delta-1 subun:
XX where the ligands identified are useful for treating disorders (:
XX nervous system, including pain -
XX Claim 8; Page 132-135; 158pp; English.
XX The invention relates to a new method for screening ligands wh:
XX cerebral cortical voltage-dependent calcium channel alpha2delta
XX preferably alpha2delta-1 subunit. The method comprises contacti:
XX secreted soluble recombinant alpha2delta-1 subunit with a ligand
XX interest and a labelled compound which binds the subunit, follow
XX measuring the level of binding of the labelled compound to alpha
XX subunit. The method is useful for screening ligands, preferably
XX biologically active products that modulate a nervous system fun:
XX which bind a cerebral cortical voltage-dependent calcium channe:
XX alpha2delta-1 subunit. The ligands identified by the method are
XX for treating disorders of the nervous system, including pain, ei
XX and anxiety. The present sequence represents a porcine calcium (:
XX alpha2delta subunit.

Query Match 100.0%; Score 5346; DB 22; Length 1036;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0;
Qy 1 MAACGLALTLTLFQSLILIGSPSEPPSAVTIKSWVDKMQEDLVTLAKTAGSVI
Db 1 MAACGLALTLTLFQSLILIGSPSEPPSAVTIKSWVDKMQEDLVTLAKTAGSVI
Qy 61 YEKQDLYTYVEPNNAQQLVEIARDEIKLLSNRSKALVSLALEAEKQVAAHQRWRI
Db 61 YEKQDLYTYVEPNNAQQLVEIARDEIKLLSNRSKALVSLALEAEKQVAAHQRWRI
Qy 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROI SYQHAHVHIPTDIYEX
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROI SYQHAHVHIPTDIYEX
Qy 181 NELNWTLSALDEVFKKREEDPSLLQVFGSATGLARYYPASVPWVDSNRTPNKIDI
Db 181 NELNWTLSALDEVFKKREEDPSLLQVFGSATGLARYYPASVPWVDSNRTPNKIDI
Qy 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLTSLDDDFVNVASFP
Db 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLTSLDDDFVNVASFP
Qy 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCKI

FOHLVQANVENKVKLDVANNITAKGITYDKGFSFAFEQLLNNYSRANCNKIIML 360
3GERAQEIIFNKYNKDKKVVFRFSGVQHNVERGPIQWMACENKGYIYEIPSGAIR 420
3GERAQEIIFNKYNKDKKVVFRFSGVQHNVERGPIQWMACENKGYIYEIPSGAIR 420
3EYLDVLRPMVLADGKAKQVQWNTVYLDLALGLVITGTLPVFNITGQFENKTNLK 480
3EYLDVLRPMVLADGKAKQVQWNTVYLDLALGLVITGTLPVFNITGQFENKTNLK 480
ILGVMGVDSLEDIKRLTPFTLCPNGYYFAIDPBGVYLLHPNLQPNKPSQBPVTL 540
ILGVMGVDSLEDIKRLTPFTLCPNGYYFAIDPBGVYLLHPNLQPNKPSQBPVTL 540
DAELNDIKVEIRNMKIDGESGKFTLTKVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
DAELNDIKVEIRNMKIDGESGKFTLTKVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
LPTYSFYIYKAKLEETITQARSKKGMKDSITLKPDPFESGYTFIAPRDYCNLDKI 660
LPTYSFYIYKAKLEETITQARSKKGMKDSITLKPDPFESGYTFIAPRDYCNLDKI 660
NTEFLNPNFIDRKTNNPNSCNADLINRVLLDAGFTNELVQWYWSKQNKIKGYKAR 720
NTEFLNPNFIDRKTNNPNSCNADLINRVLLDAGFTNELVQWYWSKQNKIKGYKAR 720
IDGIGITRVYKPEAGENQENPETVEDSFYKRSILDNDNYVTAPYFNKSGPGAYESGI 780
IDGIGITRVYKPEAGENQENPETVEDSFYKRSILDNDNYVTAPYFNKSGPGAYESGI 780
KAVEIYIQGKLLKPAVYGIKIDVNSWTFENFTKTSIRDPKAGVPCDCRNSDVMDCVI 840
KAVEIYIQGKLLKPAVYGIKIDVNSWTFENFTKTSIRDPKAGVPCDCRNSDVMDCVI 840
3GFLLMANHDYTNQIGRFFGEIDPFLMRHLVNI SVYAFNKSVDYQSVCEPAGAPKQ 900
3GFLLMANHDYTNQIGRFFGEIDPFLMRHLVNI SVYAFNKSVDYQSVCEPAGAPKQ 900
3RAYSVPVSADIIQIGHWATAAWSIIQQFLSLTFFPRLEAVEMEDDDFTASLSKQ 960
3RAYSVPVSADIIQIGHWATAAWSIIQQFLSLTFFPRLEAVEMEDDDFTASLSKQ 960
TEQTQYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIIFIMVESKTCPCDTRL 1018
TEQTQYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIIFIMVESKTCPCDTRL 1018

ndard; Protein; 1063 AA.

(first entry)

ed soluble alphas2delta calcium channel subunit #14 protein.

ted calcium channel alphas2delta subunit; alphas2delta-2;
3; alphas2delta-4; voltage-dependent calcium channel; VDCC;
scintillation proximity assay; SPA; nickel flashplate assay;
ng assay; wheat germ lectin flashplate assay.

A2.

2000WO-EP09137.

99US-0397550.

(WARN) WARNER LAMBERT CO.
Brown JP, Bertelli F;
WPI: 2001-235262/24.
N-PSDB; AA501425.
Calcium channel alphas2delta subunits, useful in e.g. SPA assays,
Flashplate assays, Nickel Flashplate assays, Filter binding ass
Wheat Germ Lectin Flashplate assays -
Claim 31; Page 137-140; 160pp; English.
The present sequence represents human secreted calcium channel
alphas2delta subunit #14 which is soluble and retains the functio
characteristics of the full length or wild type alphas2delta subu
(AAU01025) from which it is derived. The invention relates to tr
alphas2delta-2, alphas2delta-3 or alphas2delta-4 subunit soluble pr
which retain their affinity for radioactively labelled gabapenti
alphas2delta subunit is 1 of the components of the heteromultimer
voltage-dependent calcium channel (VDCC) complexes present in ne
and non-neuronal tissues including heart and skeletal muscle. Nu
soluble forms of the human calcium channel alphas2delta subunits
(AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of
porcine calcium channel alphas2delta subunits (AAU01027-AAU01031)
described. The secreted soluble alphas2delta subunit may be used
e.g. scintillation proximity assay (SPA), flashplate, nickel fla
filter binding or wheat germ lectin flashplate assays to detect
measure the binding or interaction of a ligand (e.g. gabapentin,
L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isol
L-valine, Spermine and/or L-Phenylalanine) of a calcium channel
alphas2delta subunit.

Sequence 1063 AA;

Query Match 100.0%; Score 5346; DB 22; Length 1063;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0;

QY 1 MAAGCLLALTLTIFQSLIIGPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVN
DB 1 MAAGCLLALTLTIFQSLIIGPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVN
QY 61 YEYQDLTYTVEPNARQOLVEIAARDIEKLLSNRSKALVSLAEAKVQAAHORE
DB 61 YEYQDLTYTVEPNARQOLVEIAARDIEKLLSNRSKALVSLAEAKVQAAHORE
QY 121 EVVYNAKDDLDPEKNDSPGSGORIKPVFTEDANFGROI SYQHAHVHIPTDIYEG
DB 121 EVVYNAKDDLDPEKNDSPGSGORIKPVFTEDANFGROI SYQHAHVHIPTDIYEG
QY 181 NELNWTLSALDEVFKONREEDPSLLMQVFGSATGLARYYPASPWVDSRTPNKIDI
DB 181 NELNWTLSALDEVFKONREEDPSLLMQVFGSATGLARYYPASPWVDSRTPNKIDI
QY 241 RPYIYQGAASPKDMLILVDVSGVSGLTILKLRITSVSEMLETLSDDDDFNVASFN
DB 241 RPYIYQGAASPKDMLILVDVSGVSGLTILKLRITSVSEMLETLSDDDDFNVASFN
QY 301 VSCFQHLVQANVKNKVLKDAVNNTAKGITYDKGFSFAFEQLLNNYSRANCN
DB 301 VSCFQHLVQANVKNKVLKDAVNNTAKGITYDKGFSFAFEQLLNNYSRANCN
QY 361 FTDGGERAQEIIFNKYNKDKKVVFRFSGVQHNVERGPIQWMACENKGYIYEIP
DB 361 FTDGGERAQEIIFNKYNKDKKVVFRFSGVQHNVERGPIQWMACENKGYIYEIP
QY 421 INTQEYLDVLRPMVLADGKAKQVQWNTVYLDLALGLVITGTLPVFNITGQFEN
DB 421 INTQEYLDVLRPMVLADGKAKQVQWNTVYLDLALGLVITGTLPVFNITGQFEN
QY 481 NQLILGVMGVDSLEDIKRLTPFTLCPNGYYFAIDPBGVYLLHPNLQPNKPSQ

ILGVMGVDVSLIEDIKRLTPRTLCNGYFAIDPNGYVLLHPNLQPKNPKSQEPVTL 540
 DAELNDIKVIRNKMIDGESGKTRTLVKSQDERYIDKGNRYTWTTPVNGTDYSL 600
 DAELNDIKVIRNKMIDGESGKTRTLVKSQDERYIDKGNRYTWTTPVNGTDYSL 600
 LPTYSFYVIKAKLEETITQARSKKGMKDSSTLKPDPNPEESGYTFIAPRDYCNLDKI 660
 LPTYSFYVIKAKLEETITQARSKKGMKDSSTLKPDPNPEESGYTFIAPRDYCNLDKI 660
 NTEFLANFNEIDRKTNNPSCNADLINRVLLDAGFTNELVQYWSKQKNIKGKVKAR 720
 NTEFLANFNEIDRKTNNPSCNADLINRVLLDAGFTNELVQYWSKQKNIKGKVKAR 720
 TDGGITRVYPKEAGENQENPETVEDSYKRSNDNDNVFTAPYFNKSGPGAYESGI 780
 TDGGITRVYPKEAGENQENPETVEDSYKRSNDNDNVFTAPYFNKSGPGAYESGI 780
 KAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
 KAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
 GGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
 GGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
 HRSAYVPSVADILQIGMWATAAAMSILQOFLLSLTFFPRLLEAVEMEDDDFTASLSKQ 960
 HRSAYVPSVADILQIGMWATAAAMSILQOFLLSLTFFPRLLEAVEMEDDDFTASLSKQ 960
 TEOTQYFFDNDKSPSGVLDGNCRSRIIFHGEKLMNTNLIIFIMVSKGTCPCDTRL 1018
 TEOTQYFFDNDKSPSGVLDGNCRSRIIFHGEKLMNTNLIIFIMVSKGTCPCDTRL 1018

ndard; Protein; 1063 AA.

(first entry)

ium channel alpha2delta subunit.

nel alpha2delta subunit; alpha2delta-1; cerebral cortex;
 em disorder; pain; epilepsy; anxiety; pig.

32.

2000WO-EP09136.

99US-0397549.

BER LAMBERT CO.

Brown JP, Dissanayake V, Suman-Chauban N, Gee NS;

7902/26.

7562.

binding assay for screening ligands which bind a cerebral
 tage-dependent calcium channel alpha2-delta-1 subunit,
 gands identified are useful for treating disorders of the
 .em, including pain -

re 135-139; 158pp; English.

on relates to a new method for screening ligands which bind a

CC cerebral cortical voltage-dependent calcium channel alpha2delta
 CC preferably alpha2delta-1 subunit. The method comprises contactir
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand
 CC interest and a labelled compound which binds the subunit, follow
 CC measuring the level of binding of the labelled compound to alpha
 CC subunit. The method is useful for screening ligands, preferably
 CC biologically active products that modulate a nervous system func
 CC which bind a cerebral cortical voltage-dependent calcium channel
 CC alpha2delta-1 subunit. The ligands identified by the method are
 CC for treating disorders of the nervous system, including pain, ef
 CC and anxiety. The present sequence represents a porcine calcium c
 CC alpha2delta subunit.
 XX

SQ Sequence 1063 AA;

Query Match 100.0%; Score 5346; DB 22; Length 1063;
 Best Local Similarity 100.0%; Pred No. 0;
 Matches 1018; Conservative 0; Mismatches 0; Indels 0;

Qy 1 MAAGCLLALTLTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGV
 Db 1 MAAGCLLALTLTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGV
 Qy 61 YEKYQDLYTVEPNARQLVEIARDTEKLSNESKALVSLALEAEKVQAAHORE
 Db 61 YEKYQDLYTVEPNARQLVEIARDTEKLSNESKALVSLALEAEKVQAAHORE
 Qy 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYEC
 Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYEC
 Qy 181 NELNWTSALEVPKKNREDDPSLLMQVFGSATGLARYYPASPWVDNRSRTNKKIDI
 Db 181 NELNWTSALEVPKKNREDDPSLLMQVFGSATGLARYYPASPWVDNRSRTNKKIDI
 Qy 241 RPWYIQGAASPDKMLILVDVSGVSGITLKLIRTSVSEMLETISDDDFVNVASF
 Db 241 RPWYIQGAASPDKMLILVDVSGVSGITLKLIRTSVSEMLETISDDDFVNVASF
 Qy 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLNNTNVSBRANC
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLNNTNVSBRANC
 Qy 361 FTDGGEERAQEIIFNKYNKDKKVRVFRFSVQGHNYERGFIOVMACENKGYTYEIP
 Db 361 FTDGGEERAQEIIFNKYNKDKKVRVFRFSVQGHNYERGFIOVMACENKGYTYEIP
 Qy 421 INTQEYLDVLGRPMVLADGKAKOVQNTNVYLDALGLGLVITGLPVFNITGQFEN
 Db 421 INTQEYLDVLGRPMVLADGKAKOVQNTNVYLDALGLGLVITGLPVFNITGQFEN
 Qy 481 NQLILGVMGVDVSLIEDIKRLTPRTLCNGYFAIDPNGYVLLHPNLQPKNPKS
 Db 481 NQLILGVMGVDVSLIEDIKRLTPRTLCNGYFAIDPNGYVLLHPNLQPKNPKS
 Qy 541 DFDAELENDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRYTWTTPVNC
 Db 541 DFDAELENDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRYTWTTPVNC
 Qy 601 ALVLPYTSFYVIKAKLEETITQARSKKGMKDSSTLKPDPNPEESGYTFIAPRDY
 Db 601 ALVLPYTSFYVIKAKLEETITQARSKKGMKDSSTLKPDPNPEESGYTFIAPRDY
 Qy 661 SDNNTEFLANFNEIDRKTNNPSCNADLINRVLLDAGFTNELVQYWSKQKNIK
 Db 661 SDNNTEFLANFNEIDRKTNNPSCNADLINRVLLDAGFTNELVQYWSKQKNIK
 Qy 721 FVVTGCGITRVYPKEAGENQENPETVEDSYKRSNDNDNVFTAPYFNKSGPGF
 Db 721 FVVTGCGITRVYPKEAGENQENPETVEDSYKRSNDNDNVFTAPYFNKSGPGF
 Qy 781 MVSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDI

95US-0450562.
 88US-0176899.
 90US-0482384.
 90US-0603751.
 90US-0620250.
 91US-0745206.
 92US-0868354.
 92US-0914231.
 93US-0105536.
 93US-0149097.
 94US-0193078.
 94US-0223305.
 94US-0290012.
 94US-0311363.
 94US-0314083.
 94US-0336257.
 95US-0404950.
 NEUROSCIENCES INC.
 Williams ME, McCue AF, Harpold MM;
 230/50.
 707.
 channel beta subunit polynucleotides, useful for
 ombinant eukaryotic cells and for diagnosing Lambert Eaton
 column 135-144; 153pp; English.
 n describes a novel isolated DNA molecule (I) comprising a
 ding a beta3-1 subunit of a human calcium channel.
 probes comprising 14-30 contiguous nucleotides of
 t encoding DNA are useful for isolation and cloning of
 el subunit-encoding DNA. Recombinant eukaryotic cells that
 ologous calcium channel are useful for identifying compounds
 calcium channel activity and in assays for identifying
 antagonists of calcium channel activity in humans. Human
 el subunit or eukaryotic cells expressing the channel are
 agnosing Lambert Eaton Syndrome (LES) in a human. This
 essents the human calcium channel alpha-2 subunit which is
 the method of the invention.
 91 AA;
 100.0%; Score 5346; DB 21; Length 1091;
 arity 100.0%; Pred. No. 0;
 onservative 0; Mismatches 0; Indels 0; Gaps 0;
 CLALTLTLFOSLLIGSSSEPPPSAVTIKSWDKMOEDLVTLAKTAGVNLVDI 60
 CLALTLTLFOSLLIGSSSEPPPSAVTIKSWDKMOEDLVTLAKTAGVNLVDI 60
 QDLTYVEPNNAQLVEIAARDIEKLLSNRSLALVSLAEKQAAHQWRDPASN 120
 QDLTYVEPNNAQLVEIAARDIEKLLSNRSLALVSLAEKQAAHQWRDPASN 120
 YNAKDDLPEKNDSEPGSQRIKPVFIEDANFGROIQSQAHAHPTDIYEGSTIVL 180
 YNAKDDLPEKNDSEPGSQRIKPVFIEDANFGROIQSQAHAHPTDIYEGSTIVL 180
 WTSALDEVFKKRNREDESLLMQVFGSATGLARYYPASPWVDNSTRPNKIDLYDVR 240
 WTSALDEVFKKRNREDESLLMQVFGSATGLARYYPASPWVDNSTRPNKIDLYDVR 240

241 RPWYIQGAASPKOMLILVDVSGSVGLTLKLIRTSVSEMLETSLSDDDFVNVSFNI
 241 RPWYIQGAASPKOMLILVDVSGSVGLTLKLIRTSVSEMLETSLSDDDFVNVSFNI
 301 VSCFOHLVQAVNRNKKVLKDAVNNTAKGITDYKKGFSAFEQLLNYNVSRANCNI
 301 VSCFOHLVQAVNRNKKVLKDAVNNTAKGITDYKKGFSAFEQLLNYNVSRANCNI
 361 FTGGEERAQEIFNKYNKKVVRFRPSVGOHNYERGPIONMACENKGYTYEIPS.
 361 FTGGEERAQEIFNKYNKKVVRFRPSVGOHNYERGPIONMACENKGYTYEIPS.
 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVYLDALDELGLVITGTLFPVFNITQGFENI
 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVYLDALDELGLVITGTLFPVFNITQGFENI
 481 NQLILGVNMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPLOPKPKSQI
 481 NQLILGVNMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPLOPKPKSQI
 541 DPLDAELENDIKVIRNKKMIDGESCKTFRTLVKSODERYIDKGNRTYTWTPVNG
 541 DPLDAELENDIKVIRNKKMIDGESCKTFRTLVKSODERYIDKGNRTYTWTPVNG
 601 ALVLPYTSFYIYIKAKLEETITQARSKKGMKMDSETLKPDPNFEEGYTFIAPRDYCI
 601 ALVLPYTSFYIYIKAKLEETITQARSKKGMKMDSETLKPDPNFEEGYTFIAPRDYCI
 661 SDNNTFELINFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQKNIKI
 661 SDNNTFELINFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQKNIKI
 721 FVVDGGITRVYPKEAGENMOENPETYEDSFYKSLDNDNVFTAPYFNKSGPGA
 721 FVVDGGITRVYPKEAGENMOENPETYEDSFYKSLDNDNVFTAPYFNKSGPGA
 781 MVSKAVEIYIQGLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCCKRNSDVN
 781 MVSKAVEIYIQGLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCCKRNSDVN
 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGI
 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGI
 901 GAGRSVAVPSVADILQIGWATAAANSILQOFLLSLTFPRLLEAVEMEDDDFTAS
 901 GAGRSVAVPSVADILQIGWATAAANSILQOFLLSLTFPRLLEAVEMEDDDFTAS
 961 SCITEQTYQYFPDNDKSPSGVLDGNCNSRIIPHGEKLMNTNLIIFIMVESKGTCPCDI
 961 SCITEQTYQYFPDNDKSPSGVLDGNCNSRIIPHGEKLMNTNLIIFIMVESKGTCPCDI
 RESULT 10
 AAU01035
 ID AAU01035 standard; Protein; 1091 AA.
 XX
 AC AAU01035;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human secreted soluble alpha2delta calcium channel subunit #15 pr
 KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel;
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate
 KW filter binding assay; wheat germ lectin flashplate assay.
 OS Homo sapiens.
 XX
 FN WO200119870-A2.
 XX

2000WO-EP09137.
 99US-0397550.
 IER LAMBERT CO.
 Bertelli F;
 15262/24.
 11426.
 mel alpha2delta subunits, useful in e.g. SPA assays,
 assays, Nickel Flashplate assays, Filter binding assays or
 actin Flashplate assays -
 age 141-144; 160pp; English.
 sequence represents human secreted calcium channel
 subunit #15 which is soluble and retains the functional
 ics of the full length or wild type alpha2delta subunit
 from which it is derived. The invention relates to truncated
 2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
 i their affinity for radioactively labelled gabapentin. The
 subunit is 1 of the components of the heteromultimeric
 ndent calcium channel (VCC) complexes present in neuronal
 onal tissues including heart and skeletal muscle. Numerous
 is of the human calcium channel alpha2delta subunits
 u01024 and AAU01032-AAU01038) and 5 soluble forms of the
 um channel alpha2delta subunits (AAU01027-AAU01031) are
 he secreted soluble alpha2delta subunit may be used in assays
 .ation proximity assay (SPA), flashplate, nickel flashplate,
 ng or wheat germ lectin flashplate assays to detect or
 binding or interaction of a ligand (e.g. gabapentin,
 ;, L-Allo-isoleucine, L-methionine, L-leucine, L-isoleucine,
 ermine and/or L-Phenylalanine) of a calcium channel
 subunit.
 .091 AA;
 100.0%; Score 5346; DB 22; Length 1091;
 .larity 100.0%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AGCLLATLTTLFQSLIGPSSEPPSPSANTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
 AGCLLATLTTLFQSLIGPSSEPPSPSANTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
 TYQDLTYVPNNARQLVEIARDIEKLSNRSKALVSLALEAKVQAAHQWREDFASN 120
 TYQDLTYVPNNARQLVEIARDIEKLSNRSKALVSLALEAKVQAAHQWREDFASN 120
 TYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROIYSQHAHVHPTDIYEGSTIVL 180
 TYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROIYSQHAHVHPTDIYEGSTIVL 180
 ANWTSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPVWDSNRTPNKIDLYVRR 240
 ANWTSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPVWDSNRTPNKIDLYVRR 240
 WYIQAASPKDMLILVDVSGVSGLTCLKIRTSVSEMLETLSDDDDFVNVASFNNAQD 300
 WYIQAASPKDMLILVDVSGVSGLTCLKIRTSVSEMLETLSDDDDFVNVASFNNAQD 300
 FQHLVQANVRNKKVLKDAVNNITAKGIDTYKGFSPFAFEPOLLNVNVRANCKIIML 360
 FQHLVQANVRNKKVLKDAVNNITAKGIDTYKGFSPFAFEPOLLNVNVRANCKIIML 360
 XGGEERAQELFNKYNKDKKVRFRPSVGVGHNYERGPQWACENKGYIYIPIGAI 420
 XGGEERAQELFNKYNKDKKVRFRPSVGVGHNYERGPQWACENKGYIYIPIGAI 420

421 INTOEYLDVLGRPMVLGADKAKQVQWNTNVYLDALGLVITGTLPVENITQCFE
 421 INTOEYLDVLGRPMVLGADKAKQVQWNTNVYLDALGLVITGTLPVENITQCFE
 481 NQLILGVMGVDVLSLEDIKRLTPFTLCPNGYFFAIDPNGYVLLHPNLQPKPKS
 481 NQLILGVMGVDVLSLEDIKRLTPFTLCPNGYFFAIDPNGYVLLHPNLQPKPKS
 541 DFLDAELENDIKVEIRNKWIDGSEKTFRTLVKSQDERYIDKGNRTYVTPVVK
 541 DFLDAELENDIKVEIRNKWIDGSEKTFRTLVKSQDERYIDKGNRTYVTPVVK
 601 ALVLPTYSFYIYKAKLEETITQARSKKGKMKDSITLKPDPFEESGYTFIAPRDY
 601 ALVLPTYSFYIYKAKLEETITQARSKKGKMKDSITLKPDPFEESGYTFIAPRDY
 661 SDNTEFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQNTWSKQKNI
 661 SDNTEFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQNTWSKQKNI
 721 FVVTDDGGITRVYPKEAGENQWENPETVEDSFYKRSNDNDYVFTAPYFNKSGPGI
 721 FVVTDDGGITRVYPKEAGENQWENPETVEDSFYKRSNDNDYVFTAPYFNKSGPGI
 781 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGPVCDCCKNSD
 781 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGPVCDCCKNSD
 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSIMRHLVNI SVYAFNKS YDYQSVCEK
 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSIMRHLVNI SVYAFNKS YDYQSVCEK
 901 GAGHRSAYVPSVADILQIGWATAAAMSILQOFLLSLTFFPRLLEAVEMEDDDFTI
 901 GAGHRSAYVPSVADILQIGWATAAAMSILQOFLLSLTFFPRLLEAVEMEDDDFTI
 961 SCITEQTYFFDNDKSFSGVLDCGNC SRIFPHGKLMNTMLIFIMVBSKGTCPCI
 961 SCITEQTYFFDNDKSFSGVLDCGNC SRIFPHGKLMNTMLIFIMVBSKGTCPCI
 RESULT 11
 AAB62259
 ID AAB62259 standard; Protein; 1091 AA.
 XX
 AC AAB62259;
 XX
 DT 11-JUN-2001 (first entry)
 XX
 DE Porcine calcium channel alpha2delta subunit.
 XX
 KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral co
 XX nervous system disorder; pain; epilepsy; anxiety; pig.
 XX
 OS Sus scrofa.
 XX
 FN WO200120336-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 18-SEP-2000; 2000WO-EP09136.
 XX
 PR 16-SEP-1999; 99US-0397549.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee N
 XX
 DR WPI; 2001-257902/26.
 XX
 DR N-PSDB; AAF57563.
 XX
 PT Competitive binding assay for screening ligands which bind a cel
 PT cortical voltage-dependent calcium channel alpha2delta-1 subuni

VTEFGLNFNEFLDKKIPNNFSCNADLLINKVLLDAGFINELTVQNIWSKQANIRGVAAAR 720

CC The present invention relates to novel human calcium channel proteins and polynucleotides encoding such proteins. The invention also relates to eukaryotic cells expressing a functional heterologous human calcium channel alpha 1, alpha 2, beta and gamma subunits. The eukaryotic cells are useful for studying the function of the calcium channel subunits.

or screening for potential calcium channel antagonists or select compounds that have potential as disease or tissue-repauetic agents. The subunits may be used in diagnostic he autoimmune disease Lambert Eaton Syndrome. The present human calcium channel alpha 2b subunit protein.

091 AA;

larity 100.0%; Score 5346; DB 23; Length 1091;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GCLIALTLTLFQSLILIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60

GCLIALTLTLFQSLILIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKVAQAAHQWREDFASN 120

Db 901 GAGHSAYVPSVADILQIGWATAAAWSILQOFLLSLTPRLLEAVEMEDDDFTA
QY 961 SCITEQTOYFFNDKSKFSVGLDCGNCNCSRIHFGEKLMNTNLIFIMVESKGTCPCL
Db 961 SCITEQTOYFFNDKSKFSVGLDCGNCNCSRIHFGEKLMNTNLIFIMVESKGTCPCL

RESULT 13

AAW37879

ID AAW37879 standard; Protein; 1091 AA.

XX AAW37879;

XX 28-AUG-1998 (first entry)

XX Human calcium channel a2d subunit.

XX Calcium channel; human; central nervous system disorder;

XX Lambert-Eaton syndrome; diagnosis; therapy.

XX Homo sapiens.

XX WO9811131-A2.

XX 19-MAR-1998.

XX 11-SEP-1997; 97WO-US16146.

XX 16-SEP-1996; 96US-0713118.

XX (AMHP) AMERICAN HOME PROD CORP.

XX Chen ARS, Franco R, Shuey DJ;

XX WPI; 1998-207325/18.

XX N-PSDB; AAV29060.

XX DNA encoding human neuronal calcium channel subunit(s) - useful

XX diagnosis of and treatment of central nervous system disorders,

XX Lambert-Eaton syndrome

XX Disclosure; Fig 2; 89pp; English.

XX This polypeptide comprises the a2d subunit of the human neuronal

XX calcium channel. cDNA clones (see AAV29059-61) encoding the a1b

XX subunit (see AAW37878), the a2d subunit and a b3 subunit (see AA

XX have been isolated. These have been inserted into expression

XX vectors and are stably expressed in transformed cell lines. The

XX transformed cells show omega-conotoxin GVIA binding activity,

XX and omega-conotoxin GVIA toxin sensitive potassium-stimulated

XX calcium uptake, indicating that the proteins expressed by the

XX clones are capable of forming a functioning calcium channel.

XX Nucleic acids encoding the 3 subunits, as well as vectors, host

XX cells and methods of isolating nucleic acids encoding related

XX calcium channels are disclosed. Fusion proteins incorporating t

XX subunit proteins, antibodies, and assays for identifying agents

XX that modulate calcium channel activity are also provided. Such

XX agents can be used to treat certain central nervous system

XX disorders by altering calcium channel activity. Methods of

XX diagnosing diseases associated with particular calcium channels,

XX such as Lambert-Eaton syndrome, are disclosed.

XX Sequence 1091 AA;

Query Match 99.9%; Score 5342; DB 19; Length 1091;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1017; Conservative 0; Mismatches 1; Indels 0;

QY 1 MAAGCCLALTLTLFQSLILIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVGN

Db 1 MAAGCCLALTLTLFQSLILIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVGN

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 QDLTVFPNNARQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHOMREDFASN 120
 YNAKDDLDPEKNDSEPGSQRKIPVFIEDANFGRIQSYQAAVHIPTDIYEGSTIVL 180
 YNAKDDLDPEKNDSEPGSQRKIPVFIEDANFGRIQSYQAAVHIPTDIYEGSTIVL 180
 WTSALDEVFPKNNREDEPDLQVFGSATGLARYYPASPWVDSNRPNKIDLYDVR 240
 WTSALDEVFPKNNREDEPDLQVFGSATGLARYYPASPWVDSNRPNKIDLYDVR 240
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 QHLVQANVRNKKVLKDAVNNITAKGITYKKGFSFAFQLLNINYSRANCNKIIML 360
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 KGEERAQEIENKYNKDKKVRFPSPVSGQNYERGPQMMACENKGYIYIPIPSIGAIR 420
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 JELVDVLRPMVLGAKAQVQWNTVYLDALGLVITGTLPVFNITGOFENKTNLK 480
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 LGVMGVDSVLEDIKRLTRFTLCPNGYYPADIPNGYVLLHPLNLPKNPKSQEPVTL 540
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 KAVEIYITQGLKLPVAVGKIDVNSWIENTFKTSIRDPKAGPVCDCRNSDVMDCVI 840
 KAVEIYITQGLKLPVAVGKIDVNSWIENTFKTSIRDPKAGPVCDCRNSDVMDCVI 840
 JGFLMANHDDYTNQIGRFGETIDPSLMRHLVNI SVYAFNKSVDYQSVCPGAPKQ 900
 JGFLMANHDDYTNQIGRFGETIDPSLMRHLVNI SVYAFNKSVDYQSVCPGAPKQ 900
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 TEQTQYFFDNDKSKFSFGLDCGNSRIFHGEKLMNTNLII FIMVESKGTCPCDTEL 1018
 TEQTQYFFDNDKSKFSFGLDCGNSRIFHGEKLMNTNLII FIMVESKGTCPCDTEL 1018

ndard; Protein; 1091 AA.

(updated)
(first entry)

XX Sequence of the alpha 2 human calcium channel subunit.
 DE Human calcium channel subunit; diagnosis; agonist; antagonist;
 KW Lambert Eaton syndrome.
 XX Homo sapiens.
 XX WO9304083-A1.
 XX 04-MAR-1993.
 XX 14-AUG-1992; 92WO-US06903.
 XX 15-AUG-1991; 91US-0745206.
 XX 10-APR-1992; 92US-0868354.
 XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
 XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
 XX Williams ME;
 XX WPI: 1993-093936/11.
 XX N-PSDB; AAQ37821.
 XX DNA encoding specific human calcium channel sub-units - used for
 XX identifying calcium channel agonists and antagonists and
 XX diagnosing Lambert Eaton syndrome
 XX Disclosure; Page 134-138; 150pp; English.
 XX DNA encoding a human neuronal calcium channel alpha 2 subunit wa
 XX isolated from a human genomic DNA library probed under low and h
 XX stringency conditions with a fragment of DNA encoding the rabbit
 XX skeletal muscle calcium channel alpha 2 subunit. The fragment
 XX included nucleotides having a sequence corresponding to the
 XX nucleotide sequence between nucleotides 43 and 272 inclusive of
 XX rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA
 XX PCR analysis identified splice variants of the human calcium alp
 XX 2 subunit transcript. In particularly preferred embodiments, the
 XX DNA encoding the alpha 2 subunit is produced by alternative
 XX processing of a primary transcript that includes DNA encoding th
 XX amino acids set forth in AAR3353 and the DNA of AAQ37823 insert
 XX between nucleotides 1624 and 1625 of AAQ37821.
 XX (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 1091 AA;
 SQ
 Query Match 99.9%; Score 5340; DB 14; Length 1091;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1017; Conservative 0; Mismatches 1; Indels 0;
 QY 1 MAAGCLLALTLTIFQSLILGPSEEPFSAVTTIKSWDKMQEDLVLTAKTASGVN
 DB 1 MAAGCLLALTLTIFQSLILGPSEEPFSAVTTIKSWDKMQEDLVLTAKTASGVN
 QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHOMRE
 DB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHOMRE
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRKIPVFIEDANFGRIQSYQAAVHIPTDIYEG
 DB 121 EVVYNAKDDLDPEKNDSEPGSQRKIPVFIEDANFGRIQSYQAAVHIPTDIYEG
 QY 181 NELNWTLSALDEVFPKNNREDEPDLQVFGSATGLARYYPASPWVDSNRPNKIDL
 DB 181 NELNWTLSALDEVFPKNNREDEPDLQVFGSATGLARYYPASPWVDSNRPNKIDL
 QY 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLRISVSEMLETSDDDFYNVASFN
 DB 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLRISVSEMLETSDDDFYNVASFN
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITYKKGFSFAFQLLNINYSRANC

FOHLVQANVRNKKVLDKDAVNNTAKGIDTYKKGSFAFEQLLNTVNSRANCKIIML 360
GGGERAQEIIFNKYNKDKKVRPVSQGHNVYERPIQWMAKCNKGYVEIPSGAIR 420
GGGERAQEIIFNKYNKDKKVRPVSQGHNVYERPIQWMAKCNKGYVEIPSGAIR 420
QEYLDVLGRPMVLADGAKAKQVQWNTVYLDALGLVITGTLPVFNITQGFENKTNLK 480
QEYLDVLGRPMVLADGAKAKQVQWNTVYLDALGLVITGTLPVFNITQGFENKTNLK 480
ILGVMGVDSLEDKRLTPRTLCPNGYFPAIDPNGYVLLHPNLQPKNPKSQBPVTL 540
ILGVMGVDSLEDKRLTPRTLCPNGYFPAIDPNGYVLLHPNLQPKNPKSQBPVTL 540
DAELENIDKVEIRNKMIDGESGKFTFLVKSQDERVIDKGNRYTWTVPVNGTDYSL 600
DAELENIDKVEIRNKMIDGESGKFTFLVKSQDERVIDKGNRYTWTVPVNGTDYSL 600
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LPTYSFYIIRAKLEETITQARSKKGMKDSITLKPDPFESGYTFIAPRDYCNLDKI 660
NTEFLNFEIIRKTNPNPCNADLNRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
NTEFLNFEIIRKTNPNPCNADLNRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
TDGGITRVYKPEAGENQENPETYEDSFYKRSNDNDNVVFTAPYFNKSGPGAYESGI 780
TDGGITRVYKPEAGENQENPETYEDSFYKRSNDNDNVVFTAPYFNKSGPGAYESGI 780
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GGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNLISVYAFNKSVDYQSVCEPFGAPKQ 900
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HRSAYVFSVADILQIGMWATAAASILQQFLLSITFPRLLEAVEMEDDDFTASLSKQ 960
TEQTQYFPDNDKSGFSGVLDGNGCSRIFPHGKLANNTNLIFIMVBSKGTCPDTRL 1018
TEQTQYFPDNDKSGFSGVLDGNGCSRIFPHGKLANNTNLIFIMVBSKGTCPDTRL 1018

ndard; Protein; 1110 AA.

(updated)
(first entry)

m channel alpha-2 subunit.

nit; human; calcium channel; assay; detection;
tion; Lambert Eaton Syndrome; LES; diagnosis.

95US-0455543.

94US-0223305.

88US-0176899.

89WO-US01408.

20-FEB-1990; 90US-0482384.
08-NOV-1990; 90US-0603751.
30-NOV-1990; 90US-0620250.
15-AUG-1991; 91US-0745206.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX
XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
Williams ME;
XX WPI; 1998-456192/39.
XX N-PSDB; AAV42694.
XX
XX DNA encoding human calcium channel alpha 1B subunit protein -
XX useful for recombinant production of the channel for screening c
XX its modulators, and diagnosis of Lambert Eaton Syndrome
XX
XX Disclosure; Columns 131-138; 166pp; English.
XX
XX The present sequence represents the alpha-2 subunit of a human c
XX channel. Calcium channels are membrane-spanning, multi-subunit p
XX that allow controlled entry of calcium ions into cells. This lea
XX to depolarisation events required for muscle contraction. The re
XX subunit, when expressed with nucleic acids encoding the complete
XX channel, can be used in assays for the detection and characteris
XX compounds that modulate the channel. The DNA encoding the subun
XX be alternatively spliced when transcribed, giving more than one
XX the protein from the same transcript, each having slightly diffe
XX properties. In addition, the reactivity of the alpha 1 subunit w
XX molecules from the serum of an individual with Lambert Eaton Syn
XX (LES) can be used as a diagnostic for the disease.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX

XX Sequence 1110 AA;

Query Match 99.6%; Score 5326.5; DB 19; Length 1110;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 19;

QY 1 MAAGCLLALTTLTFLQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVN
DB 1 MAAGCLLALTTLTFLQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVN
QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAKVQAAHORE
DB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAKVQAAHORE
QY 121 EVVYNAKDDLOPEKNDSEPGSORIKPVFTEDANFGROIYSQHAHVHPTDIYEG
DB 121 EVVYNAKDDLOPEKNDSEPGSORIKPVFTEDANFGROIYSQHAHVHPTDIYEG
QY 181 NELNWTSSALDEVPKQNEEDPSLLQWVFGSATGLARYYPASPWVDSRTPNKIDI
DB 181 NELNWTSSALDEVPKQNEEDPSLLQWVFGSATGLARYYPASPWVDSRTPNKIDI
QY 241 RPWYIQGAASPKDMLILVDVSGSVSGITLKLIRTSVSEMLETSLDDDFVNVASFN
DB 241 RPWYIQGAASPKDMLILVDVSGSVSGITLKLIRTSVSEMLETSLDDDFVNVASFN
QY 301 VSCFQHLVQANVRNKKVLDKDAVNNTAKGIDTYKKGSFAFEQLLNTVNSRANCK
DB 301 VSCFQHLVQANVRNKKVLDKDAVNNTAKGIDTYKKGSFAFEQLLNTVNSRANCK
QY 361 FTDGGERAQEIIFNKYNKDKKVRPVSQGHNVYERPIQWMAKCNKGYVEIPSG
DB 361 FTDGGERAQEIIFNKYNKDKKVRPVSQGHNVYERPIQWMAKCNKGYVEIPSG
QY 421 INTQEVYLDVLGRPMVLADGAKAKQVQWNTVYLDALGLVITGTLPVFNITQGFEN
DB 421 INTQEVYLDVLGRPMVLADGAKAKQVQWNTVYLDALGLVITGTLPVFNITQGFEN
QY 481 NQILGVMGVDSLEDKRLTPRTLCPNGYFPAIDPNGYVLLHPNLQPKNPKSQBPVTL

GenCore version 5.1.6
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in search, using sw model

bruary 20, 2004, 16:47:50 ; Search time 37.5579 Seconds
(without alignments)
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i-10-090-827-14

43

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OSUM62

pop 10.0 , Gapext 0.5

.07863 seqs, 158726573 residues

its satisfying chosen parameters:

1107863

length: 0

length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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s the number of results predicted by chance to have a
er than or equal to the score of the result being printed,
ved by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description
00.0	1036	22	AAU01033		Human secreted sol
00.0	1036	22	AAB62257		Porcine calcium ch
00.0	1063	22	AAU01034		Human secreted sol
00.0	1063	22	AAB62258		Porcine calcium ch
00.0	1091	16	AAU01035		Human neuronal cal
00.0	1091	19	AAW63145		Human calcium chan
00.0	1091	21	AAB10576		Human calcium chan
00.0	1091	22	AAU01035		Human secreted sol
00.0	1091	22	AAB62259		Porcine calcium ch

10	5443	100.0	1091	23	AAE24789	Human cal
11	5439	99.9	1091	19	AAW37879	Human cal
12	5437	99.9	1091	14	AAW33553	Sequence
13	5423.5	99.6	1110	19	AAW63148	Human cal
14	5403.5	99.3	1086	16	AAW71013	Human neu
15	5403.5	99.3	1086	19	AAW63153	Human cal
16	5403.5	99.3	1086	21	AAU010587	Human cal
17	5403.5	99.3	1086	23	AAE24799	Human cal
18	5386.5	99.0	1084	16	AAW71015	Human neu
19	5386.5	99.0	1084	19	AAW63155	Human cal
20	5386.5	99.0	1084	21	AAU010589	Human cal
21	5386.5	99.0	1084	23	AAE24801	Human cal
22	5380	98.8	1036	22	AAU01029	Pig secre
23	5380	98.8	1036	22	AAU01029	Pig secre
24	5380	98.8	1036	22	AAU01030	Pig secre
25	5380	98.8	1063	22	AAU01030	Pig secre
26	5380	98.8	1063	22	AAU01031	Pig secre
27	5380	98.8	1069	22	AAU01031	Pig secre
28	5380	98.8	1091	22	AAU01027	Pig secre
29	5380	98.8	1091	22	AAU01027	Pig secre
30	5367	98.6	1103	16	AAW71012	Human neu
31	5367	98.6	1103	19	AAW63151	Human cal
32	5367	98.6	1103	21	AAU010586	Human cal
33	5367	98.6	1103	23	AAE24798	Human cal
34	5347	98.2	1079	19	AAW63154	Human cal
35	5347	98.2	1079	21	AAU010588	Human cal
36	5347	98.2	1079	23	AAE24800	Human cal
37	5346	98.2	1018	22	AAU01032	Human sec
38	5346	98.2	1018	22	AAU01032	Porcine c
39	5341	98.1	1079	16	AAW71014	Human neu
40	5288	97.2	1018	22	AAU01028	Pig secre
41	5288	97.2	1018	22	AAU01028	Porcine c
42	5229.5	96.1	1106	18	AAW37712	Rabbit sk
43	5229.5	96.1	1106	18	AAW18389	Rabbit sk
44	5229.5	96.1	1106	21	AAU01035	Rabbit sk
45	5208.5	95.7	1106	16	AAW73056	Rabbit sk

ALIGNMENTS

RESULT 1

AAU01033

ID AAU01033 standard; Protein; 1036 AA.

AC AAU01033;

XX

DT 04-JUL-2001 (first entry)

XX

XX

DE Human secreted soluble alpha2delta calcium channel subunit #13 F

XX

XX

KW Human; secreted calcium channel alpha2delta subunit; alpha2delta

KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel;

KW gabapentin; scintillation proximity assay; SPA; nickel flashplat

KW filter binding assay; wheat germ lectin flashplate assay.

XX

OS Homo sapiens.

XX

PN WO200119870-A2.

XX

PD 22-MAR-2001.

XX

PF 18-SEP-2000; 2000WO-EP09137.

XX

PR 16-SEP-1999; 99US-0397550.

XX

PA (WARN) WARNER LAMBERT CO.

XX

PI Brown JP, Bertelli F;

XX

DR WPI; 2001-235262/24.

XX

DR N-PSDB; AAS01424.

XX

nel alpha2delta subunits, useful in e.g. SPA assays, assays, Nickel Flashplate assays, Filter binding assays or ectin Flashplate assays -

ge 134-137; 160pp; English.

sequence represents human secreted calcium channel subunit #13 which is soluble and retains the functional ics of the full length or wild type alpha2delta subunit from which it is derived. The invention relates to truncated 2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins their affinity for radioactively labelled gabapentin. The subunit is 1 of the components of the heteromultimeric ndent calcium channel (VDCC) complexes present in neuronal onal tissues including heart and skeletal muscle. Numerous s of the human calcium channel alpha2delta subunits 01024 and AAU01032-AAU01038) and 5 soluble forms of the um channel alpha2delta subunits (AAU01027-AAU01031) are he secreted soluble alpha2delta subunit may be used in assays lation proximity assay (SPA), flashplate, nickel flashplate, ng or wheat germ lectin flashplate assays to detect or binding or interaction of a ligand (e.g. gabapentin, L-Allo-leucine, L-methionine, L-leucine, L-isoleucine, ermine and/or L-Phenylalanine) of a calcium channel subunit.

.036 AA;

.arity 100.0%; Score 5443; DB 22; Length 1036;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGCLLALTTLFOSLLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
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 OGEERAQEIIFNKNYKDKKVRFRFVSGQNYRERGPIQWACENKGYIIPISGAIR 420
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 LILGVMGVDSLEDIKBLTRPFTLCPNGYFPAIDPNGVLLHPLNLPKNKPSQBPVTL 540
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 LDALENDIKVEIRNKMIDGESGKFTRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600
 VLPTYSFYIKAKLEETITQARSKKGMKSETLKPONFESGYTFIAPRDYCNLDKI 660

601 ALVLPYTFYIKAKLEETITQARSKKGMKSETLKPONFESGYTFIAPRDY
 661 SDNNTFRLLNFNEFIDRKTPNPNFSCNADLINRVLLDAGFTNVLQVYWSKQKNI
 661 SDNNTFRLLNFNEFIDRKTPNPNFSCNADLINRVLLDAGFTNVLQVYWSKQKNI
 721 FVYTDGGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPG
 721 FVYTDGGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPG
 781 MVSKAIVEIYQGLKLPVAVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSD
 781 MVSKAIVEIYQGLKLPVAVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSD
 841 LDGQGLLMAHDDYTNQIGRFFGEIDPISLMRHLVNI SVYAFNKSXYDQVCEK
 841 LDGQGLLMAHDDYTNQIGRFFGEIDPISLMRHLVNI SVYAFNKSXYDQVCEK
 901 GAGHRSAYVPSVADILQIGWATAAAWSIIQQOFLLSLTPRLLLEAVEMEDDDFT
 901 GAGHRSAYVPSVADILQIGWATAAAWSIIQQOFLLSLTPRLLLEAVEMEDDDFT
 961 SCITEQTOYFEDNDSKSPGVLDGCGNSRIFHGEKLMNTNLI FIMVESKGTCPCI
 961 SCITEQTOYFEDNDSKSPGVLDGCGNSRIFHGEKLMNTNLI FIMVESKGTCPCI
 1021 QAEQTSQDPNPNCDMVK 1036
 1021 QAEQTSQDPNPNCDMVK 1036

RESULT 2

AA62257

ID AA62257 standard; Protein; 1036 AA.

AC AA62257;

DT 11-JUN-2001 (first entry)

DE Porcine calcium channel alpha2delta subunit.

KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral co
 nervous system disorder; pain; epilepsy; anxiety; pig.

OS Sus scrofa.

PN WO200120336-A2.

PD 22-MAR-2001.

PF 18-SEP-2000; 2000WO-EP09136.

PR 16-SEP-1999; 99US-0397549.

PA (WARN) WARNER LAMBERT CO.

PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee N

XX WPI: 2001-257902/26.

XX N-PSDB; AAF57561.

XX Competitive binding assay for screening ligands which bind a ce
 cortical voltage-dependent calcium channel alpha2delta-1 subun
 where the ligands identified are useful for treating disorders
 nervous system, including pain -

PS Claim 8; Page 132-135; 158pp; English.

XX The invention relates to a new method for screening ligands wh
 cerebral cortical voltage-dependent calcium channel alpha2delta
 preferably alpha2delta-1 subunit. The method comprises contacti
 secreted soluble recombinant alpha2delta-1 subunit with a ligan

063 AA;	100.0%; Score 5443; DB 22; Length 1063;	
larity 100.0%; Pred. No. 0;		
Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
3CLIALTLTLFQSLLIGSSSEPPSPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60		
3CLIALTLTLFQSLLIGSSSEPPSPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60		
YQDLYTVEPNARQLVBIARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120		
YQDLYTVEPNARQLVBIARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120		
YNAKDDLDPEKNDSEPGSRIKPFVIEDANFGRIQISYQAAHVIPTDIYEGSTIVL 180		
YNAKDDLDPEKNDSEPGSRIKPFVIEDANFGRIQISYQAAHVIPTDIYEGSTIVL 180		
WNTSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPMVDNSRTPNKIDLYDVR 240		
WNTSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPMVDNSRTPNKIDLYDVR 240		
YIQGAASPKDMLILVDVSGVSGLTTLKIRTSVSEMLETSDDDFVNVAASFNSNAQD 300		
YIQGAASPKDMLILVDVSGVSGLTTLKIRTSVSEMLETSDDDFVNVAASFNSNAQD 300		
FQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEGQLLNVTNVRANCNKIIML 360		
FQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEGQLLNVTNVRANCNKIIML 360		
3GERAQEI FNKYNKOKKVRFPFSVQHNRYERGPIONMACENKGYIYEIPSGAIR 420		
3GERAQEI FNKYNKOKKVRFPFSVQHNRYERGPIONMACENKGYIYEIPSGAIR 420		
DEYLDVLRPMVLADKAKOVQNTNVDLDALEGLVITGTLPVFNITQGFENKTNLK 480		
DEYLDVLRPMVLADKAKOVQNTNVDLDALEGLVITGTLPVFNITQGFENKTNLK 480		
ILGVMGVDSLEIDIKRLTPFTLCPNGYYPAIDPNGVLLHPLNLPKNPKSQBPVTL 540		
ILGVMGVDSLEIDIKRLTPFTLCPNGYYPAIDPNGVLLHPLNLPKNPKSQBPVTL 540		
DAELNDIKVEIRNKMIDGESBKTFTLTKSQDERYIDKGNRTYTPVNGTDYSL 600		
DAELNDIKVEIRNKMIDGESBKTFTLTKSQDERYIDKGNRTYTPVNGTDYSL 600		
LPYSFYIYKALEETITQARSKKGMKDETLKPNFESGYTPIAPRDYCNLDKI 660		
LPYSFYIYKALEETITQARSKKGMKDETLKPNFESGYTPIAPRDYCNLDKI 660		
NTBFLNFEFIDRKTNNPNSCNADLNRLVLLDAGFTNELVQNWYKOKNIGVKAR 720		
NTBFLNFEFIDRKTNNPNSCNADLNRLVLLDAGFTNELVQNWYKOKNIGVKAR 720		
TDGGITRVYKPEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780		
TDGGITRVYKPEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780		
QAVEIYIQGLKLPVAVGIKIDVNSIENETKTSIRDPCAGPVCDCKRNSDVMDCVI 840		
QAVEIYIQGLKLPVAVGIKIDVNSIENETKTSIRDPCAGPVCDCKRNSDVMDCVI 840		
3GFLMANHDDYTNQIGRPFGEIDPSLRHLVNI SVYAFNKSVDYQSVCEPGAAPQ 900		
3GFLMANHDDYTNQIGRPFGEIDPSLRHLVNI SVYAFNKSVDYQSVCEPGAAPQ 900		
IRSAVYPSVADIIQIGWATAAASIIQQFLSLTTPRLLEAVEMEDDDFTASLSQ 960		
IRSAVYPSVADIIQIGWATAAASIIQQFLSLTTPRLLEAVEMEDDDFTASLSQ 960		
TEOTQVFFDNDKSKFSGLDCGNCRI FHGEKLMNTNLIPIIMVESKGTCPCTPCI 1020		
TEOTQVFFDNDKSKFSGLDCGNCRI FHGEKLMNTNLIPIIMVESKGTCPCTPCI 1020		

Db	961	SCITEQTQVFFDNDKSKFSGLDCGNCRI FHGEKLMNTNLIPIIMVESKGTCPCTPCI
Qy	1021	QAEQTSFGPNPCDMVK 1036
Db	1021	QAEQTSFGPNPCDMVK 1036
RESULT 4		
AAB62258		
ID	AAB62258	standard; Protein; 1063 AA.
XX	AAB62258;	
XX	11-JUN-2001	(first entry)
XX	Porcine calcium channel alpha2delta subunit.	
DE	Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cor	
KW	nervous system disorder; pain; epilepsy; anxiety; pig.	
XX	Sus scrofa.	
XX	WO200120336-A2.	
XX	22-MAR-2001.	
XX	18-SEP-2000; 2000WO-EP09136.	
XX	16-SEP-1999; 99US-0397549.	
XX	(WARN) WARNER LAMBERT CO.	
XX	Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS	
XX	WPI; 2001-257902/26.	
XX	N-PSDB; AAF57562.	
PT	Competitive binding assay for screening ligands which bind a cer	
PT	cortical voltage-dependent calcium channel alpha2delta-1 subuni	
PT	where the ligands identified are useful for treating disorders o	
XX	nervous system, including pain -	
PS	Claim 8; Page 135-139; 158pp; English.	
XX	The invention relates to a new method for screening ligands whi	
CC	cerebral cortical voltage-dependent calcium channel alpha2delta	
CC	secreted soluble recombinant alpha2delta-1 subunit with a ligand	
CC	interest and a labelled compound which binds the subunit, follow	
CC	measuring the level of binding of the labelled compound to alpha	
CC	subunit. The method is useful for screening ligands, preferably	
CC	biologically active products that modulate a nervous system funci	
CC	which bind a cerebral cortical voltage-dependent calcium channel	
CC	alpha2delta-1 subunit. The ligands identified by the method are	
CC	for treating disorders of the nervous system, including pain, ep	
CC	and anxiety. The present sequence represents a porcine calcium c	
CC	alpha2delta subunit.	
XX	Sequence 1063 AA;	
Qy	Query Match 100.0%; Score 5443; DB 22; Length 1063;	
Db	Best Local Similarity 100.0%; Pred. No. 0;	
XX	Matches 1036; Conservative 0; Mismatches 0; Indels 0;	
Qy	1	MAAGCCLALTTLFQSLLIGSSSEPPSPSAVTIKSWDKMQEDLVTLAKTAGVNI
Db	1	MAAGCCLALTTLFQSLLIGSSSEPPSPSAVTIKSWDKMQEDLVTLAKTAGVNI
Qy	61	YEKYQDLYTVEPNARQLVBIARDIEKLLSNRSKALVSLALEAEKVQAAHQWREI
Db	61	YEKYQDLYTVEPNARQLVBIARDIEKLLSNRSKALVSLALEAEKVQAAHQWREI
Qy	121	EVVYNAKDDLDPEKNDSEPGSRIKPFVIEDANFGRIQISYQAAHVIPTDIYEGS

EYLDVLRPMVLADGKAKQVQWNTVYLLDALEGLVITGTLFVFNITGQFENKTNLK 480
 EYLDVLRPMVLADGKAKQVQWNTVYLLDALEGLVITGTLFVFNITGQFENKTNLK 480
 LGVGVDSLEDDIKELTRPFTLCPNGYYFAIDPNGYVLLHNPLOPKPKSQEPVTL 540
 LGVGVDSLEDDIKELTRPFTLCPNGYYFAIDPNGYVLLHNPLOPKPKSQEPVTL 540
 AELENDIKVEIRNMIDGESSEKTRTLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
 AELENDIKVEIRNMIDGESSEKTRTLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
 PTYSFYIKAKLEETITQARSKGKMDSETLKPDPNPEESGYTFIAPRDYCNLDKI 660
 PTYSFYIKAKLEETITQARSKGKMDSETLKPDPNPEESGYTFIAPRDYCNLDKI 660
 TEFLLNFNEFDTRKTPNNPSCNADLINRVLLDAGFTNELVQNYWSKQNIKGVKAR 720
 TEFLLNFNEFDTRKTPNNPSCNADLINRVLLDAGFTNELVQNYWSKQNIKGVKAR 720
 DGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNVYFTAPYFNKSGPGAYESGI 780
 DGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNVYFTAPYFNKSGPGAYESGI 780
 AVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPKAGPVCCKRNSDVMDCVI 840
 AVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPKAGPVCCKRNSDVMDCVI 840
 GFLLMANHDDVTNOIGRFFGSDPSLMRHLNIVSYAFNKSIDYQSVCEPGAAPKQ 900
 GFLLMANHDDVTNOIGRFFGSDPSLMRHLNIVSYAFNKSIDYQSVCEPGAAPKQ 900
 RSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
 RSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
 EQTYFPDNDKSGSVGLDCGNCRSRIFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
 EQTYFPDNDKSGSVGLDCGNCRSRIFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
 TSDGNPCDMVK 1036
 TSDGNPCDMVK 1036

Standard; Protein; 1091 AA.

(first entry)

channel alpha-2 subunit protein.

n channel; calcium channel subunit; diagnosis;
 Syndrome; calcium channel subunit alpha-2.

95US-0450562.

88US-0176899.
 90US-0482384.
 90US-0603751.
 90US-0620250.
 91US-0745206.
 92US-0868354.
 92US-0914231.

PR 11-AUG-1993; 93US-0105536.
 PR 05-NOV-1993; 93US-0149097.
 PR 07-FEB-1994; 94US-0193078.
 PR 04-APR-1994; 94US-0223305.
 PR 11-AUG-1994; 94US-0290012.
 PR 23-SEP-1994; 94US-0311363.
 PR 28-SEP-1994; 94US-0314083.
 PR 07-NOV-1994; 94US-0336257.
 PR 13-MAR-1995; 95US-0404950.
 XX
 PA (STBI-) SIBIA NEUROSCIENCES INC.
 XX
 PI Ellis SB, Williams ME, McCue AF, Harpold MM;
 XX
 XX WPI; 2000-548230/50.
 DR N-PSDB; AAA71707.
 XX
 PT Human calcium channel beta subunit polynucleotides, useful for
 PT producing recombinant eukaryotic cells and for diagnosing Lambert
 PT Syndrome -
 XX
 PS Example IV; Column 135-144; 153pp; English.
 XX
 CC This invention describes a novel isolated DNA molecule (I) compri
 CC sequence encoding a beta3-1 subunit of a human calcium channel.
 CC Nucleic acid probes comprising 14-30 contiguous nucleotides of
 CC beta 3 subunit encoding DNA are useful for isolation and cloning
 CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cell
 CC express heterologous calcium channel are useful for identifying c
 CC that modulate calcium channel activity and in assays for identify
 CC agonists and antagonists of calcium channel activity in humans. F
 CC calcium channel subunit or eukaryotic cells expressing the channe
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. Th
 CC sequence represents the human calcium channel alpha-2 subunit whi
 CC described in the method of the invention.
 XX
 SQ Sequence 1091 AA;

Query Match 100.0%; Score 5443; DB 21; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1036; Conservative 0; Mismatches 0; Indels 0; G

QY 1 MAACCLALATLTLFQSLILIGPSSEPPFPSPAVTIKSWDKMQEDLVTLAKTASGVNC
 DB 1 MAACCLALATLTLFQSLILIGPSSEPPFPSPAVTIKSWDKMQEDLVTLAKTASGVNC
 QY 61 YEKYQDLYTVEPNARQLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREI
 DB 61 YEKYQDLYTVEPNARQLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREI
 QY 121 EVVYNAKDDLDPKNDSEPGSQRIKPVFTEDANFGRIQISYQHAHVHIPTDIYEGS
 DB 121 EVVYNAKDDLDPKNDSEPGSQRIKPVFTEDANFGRIQISYQHAHVHIPTDIYEGS
 QY 181 NELNWTSALEDEVFKCNREEDPSLLMQVFGSATGLARYYPASPWPVNSRTPNKIDLY
 DB 181 NELNWTSALEDEVFKCNREEDPSLLMQVFGSATGLARYYPASPWPVNSRTPNKIDLY
 QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSSDDDFVNVASFNS
 DB 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSSDDDFVNVASFNS
 QY 301 VSCFQHLVQANVRNKKVLKDAVNIITAKGTTDYKKGFSFAFEQLLNINVRANCNK
 DB 301 VSCFQHLVQANVRNKKVLKDAVNIITAKGTTDYKKGFSFAFEQLLNINVRANCNK
 QY 361 FTDGGERAQEIIFNKYNKDKKVRVFRFSPVSGQHNRYERGIQWMACENKGYTYEIPSI
 DB 361 FTDGGERAQEIIFNKYNKDKKVRVFRFSPVSGQHNRYERGIQWMACENKGYTYEIPSI
 QY 421 INTQEYLDVLGRPMVLADGKAKQVQWNTVYLLDALEGLVITGTLFVFNITGQFENK
 DB 421 INTQEYLDVLGRPMVLADGKAKQVQWNTVYLLDALEGLVITGTLFVFNITGQFENK

1426.

PTSYIYKAKLEETITQARSKGKMDSETLKPDNFESGYTFIAPRDYCNLKI 660
 PTSYIYKAKLEETITQARSKGKMDSETLKPDNFESGYTFIAPRDYCNLKI 660
 TEFLNFNEFIDRKTNNPNCNADLINRVLLDAGFTNBLVQYWSKQNIKGVKAR 720
 TEFLNFNEFIDRKTNNPNCNADLINRVLLDAGFTNBLVQYWSKQNIKGVKAR 720
 DGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYYVFTAPYFNKSGPGAYESGI 780
 DGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYYVFTAPYFNKSGPGAYESGI 780
 AVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRSDPCAGPVCDCRNSDVMDCVI 840
 AVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRSDPCAGPVCDCRNSDVMDCVI 840
 GFLMANHDDYTQIGRFFGEIDPSLMRLHVNISVYAFNKSYDYQSVCEPGAAPKQ 900
 GFLMANHDDYTQIGRFFGEIDPSLMRLHVNISVYAFNKSYDYQSVCEPGAAPKQ 900
 RSAYVPSVADILQIGWATAAAMSILQOFLSLTPPRLLEAVEMEDDDFTASLSKQ 960
 RSAYVPSVADILQIGWATAAAMSILQOFLSLTPPRLLEAVEMEDDDFTASLSKQ 960
 EQTYFFDNDKSPGVLDGCGNCSRIHFGEKLMNTNLIIFIMVESKGTGCPDTRLII 1020
 EQTYFFDNDKSPGVLDGCGNCSRIHFGEKLMNTNLIIFIMVESKGTGCPDTRLII 1020
 TSDGPNPCDMVK 1036
 TSDGPNPCDMVK 1036

dard; Protein; 1091 AA.

(first entry)

um channel alpha2delta subunit.

el alpha2delta subunit; alpha2delta-1; cerebral cortex;
 m disorder; pain; epilepsy; anxiety; pig.

2.

2000WO-EP09136.

9US-0397549.

R LAMBERT CO.

Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;

902/26.

563.

inding assay for screening ligands which bind a cerebral
 age-dependent calcium channel alpha2-delta-1 subunit,
 and identified are useful for treating disorders of the
 m, including pain -

139-142; 158pp; English.

relates to a new method for screening ligands which bind a
 cal voltage-dependent calcium channel alpha2delta subunit,
 pha2delta-1 subunit. The method comprises contacting a

CC secreted soluble recombinant alpha2delta-1 subunit with a ligand
 CC interest and a labelled compound which binds the subunit, follow
 CC measuring the level of binding of the labelled compound to alpha
 CC subunit. The method is useful for screening ligands, preferably
 CC biologically active products that modulate a nervous system func
 CC which bind a cerebral cortical voltage-dependent calcium channel
 CC alpha2delta-1 subunit. The ligands identified by the method are
 CC for treating disorders of the nervous system, including pain, ep
 CC and anxiety. The present sequence represents a porcine calcium C
 CC alpha2delta subunit.

XX Sequence 1091 AA;

Query Match 100.0%; Score 5443; DB 22; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1036; Conservative 0; Mismatches 0; Indels 0;

QY 1 MAAGCLLALTTLTQSLIIGPSSSEPPFSAVTIKSVVDKMQEDLVTLAKTAGVNN
 Db 1 MAAGCLLALTTLTQSLIIGPSSSEPPFSAVTIKSVVDKMQEDLVTLAKTAGVNN
 QY 61 YEKYQDLTYVFPNNARQLVEIAARDIEKLSNRSKALVSLAEAEKVQAAHQRREI
 Db 61 YEKYQDLTYVFPNNARQLVEIAARDIEKLSNRSKALVSLAEAEKVQAAHQRREI
 QY 121 EYVYNAXDDLDPKNDSEPGSQRIKPVFIEDANFGROI SYOHAHVHIPTDIYEG
 Db 121 EYVYNAXDDLDPKNDSEPGSQRIKPVFIEDANFGROI SYOHAHVHIPTDIYEG
 QY 181 NELNWTISALDEVFKKREEDPSLLWQVFGSATGLARYYPASPVDNSRTPNKIDL
 Db 181 NELNWTISALDEVFKKREEDPSLLWQVFGSATGLARYYPASPVDNSRTPNKIDL
 QY 241 RPWYIOGAASPKDMLILVDVSGSVSGLTLKLRISVSEMLETSLDDDFVNVASFNI
 Db 241 RPWYIOGAASPKDMLILVDVSGSVSGLTLKLRISVSEMLETSLDDDFVNVASFNI
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGPSFAFEQLLNNVSRANCI
 Db 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGPSFAFEQLLNNVSRANCI
 QY 361 FTDGGEERAQEI FNKYNKKVRVFRFSGVQHNYERGEPIOMMACENKGYIYEIPSI
 Db 361 FTDGGEERAQEI FNKYNKKVRVFRFSGVQHNYERGEPIOMMACENKGYIYEIPSI
 QY 421 INTOEYLDVLGRPMVLADGKAKQVQWNTNVYLDALGLVITGTLPVFNITQGFENI
 Db 421 INTOEYLDVLGRPMVLADGKAKQVQWNTNVYLDALGLVITGTLPVFNITQGFENI
 QY 481 NQLILGYMGVDVSLIEDIKRLTPRFTLCPNGYYPALDPNGYVLLHPNLPKPKSQE
 Db 481 NQLILGYMGVDVSLIEDIKRLTPRFTLCPNGYYPALDPNGYVLLHPNLPKPKSQE
 QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTVYTPVANGT
 Db 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTVYTPVANGT
 QY 601 ALVLPYTSFYIYKAKLBETITQARSKGKMDSETLKPDNFESGYTFIAPRDYCN
 Db 601 ALVLPYTSFYIYKAKLBETITQARSKGKMDSETLKPDNFESGYTFIAPRDYCN
 QY 661 SDNNTFLLNPFNEFIDRKTNNPNCNADLINRVLLDAGFTNBLVQYWSKQNIK
 Db 661 SDNNTFLLNPFNEFIDRKTNNPNCNADLINRVLLDAGFTNBLVQYWSKQNIK
 QY 721 FVVTDDGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYYVFTAPYFNKSGPGAY
 Db 721 FVVTDDGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYYVFTAPYFNKSGPGAY
 QY 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRSDPCAGPVCDCRNSDVM
 Db 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRSDPCAGPVCDCRNSDVM

[illegible]

Standard; Protein; 1091 AA.

(first entry)

n channel alpha 2b subunit protein.

um channel protein; therapeutic; autoimmune disease;
ambert Eaton Syndrome; alpha 2b subunit.

95US-0450272.

89WO-US01408.
90US-0603751.
92US-0914231.
90US-0482384.
90US-0620250.
91US-0745206.
92WO-US06903.
93US-0105536.
93US-0149097.
94US-0193078.
94US-0311363.
94US-0336257.
95US-0404354.

K & CO INC.

Ellis SB, Williams ME, McCue AF;

0318/50.
3959.

cells expressing a functional heterologous human calcium encoding nucleic acid isolated from human cerebellum for and to diagnose Lambert Eaton Syndrome -

Column 137-144; 154pp; English.

invention relates to novel human calcium channel proteins nucleotides encoding such proteins. The invention also relates to cells expressing a functional heterologous human calcium channel subunits, α_1 , α_2 , β , and γ subunits. The eukaryotic cells are useful for screening for potential calcium channel antagonists or select compounds that have potential as disease or tissue-specific therapeutic agents. The subunits may be used in diagnostic and therapeutic applications. The invention also relates to the autoimmune disease Lambert Eaton Syndrome. The present

CC	sequence is human calcium channel alpha 2b subunit protein.											
XX												
SQ	Sequence	1091 AA;										
	Query Match	100.0%;	Score	5443;	DB	23;	Length	1091;				
	Best Local Similarity	100.0%;	Pred. No.	0;								
	Matches 1036;	Conservative	0;	Mismatches	0;	Indels	0;					
QY	1	MAAGCLLALT	LTLFQSL	LIGSSSEPP	SPSATTIKSW	VDKMQED	LVT	LAKTAGS	VN			
Db	1	MAAGCLLALT	LTLFQSL	LIGSSSEPP	SPSATTIKSW	VDKMQED	LVT	LAKTAGS	VN			
QY	61	YKYYQDLV	TVPNNA	QLVETAA	RIEKL	SNKSLV	LALAE	KVQAAH	QWRE			
Db	61	YKYYQDLV	TVPNNA	QLVETAA	RIEKL	SNKSLV	LALAE	KVQAAH	QWRE			
QY	121	EVVYNA	KDDLPE	KNDSE	PGSQRIK	PVFIED	ANF	QRQISY	QAAVHI	PTDIYEG		
Db	121	EVVYNA	KDDLPE	KNDSE	PGSQRIK	PVFIED	ANF	QRQISY	QAAVHI	PTDIYEG		
QY	181	NELN	WTSALD	EVFK	KNREED	PSLLQ	WFG	SATGLA	RYPAS	PWVWNSR		
Db	181	NELN	WTSALD	EVFK	KNREED	PSLLQ	WFG	SATGLA	RYPAS	PWVWNSR		
QY	241	RPWY	TQGAAS	PKDML	LLVD	YSGS	VGITL	KIR	TSVSE	LETLS		
Db	241	RPWY	TQGAAS	PKDML	LLVD	YSGS	VGITL	KIR	TSVSE	LETLS		
QY	301	VSCFO	HLVQ	ANVR	NKKVL	KDA	VNNIT	AKGT	TDYK	KGFS		
Db	301	VSCFO	HLVQ	ANVR	NKKVL	KDA	VNNIT	AKGT	TDYK	KGFS		
QY	361	FTDGE	EAAQEI	FN	KIN	KDKV	RFR	FSV	QHN	VERG		
Db	361	FTDGE	EAAQEI	FN	KIN	KDKV	RFR	FSV	QHN	VERG		
QY	421	INTQ	BYLD	VLGR	PW	LAD	KAKQ	VO	WNT	NYV		
Db	421	INTQ	BYLD	VLGR	PW	LAD	KAKQ	VO	WNT	NYV		
QY	481	NOL	IL	GV	MG	VD	SLE	D	KRL	TP		
Db	481	NOL	IL	GV	MG	VD	SLE	D	KRL	TP		
QY	541	DFL	DAE	LE	ND	I	KV	IR	NK	MD		
Db	541	DFL	DAE	LE	ND	I	KV	IR	NK	MD		
QY	601	ALV	PT	S	F	Y	I	K	A	L		
Db	601	ALV	PT	S	F	Y	I	K	A	L		
QY	661	SDNN	T	E	F	L	L	N	E	F		
Db	661	SDNN	T	E	F	L	L	N	E	F		
QY	721	FV	TD	D	G	G	I	T	R	Y		
Db	721	FV	TD	D	G	G	I	T	R	Y		
QY	781	MV	S	K	A	V	E	I	I	O		
Db	781	MV	S	K	A	V	E	I	I	O		
QY	841	L	D	D	G	F	L	L	M	A		
Db	841	L	D	D	G	F	L	L	M	A		
QY	901	G	A	G	H	R	S	A	V	P		
Db	901	G	A	G	H	R	S	A	V	P		
QY	961	S	C	I	T	E	O	T	O	Y		

|||||
 EQTYFFDNDKSFSGVLDCGNCRIFFHGEKLMNTLIFIMVESKGTCCCTRLII 1020

TS DGNPCDMVK 1036
 |||||
 TS DGNPCDMVK 1036

Standard; Protein; 1091 AA.

(first entry)

channel a2d subunit.

el; human; central nervous system disorder;
 syndrome; diagnosis; therapy.

97WO-US16146.

96US-0713118.

CAN HOME PROD CORP.

anco R, Shuey DJ;

325/18.

060.

human neuronal calcium channel subunit(a) - useful for
 and treatment of central nervous system disorders, e.g.
 syndrome

Fig 2; 89pp; English.

ide comprises the a2d subunit of the human neuronal
 el. cDNA clones (see AAV29059-61) encoding the a1B
 AAW37878), the a2d subunit and a b3 subunit (see AAW37880)
 related. These have been inserted into expression
 are stably expressed in transformed cell lines. The
 cells show omega-conotoxin GVIA binding activity. The
 ototoxin GVIA toxin sensitive potassium-stimulated
 ke, indicating that the proteins expressed by the
 ible of forming a functioning calcium channel.
 encoding the 3 subunits, as well as vectors, host
 hods of isolating nucleic acids encoding related
 els are disclosed. Fusion proteins incorporating the
 ins, antibodies, and assays for identifying agents
 calcium channel activity are also provided. Such
 used to treat certain central nervous system
 altering calcium channel activity. Methods of
 eases associated with particular calcium channels,
 art-Eaton syndrome, are disclosed.

091 AA;

99.9%; Score 5439; DB 19; Length 1091;

larity 99.9%; Pred. No. 0;

conservative 0; Mismatches 1; Indels 0; Gaps 0;

LCALLATLTLFQSLILGPSSEEPFSAVTIKSWVDKMQEDLVTLAKTAGSVNLVDI 60

LCALLATLTLFQSLILGPSSEEPFSAVTIKSWVDKMQEDLVTLAKTAGSVNLVDI 60

QY 61 YEKYQDLYTVENPNARQLVEIAARDIEKLLSNRSLKALVSLALEAKVQAAHWRRE
 DB 61 YEKYQDLYTVENPNARQLVEIAARDIEKLLSNRSLKALVSLALEAKVQAAHWRRE
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIISYOHAAVHIPTDIYEG
 DB 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIISYOHAAVHIPTDIYEG
 QY 181 NELNWTSSALDEVFKKREDEPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
 DB 181 NELNWTSSALDEVFKKREDEPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
 QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRITSVSEMLETLSDDDDFNVASFN
 DB 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRITSVSEMLETLSDDDDFNVASFN
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFQQLLNYNVSRANCN
 DB 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFQQLLNYNVSRANCN
 QY 361 FTDGGEERAQELFNKYNDKKVRVFRFSVGOHNYERGPLOMACENKGYIYIIPS
 DB 361 FTDGGEERAQELFNKYNDKKVRVFRFSVGOHNYERGPLOMACENKGYIYIIPS
 QY 421 INTOEYLDVLGRPMVLADGKAKQVQMTNVYLDALGLVITGLTFVFNITGQFEN
 DB 421 INTOEYLDVLGRPMVLADGKAKQVQMTNVYLDALGLVITGLTFVFNITGQFEN
 QY 481 NQLILGVNGVDVSLSDIIRKLTPRFTLCPNGYYPADPNQYVLLHNPLOPKNPKSQ
 DB 481 NQLILGVNGVDVSLSDIIRKLTPRFTLCPNGYYPADPNQYVLLHNPLOPKNPKSQ
 QY 541 DFLDAELENDDIIVEIRNMIDGESSEKTRTLVKSQDERYIDKGNRTYTWTPVNG
 DB 541 DFLDAELENDDIIVEIRNMIDGESSEKTRTLVKSQDERYIDKGNRTYTWTPVNG
 QY 601 ALVLPYSFYIYIKAKLEETITQARSKKGKMDSETLKPDNPFESGYTFIAPRDYCI
 DB 601 ALVLPYSFYIYIKAKLEETITQARSKKGKMDSETLKPDNPFESGYTFIAPRDYCI
 QY 661 SDNTEFLINFEPIIDRKTNNPNSCNADLINRVLLDAGFTNBLVONTYWSKQNNIK
 DB 661 SDNTEFLINFEPIIDRKTNNPNSCNADLINRVLLDAGFTNBLVONTYWSKQNNIK
 QY 721 FVVTGGITRVVYKAGENQENPETYSDSFYKRSILDNDNVYFTAPYFNKSGPGA
 DB 721 FVVTGGITRVVYKAGENQENPETYSDSFYKRSILDNDNVYFTAPYFNKSGPGA
 QY 781 MYSKAVEIYIQGLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVI
 DB 781 MYSKAVEIYIQGLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVI
 QY 841 LDGCGFLLMANHDDYTNGIRPFGEIDPSLMHNLNIVSYAFNKSYDYQSVCEPG
 DB 841 LDGCGFLLMANHDDYTNGIRPFGEIDPSLMHNLNIVSYAFNKSYDYQSVCEPG
 QY 901 GAGHSAYVPSVADILQIGWATAAWSILOQFLLSLTFPRLEAEMEDDDFTFA
 DB 901 GAGHSAYVPSVADILQIGWATAAWSILOQFLLSLTFPRLEAEMEDDDFTFA
 QY 961 SCITEQTQYFFDNDKSFSGVLDCGNCRSRIIFHGEKLMNTLIFIMVESKGTCCPD
 DB 961 SCITEQTQYFFDNDKSFSGVLDCGNCRSRIIFHGEKLMNTLIFIMVESKGTCCPD
 QY 1021 QABQTS DGNPCDMVK 1036
 DB 1021 QABQTS DGNPCDMVK 1036

RESULT 12

AAR33553

ID AAR33553 standard; Protein; 1091 AA.

XX

(updated)
(first entry)

the alpha 2 human calcium channel subunit.

m channel subunit; diagnosis; agonist; antagonist;
n syndrome.

92WO-US06903.

91US-0745206.
92US-0868354.

INST BIOTECHNOLOGY IND ASSOC.

Ellis SB, Feldman DH, Harpold MM, McCue AF;
3936/11.
7821.

specific human calcium channel sub-units - used for
calcium channel agonists and antagonists and
ambert Eaton syndrome

Page 134-138; 150pp; English.

a human neuronal calcium channel alpha 2 subunit was
m a human genomic DNA library probed under low and high
conditions with a fragment of DNA encoding the rabbit
cle calcium channel alpha 2 subunit. The fragment
leotides having a sequence corresponding to the
skeletal muscle calcium channel alpha 2 subunit cDNA.
identified splice variants of the human calcium alpha
anscript. In particularly preferred embodiments, the
the alpha 2 subunit is produced by alternative
f a primary transcript that includes DNA encoding the
set forth in AAR33553 and the DNA of AAQ37823 inserted
eotides 1624 and 1625 of AAQ37821.
25-MAR-2003 to correct PN field.)

091 AA;
Larity 99.9%; Score 5437; DB 14; Length 1091;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GCLLALTLTFLQSLIGSPSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
GCLLALTLTFLQSLIGSPSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60

YQDLYTVPPNNARQLVEIARDIEKLISNRSKALVSLALEAEKVQAAHQWRDPASN 120
YQDLYTVPPNNARQLVEIARDIEKLISNRSKALVSLALEAEKVQAAHQWRDPASN 120

YYNKADDLDPKNDSEPGSQRIKPVFTEDANFGQISYQHAHVHPTDIVEGSTITVL 180
YYNKADDLDPKNDSEPGSQRIKPVFTEDANFGQISYQHAHVHPTDIVEGSTITVL 180

NWTSALDEVFKKNEEPPSLIQVFGSATGLARYYPASPVVDNSRTNPKIDLYDVR 240
NWTSALDEVFKKNEEPPSLIQVFGSATGLARYYPASPVVDNSRTNPKIDLYDVR 240

YIQGAASPOMLILVDVSGSVGLTLKLRISVSEMLETLSDDDDFNVASFNQAQD 300

Db 241 RPWYIQGAASPOMLILVDVSGSVGLTLKLRISVSEMLETLSDDDDFNVASFN
Qy 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFQOLLNYSRANCN
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFQOLLNYSRANCN
Qy 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVQGHNYERGP IQMMACENKGYEYIIPS
Db 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVQGHNYERGP IQMMACENKGYEYIIPS
Qy 421 INTQEYLDVLGRPMVLGAKAKQVQWNTVYLDALGLGLVITGLTPVFNITGQFEN
Db 421 INTQEYLDVLGRPMVLGAKAKQVQWNTVYLDALGLGLVITGLTPVFNITGQFEN
Qy 481 NQLILGVMGVDVLSLEDKRLTPFTLCPNGYYFAIDPNGVYLLHPNLQPNPKSQ
Db 481 NQLILGVMGVDVLSLEDKRLTPFTLCPNGYYFAIDPNGVYLLHPNLQPNPKSQ
Qy 541 DFLDAELENDAIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTTWTPVNG
Db 541 DFLDAELENDAIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTTWTPVNG
Qy 601 ALVLPTYSFYIKAKLEETITQARSKKGKMKDSETLKPDNFESGYTFIAPRDYC
Db 601 ALVLPTYSFYIKAKLEETITQARSKKGKMKDSETLKPDNFESGYTFIAPRDYC
Qy 661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNGLVQVNSKQKNIK
Db 661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNGLVQVNSKQKNIK
Qy 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKXSLDNDNYVFTAPYFNKSGPGA
Db 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKXSLDNDNYVFTAPYFNKSGPGA
Qy 781 MYSKAYEIIYQGLKLPKPAVVGKIDVNSWIENFTKTSIRDPKAGPVCDCKRNSDV
Db 781 MYSKAYEIIYQGLKLPKPAVVGKIDVNSWIENFTKTSIRDPKAGPVCDCKRNSDV
Qy 841 LDGSGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYOSVCEPG
Db 841 LDGSGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYOSVCEPG
Qy 901 GAGHSAYVPSVADIIQIGWATAAAWSILQQFLLSLTTPRLLEAVEMEDDDFTFA
Db 901 GAGHSAYVPSVADIIQIGWATAAAWSILQQFLLSLTTPRLLEAVEMEDDDFTFA
Qy 961 SCITEQTQYFFDNDKSFSGVLDGCGNSRIFHGEKLMNTNLIIFIMVESKGTCPCL
Db 961 SCITEQTQYFFDNDKSFSGVLDGCGNSRIFHGEKLMNTNLIIFIMVESKGTCPCL
Qy 1021 QAEQTS DGNPCDMVK 1036
Db 1021 QAEQTS DGNPCDMVK 1036

RESULT 13
AAW63148
ID AAW63148 standard; Protein; 1110 AA.
XX AAW63148;
XX
DT 25-MAR-2003 (updated)
DT 12-OCT-1998 (first entry)
XX Human calcium channel alpha-2 subunit.
XX Alpha-2 subunit; human; calcium channel; assay; detection;
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.
XX Homo sapiens.
XX US95792846-A.
PN

95US-0455543.
94US-0223305.
88US-0176899.
89WO-US01408.
90US-0482384.
90US-0603751.
90US-0620250.
91US-0745206.
NEUROSCIENCES INC.
llie SB, Feidman DH, Harpold MM, McCue AF;
192/39.
594.
human calcium channel alpha 1B subunit protein -
combinant production of the channel for screening of
3, and diagnosis of Lambert Eaton Syndrome
columns 131-138; 166pp; English.
sequence represents the alpha-2 subunit of a human calcium
ium channels are membrane-spanning, multi-subunit proteins
attrolled entry of calcium ions into cells. This leads
ion events required for muscle contraction. The recombinant
expressed with nucleic acids encoding the complete calcium
be used in assays for the detection and characterization of
e modulate the channel. The DNA encoding the subunits can
ely spliced when transcribed, giving more than one form of
rom the same transcript, each having slightly different
a addition, the reactivity of the alpha 1 subunit with IgG
n the serum of an individual with Lambert Eaton Syndrome
used as a diagnostic for the disease.
5-MAR-2003 to correct PR field.)
10 AA;
arity 99.6%; Score 5423.5; DB 19; Length 1110;
nservative 0; Mismatches 0; Indels 19; Gaps 1;
CLALTLTLFQSLILIGPSSREPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
CLALTLTLFQSLILIGPSSREPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
QDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAKVQAARHOREDFASN 120
QDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAKVQAARHOREDFASN 120
YNAKDDLDPKNDSEPSQRIKPVIFEDANFGROIYQHAHVHPTDIYEGSTIVL 180
YNAKDDLDPKNDSEPSQRIKPVIFEDANFGROIYQHAHVHPTDIYEGSTIVL 180
WTSALDVEFKKREEDPSLLMQVFGSATGLARYYPASPVDNSRTPNKIDLYDVR 240
WTSALDVEFKKREEDPSLLMQVFGSATGLARYYPASPVDNSRTPNKIDLYDVR 240
IQGAASPKDMLILVDVSGVSGTLKLIKRTSVSEMLTSLDDDFNVASFNNAQD 300
IQGAASPKDMLILVDVSGVSGTLKLIKRTSVSEMLTSLDDDFNVASFNNAQD 300
QHLVQANVRNKKVLKDAVNNITAKGIDTYKGFSAFQELLNVNVRANCKMIIML 360
QHLVQANVRNKKVLKDAVNNITAKGIDTYKGFSAFQELLNVNVRANCKMIIML 360
GEERAQEI FNKYNDKKVRFVSGVGHNYERGPIQWMACENKGYVEIPSI 420

361 FTGGGERAQEI FNKYNDKKVRFVSGVGHNYERGPIQWMACENKGYVEIPSI
421 INTQEYLDVLGRPMVLADKAKQVQWNTNVYLDALGLVITGLPVNITQGFENK
421 INTQEYLDVLGRPMVLADKAKQVQWNTNVYLDALGLVITGLPVNITQGFENK
481 NQILILGVMGVDSLEDIKRLTPRTFLCPNGYYFAIDPNGVVLHPNLQPK-----
481 NQILILGVMGVDSLEDIKRLTPRTFLCPNGYYFAIDPNGVVLHPNLQPKIGVGI
531 -----NPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESSEKTFRLVKSQD
541 LRKERPNIQPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESSEKTFRLVKSQD
582 DGNRTYTTWTPVNGTDYSLALVLPYTSFYIYKAKLEETITQARSKGKMKDSETLK
601 DGNRTYTTWTPVNGTDYSLALVLPYTSFYIYKAKLEETITQARSKGKMKDSETLK
642 EESGYTFIAPRDYCNLDKISDNNTEFLNFEFIDRKTNNPNSCNADLINRVLLDA
661 EESGYTFIAPRDYCNLDKISDNNTEFLNFEFIDRKTNNPNSCNADLINRVLLDA
702 ELQNVYWSKQNIKGKVFVTDGGITRVYPKEAGENWOENPETYEDSFYKRSLD
721 ELQNVYWSKQNIKGKVFVTDGGITRVYPKEAGENWOENPETYEDSFYKRSLD
762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTS
781 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTS
822 CAGPVCDCKNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNI
841 CAGPVCDCKNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNI
882 FNKSYDYQSCECAAPKQAGHRSAYVPSVADILQIGMWATAAASILQOFLLSL
901 FNKSYDYQSCECAAPKQAGHRSAYVPSVADILQIGMWATAAASILQOFLLSL
942 LLRAVENEDDDFTASLSKQSCITEQTQYFFDNDSKSPSGVLDCNCRSRIFHGEKLM
961 LLRAVENEDDDFTASLSKQSCITEQTQYFFDNDSKSPSGVLDCNCRSRIFHGEKLM
1002 IFIMVESKGTCPDCTRLLIQAEQTS DGNPCDMVK 1036
1021 IFIMVESKGTCPDCTRLLIQAEQTS DGNPCDMVK 1055
RESULT 14
AAR71013
ID AAR71013 standard; Protein; 1086 AA.
XX AAR71013;
AC AAR71013;
XX AAR71013;
DT 25-MAR-2003 (updated)
DT 01-DEC-1995 (first entry)
XX Human neuronal calcium channel subunit alpha 2c.
DE Calcium channel subunit; antagonist; agonist; diagnosis;
KW Lambert Eaton Syndrome.
XX Homo sapiens.
XX WO9504822-A1.
XX 16-FEB-1995.
XX 11-AUG-1994; 94WO-US09230.
XX 11-AUG-1993; 93US-0105536.
XX 05-NOV-1993; 93US-0149097.
XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.

192/39.
702.

human calcium channel alpha 1B sub:unit protein -
combinant production of the channel for screening of
s, and diagnosis of Lambert Eaton Syndrome

mus 293-300; 156pp; English.

sequence represents the alpha-2c subunit of a human calcium
ium channels are membrane-spanning, multi-subunit proteins
ntrolled entry of calcium ions into cells. This leads
tion events required for muscle contraction. The recombinant
expressed with nucleic acids encoding the complete calcium
be used in assays for the detection and characterisation of
it modulate the channel. The DNA encoding the subunits can
ely spliced when transcribed, giving more than one form of
rom the same transcript, each having slightly different
n addition, the reactivity of the alpha 1 subunit with IgG
m the serum of an individual with Lambert Eaton Syndrome
used as a diagnostic for the disease.
(5-MAR-2003 to correct PR field.)

186 AA;

99.3%; Score 5403.5; DB 19; Length 1086;
larity 99.5%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 5; Gaps 1;

LCLLALTLTLFQSLILGPSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
LCLLALTLTLFQSLILGPSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
QDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALRAEKVQAAHQWREDFASN 120
QDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALRAEKVQAAHQWREDFASN 120
YNAKDDILPEKNDSPGSGRIKPVFTEDANFGROI SQYHAAVHIPTDIYEGSTIVL 180
YNAKDDILPEKNDSPGSGRIKPVFTEDANFGROI SQYHAAVHIPTDIYEGSTIVL 180
WTSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
WTSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
TQGAASPDKMLTLVDVSGSVGLTLKILRTSVSEMLETISDDDFVNVASFNSNAQD 300
TQGAASPDKMLTLVDVSGSVGLTLKILRTSVSEMLETISDDDFVNVASFNSNAQD 300
QHLVQANVRNKKVLQDAVNNITAKGIDTVYKGFSPAPEQLLNVSRANCKLIIML 360
QHLVQANVRNKKVLQDAVNNITAKGIDTVYKGFSPAPEQLLNVSRANCKLIIML 360
QGEERAQEIFNKYNKDKKVRFRFSVQGHNYERGPQIMWACENKGYTIEPSIGAIR 420
QGEERAQEIFNKYNKDKKVRFRFSVQGHNYERGPQIMWACENKGYTIEPSIGAIR 420
DEYLDVLRPMVLQAGKAKQVQWTVNVYLDALIELGLVITGTLPVFNITGQPFKNKMLK 480
DEYLDVLRPMVLQAGKAKQVQWTVNVYLDALIELGLVITGTLPVFNITGQPFKNKMLK 480
ILGVMGVDVLSLEDIKRLTPRTLCPNGYFYFAIDPNGVYLLHPNLQPKPKSQBPVTL 540
ILGVMGVDVLSLEDIKRLTPRTLCPNGYFYFAIDPNGVYLLHPNLQPKPKSQBPVTL 540
LAELENDIKVEIRNKMIDGSSGEKFTRLVKSQDERYIDKGNRTYTWTVPVNGTDYSL 600
LAELENDIKVEIRNKMIDGSSGEKFTRLVKSQDERYIDKGNRTYTWTVPVNGTDYSL 595
LPTYSFYIKAKLEETITQARSKKGKMKOSTLKPDPNPFESGYTFIAPRDYCNLDIKI 660
LPTYSFYIKAKLEETITQARSKKGKMKOSTLKPDPNPFESGYTFIAPRDYCNLDIKI 655

QY	661	SDNNTEFLLNNEFI	DRKTPNNPSCNADL	INRVLLDAGFTNEL	VQNYNSKQXN	KIK
Db	656	SDNNTEFLLNNEFI	DRKTPNNPSCNADL	INRVLLDAGFTNEL	VQNYNSKQXN	KIK
QY	721	FVWTDGGITR	YYPKEAGENQEN	PETVEDSFYKRS	LDNDNYFT	PAPYFNKSGFGA
Db	716	FVWTDGGITR	YYPKEAGENQEN	PETVEDSFYKRS	LDNDNYFT	PAPYFNKSGFGA
QY	781	MVSKAVEI	YIOGKLLKPA	VGVGIKIDVNS	WTENFTKTS	IRDPCAGPVCDCRNSDVI
Db	776	MVSKAVEI	YIOGKLLKPA	VGVGIKIDVNS	WTENFTKTS	IRDPCAGPVCDCRNSDVI
QY	841	LDGCGFLMA	NHDDYTQIO	IGRPFGEIDPS	LMRHLVNI	SVYAFNKSVDYOSVCEPGI
Db	836	LDGCGFLMA	NHDDYTQIO	IGRPFGEIDPS	LMRHLVNI	SVYAFNKSVDYOSVCEPGI
QY	901	GAGHRS	AVPVS	VADILOIGW	ATAA	WSILQQFLLSLTFPRLLLEAVEMEDDDFTA
Db	896	GAGHRS	AVPVS	VADILOIGW	ATAA	WSILQQFLLSLTFPRLLLEAVEMEDDDFTA
QY	961	SCITEQ	TOYFPD	NSKFS	GVLD	CNCSRIFHGEKLMNTNLI
Db	956	SCITEQ	TOYFPD	NSKFS	GVLD	CNCSRIFHGEKLMNTNLI
QY	1021	QAEQTS	DGPN	CDMWK	1036	
Db	1016	QAEQTS	DGPN	CDMWK	1031	

Search completed: February 20, 2004, 16:55:15
Job time : 40.5579 secs

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in search, using sw model

bruary 20, 2004, 16:53:09 ; Search time 18.0748 Seconds
(without alignments)
2488.357 Million cell updates/sec

10-090-827-15

99

MAAGCLLALTLFQSLIG.....PDVCFDNNVLEDYDCGGVS 1063

OSUM62

pop 10.0 , Gapext 0.5

8717 seqs, 42310858 residues

ts satisfying chosen parameters: 328717

gth: 0

gth: 2000000000

inimum Match 0%

aximum Match 100%

isting first 45 summaries

ssued Patents AA:*

/cgn2_6/ptodata/1/1aa/5A_COMB.pap:*

/cgn2_6/ptodata/1/1aa/5B_COMB.pap:*

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/cgn2_6/ptodata/1/1aa/6B_COMB.pap:*

/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pap:*

/cgn2_6/ptodata/1/1aa/backfiles.pap:*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

ery	tch	Length	DB	ID	Description
0.0	0.0	1091	1	US-07-745-206A-25	Sequence 25, Appl
0.0	0.0	1091	1	US-08-455-543A-52	Sequence 52, Appl
0.0	0.0	1091	2	US-08-223-305C-52	Sequence 52, Appl
0.0	0.0	1091	2	US-08-311-363-25	Sequence 25, Appl
9.9	9.9	1091	3	US-08-713-118-4	Sequence 4, Appl
9.9	9.9	1091	3	US-09-452-007-4	Sequence 4, Appl
9.3	9.3	1086	1	US-08-455-543A-54	Sequence 54, Appl
9.3	9.3	1086	2	US-08-223-305C-54	Sequence 54, Appl
9.0	9.0	1084	1	US-08-455-543A-56	Sequence 56, Appl
9.0	9.0	1084	2	US-08-223-305C-56	Sequence 56, Appl
8.6	8.6	1103	1	US-08-455-543A-53	Sequence 53, Appl
8.6	8.6	1103	2	US-08-223-305C-53	Sequence 53, Appl
8.3	8.3	1079	1	US-08-455-543A-55	Sequence 55, Appl
8.3	8.3	1079	2	US-08-223-305C-55	Sequence 55, Appl
6.2	6.2	1106	1	US-08-435-675B-5	Sequence 5, Appl
5.9	5.9	1106	1	US-08-336-257A-8	Sequence 8, Appl
1.7	1.7	1086	6	5386025-8	Patent No. 5386025
13.7	13.7	1145	4	US-09-470-443-2	Sequence 2, Appl
13.7	13.7	1145	4	US-09-470-443-4	Sequence 4, Appl
13.3	13.3	1076	4	US-09-470-443-6	Sequence 6, Appl
16.1	16.1	508	1	US-08-435-675B-6	Sequence 6, Appl
3.3	3.3	885	3	US-09-074-579-5	Sequence 5, Appl
3.3	3.3	885	3	US-09-388-774-5	Sequence 5, Appl
3.3	3.3	885	3	US-09-388-774-5	Sequence 5, Appl
2.8	2.8	946	3	US-09-074-579-3	Sequence 3, Appl
2.8	2.8	946	3	US-09-388-774-3	Sequence 3, Appl
2.8	2.8	894	4	US-09-071-035-248	Sequence 248, App
2.8	2.8	962	4	US-09-071-035-246	Sequence 246, App

28	158.5	2.8	962	4	US-09-071-035-250	Sequence
29	158.5	2.8	962	4	US-09-071-035-254	Sequence
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34	154	2.8	903	1	US-08-021-601-12	Sequence
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41	152.5	2.7	789	2	US-08-470-566B-32	Sequence
42	152.5	2.7	789	2	US-08-838-219B-4	Sequence
43	152.5	2.7	789	2	US-08-469-334-32	Sequence
44	152.5	2.7	789	3	US-09-300-529-32	Sequence
45	152.5	2.7	789	3	US-09-233-336A-4	Sequence

ALIGNMENTS

RESULT 1
US-07-745-206A-25
; Sequence 25, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 S. LaSalle
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07745.206A
; FILING DATE: 19910815
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feder, Scott B
; REFERENCE/DOCKET NUMBER: 51504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-372-7842
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-745-206A-25

Query Match 100.0%; Score 5599; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0;
QY 1 MAAGCLLALTLFQSLIGPSSPPFPFSAVTIKSWDKMOEDLVTLAKTAGVNM
DB 1 MAAGCLLALTLFQSLIGPSSPPFPFSAVTIKSWDKMOEDLVTLAKTAGVNM

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YTSNGNPNCDMWKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063

Patent No. 5951824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0999
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-52

Query Match 100.0%; Score 5599; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0;
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DB 1 MAAGCLLALTLTLPQSLIGPSSBEPFSAVTIKSWDKMQEDLVTLAKTAGVNN
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Application US/08311363

5958

ATION:

```

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
METHODS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-311-363-25

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Query Match 100.0%; Score 5599; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0;

Qy 1 MAACGLLALTLTLFQSLILIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGV
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ication US/08713118
36
TION:
ranco, Rodrigo
un Chen, Ai Ru
ney, David J.
TION: NUCLEIC ACID ENCODING HUMAN NEURONAL
TION: CALCIUM CHANNEL SUBUNITS
JENCES: 6
E ADDRESS:
Hamilton, Brook, Smith & Reynolds, P.C.
o Militia Drive
ngton
ISA
}-4799
ABLE FORM:
3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patent In Release #1.0, Version #1.30
CATION DATA:
3 NUMBER: US/08/713,118
3: 16-SEP-1996
TION: 435

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; ATTORNEY/AGENT INFORMATION:
; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-713-118-4

Query Match      99.9%; Score 5595; DB 3; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 1; Indels 0; (

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Db 1 MAAGCLLALTLTLFQSLILIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTAGVNM
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lication US/09452007

485

ATTION:

Franco, Rodrigo

Sun Chen, Ai Ru

Suey, David J.

ENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL

ENTION: CALCIUM CHANNEL SUBUNITS

SEQUENCES: 6

CE ADDRESS:

Hamilton, Brook, Smith & Reynolds, P.C.

wo Militia Drive

ington

USA

3-4799

DABLE FORM:

E: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

Patentin Release #1.0, Version #1.30

ICATION DATA:

IN NUMBER: US/09/452,007

E:

ATION:

ATION DATA:

IN NUMBER: US/08/713,118

E: 16-SEP-1996

INT INFORMATION:

a, Elizabeth W.

ON NUMBER: 38,236

DOCKET NUMBER: ACC96-01

ATION INFORMATION:

: 617-861-6240

617-861-9540

OR SEQ ID NO: 4:

ARACTERISTICS:

1091 amino acids

ino acid

linear

E: protein

ilarity 99.9%; Score 5595; DB 3; Length 1091;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AGCLLALTTLFQSLIGPSEPPFPFSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
 AGCLLALTTLFQSLIGPSEPPFPFSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
 KYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWREDFASN 120

Db 61 YEYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWRE
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGRQISYQHAHVHIPTDIYEG
 Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGRQISYQHAHVHIPTDIYEG
 QY 181 NELNWTLSALDEVFKKREEDPSSLWQVFGSATGLARYYPASPWVDSRPNKIDLI
 Db 181 NELNWTLSALDEVFKKREEDPSSLWQVFGSATGLARYYPASPWVDSRPNKIDLI
 QY 241 RPYWIOGAASPDKMLILVDVSGSVGLTLKLRITSVSEMLETLSDDDFVNVSFN
 Db 241 RPYWIOGAASPDKMLILVDVSGSVGLTLKLRITSVSEMLETLSDDDFVNVSFN
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNNVSRANCK
 Db 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNNVSRANCK
 QY 361 FTDGGERAQEIEFNKYNKOKKVVFRFSPVQGHYERGPIONMACENKGYIYEIPE
 Db 361 FTDGGERAQEIEFNKYNKOKKVVFRFSPVQGHYERGPIONMACENKGYIYEIPE
 QY 421 INTOEYLDVLGRPMVLADGKAKOVQNTVYLDALGLVITGLTPVFNITQGFEN
 Db 421 INTOEYLDVLGRPMVLADGKAKOVQNTVYLDALGLVITGLTPVFNITQGFEN
 QY 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYYPADIPNGYVLLHPLNLPKNPKSC
 Db 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYYPADIPNGYVLLHPLNLPKNPKSC
 QY 541 DFLDAELENDIKVEIRNKMIDGESGKTPRTLVKSQDERVIDKGNRTYTWTVPNC
 Db 541 DFLDAELENDIKVEIRNKMIDGESGKTPRTLVKSQDERVIDKGNRTYTWTVPNC
 QY 601 ALVLPYTSFYIYIKALBEITITQARSKGKMKDSETLKPDNFESGYTFIAPRDYK
 Db 601 ALVLPYTSFYIYIKALBEITITQARSKGKMKDSETLKPDNFESGYTFIAPRDYK
 QY 661 SDNNTFELNFEFIDRKTTPNPNSCNADLINRVLLDAGFTNELVQNTWSQKNII
 Db 661 SDNNTFELNFEFIDRKTTPNPNSCNADLINRVLLDAGFTNELVQNTWSQKNII
 QY 721 FVVTGGGITRVPYKBAENQENPETYEDSFYKRSLDNDNVVFTAPYFNKSGPGI
 Db 721 FVVTGGGITRVPYKBAENQENPETYEDSFYKRSLDNDNVVFTAPYFNKSGPGI
 QY 781 MVSKAVEIYIQGLKLLPAVVGKIDVNSWIENFTKTSIRDPGAPVCDCKRNSDY
 Db 781 MVSKAVEIYIQGLKLLPAVVGKIDVNSWIENFTKTSIRDPGAPVCDCKRNSDY
 QY 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPDLMRHLVNI SVAFNKS YDYQSVCEPK
 Db 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPDLMRHLVNI SVAFNKS YDYQSVCEPK
 QY 901 GAGHSAYVPSVADILQIGMWATAAAWSILQQFLSLTFFPRLLEAVEMEDDDFTI
 Db 901 GAGHSAYVPSVADILQIGMWATAAAWSILQQFLSLTFFPRLLEAVEMEDDDFTI
 QY 961 SCITEQTYQYFPDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIFIMVESKGTCPCI
 Db 961 SCITEQTYQYFPDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIFIMVESKGTCPCI
 QY 1021 QAEQTSQGPNCMDVKQPRYRKGPVDFDNNVLEDYDCCGV 1063
 Db 1021 QAEQTSQGPNCMDVKQPRYRKGPVDFDNNVLEDYDCCGV 1063

RESULT 7

US-08-455-543A-54

; Sequence 54, Application US/08455543A

; Patent No. 5792846

; GENERAL INFORMATION:

arpold, Michael
 lls, Steven
 illiams, Mark
 eldman, Daniel
 Cue, Ann
 renner, Robert
 NTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 NCES: 57
 ADDRESS:
 Brown, Martin, Haller & McClain
 60 Union Street
 Diego
 ifornia
 SA

-2926
 ABLE FORM:
 : Diskette
 IBM Compatible
 YSTEM: DOS
 FastSEQ Version 1.5
 CATION DATA:
 : May 31, 1995
 : NUMBER: US/08/455.543A
 TION DATA:
 : April 4, 1994
 : NUMBER: 08/223.305
 TION DATA:
 : April 10, 1992
 : NUMBER: 07/868.354
 TION DATA:
 : April 10, 1992
 : NUMBER: 07/745.206
 TION DATA:
 : 15-AUG-1991
 : NUMBER: US 07/620,250
 TION DATA:
 : 30-NOV-1990
 : NUMBER: US 07/482,384
 TION DATA:
 : 20-FEB-1990
 : NUMBER: WO PCT/US89/01408
 : 04-APR-1989
 TION DATA:
 : NUMBER: US 07/176,899
 : 04-APR-1988
 T INFORMATION:
 man, Stephanie L.
 IN NUMBER: 33,779
 XCKET NUMBER: 6362-52517
 TION INFORMATION:
 (619)238-0999
 (619)238-0062
 r SEQ ID NO: 54:
 RACTERISTICS:
 86 amino acids
 to acid
 3S: single
 linear
 3: protein
 3: internal

99.3%; Score 5559.5; DB 1; Length 1086;
 larity 99.5%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 5; Gaps 1;

3CLLALTLTLFQSLILGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
 |||||
 3CLLALTLTLFQSLILGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREI
 DB 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREI
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHAVHPTDIYEGS
 DB 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHAVHPTDIYEGS
 QY 181 NELNWTSALEDEVFKCNREEDPSLLWQVFGSATGLARYYPASPWVDNSRTNPKIDLY
 DB 181 NELNWTSALEDEVFKCNREEDPSLLWQVFGSATGLARYYPASPWVDNSRTNPKIDLY
 QY 241 RPWYIQGAASPKOMLILVDVSGSVGLTLKLIRTSVSEMLETLSDDDDFVNVASFNE
 DB 241 RPWYIQGAASPKOMLILVDVSGSVGLTLKLIRTSVSEMLETLSDDDDFVNVASFNE
 QY 301 VSCFHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAPEQLLNVNVRANCNF
 DB 301 VSCFHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAPEQLLNVNVRANCNF
 QY 361 FTDGGEERAQEIFNKYNKDKKRVFRFSVGOHNYERGEPIOMWACENKGYIYEIPSI
 DB 361 FTDGGEERAQEIFNKYNKDKKRVFRFSVGOHNYERGEPIOMWACENKGYIYEIPSI
 QY 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVDLDALEGLVITGTLPVFNITQGFENI
 DB 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVDLDALEGLVITGTLPVFNITQGFENI
 QY 481 NQLILGVNGVDVSLIEDIKLTPRFTLCPNGYVFAIDPNGYVLLHNLQPKPKSQI
 DB 481 NQLILGVNGVDVSLIEDIKLTPRFTLCPNGYVFAIDPNGYVLLHNLQPKPKSQI
 QY 541 DFLDALENDIKVEIRNKMIDGSEKTRTLVKSQDERYIDKGNRTYVTPVNG
 DB 536 DFLDALENDIKVEIRNKMIDGSEKTRTLVKSQDERYIDKGNRTYVTPVNG
 QY 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSITLKPONFEESYTTIAPRDYCI
 DB 596 ALVLPYTFYIYKAKLEETITQARSKKGMKDSITLKPONFEESYTTIAPRDYCI
 QY 661 SDNTEFLLNFNEFIDRKTNNPNSCNADLINRLLDAGFTNELVQNYWSKQKNIKI
 DB 656 SDNTEFLLNFNEFIDRKTNNPNSCNADLINRLLDAGFTNELVQNYWSKQKNIKI
 QY 721 FVVTGGITRVYPKEAGENWQENPTYEDSFYKRSIDNDNYVFTAPYFNKSGPGA
 DB 716 FVVTGGITRVYPKEAGENWQENPTYEDSFYKRSIDNDNYVFTAPYFNKSGPGA
 QY 781 MVSKAVEIYIQGLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGVPCCKRNSDV
 DB 776 MVSKAVEIYIQGLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGVPCCKRNSDV
 QY 841 LDDGGFLMANHDDVTNOIGRPFGEIDPSLMHNLVNI SVYAFNKSVDYQSVCEPGI
 DB 836 LDDGGFLMANHDDVTNOIGRPFGEIDPSLMHNLVNI SVYAFNKSVDYQSVCEPGI
 QY 901 GAGHSAYVPSVADILQIGMWATAAASILQOFLSLTFPRLLEAVEMEDDDFTAI
 DB 896 GAGHSAYVPSVADILQIGMWATAAASILQOFLSLTFPRLLEAVEMEDDDFTAI
 QY 961 SCITEQTQYFFDNDKSFSGVLDCGNCRSRI FHGEKLMNTNLI FIMVESKGTGCPD
 DB 956 SCITEQTQYFFDNDKSFSGVLDCGNCRSRI FHGEKLMNTNLI FIMVESKGTGCPD
 QY 1021 QAEQTSDEGNPCDMVKQPRYKGPVCFDNNVLEDTDCGGVS 1063
 DB 1016 QAEQTSDEGNPCDMVKQPRYKGPVCFDNNVLEDTDCGGVS 1058

RESULT 8
 US-08-223-305C-54
 ; Sequence 54, Application US/08223305C
 ; Patent No. 5851824

ATION:
 Harpold, Michael
 Illis, Steven
 Williams, Mark
 Feldman, Daniel
 McCue, Ann
 Brenner, Robert
 ION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ION: METHODS
 JENCES: 57
 Brown, Martin, Haller & McClain
 560 Union Street
 Diego
 lifornia
 USA
 1-2926
 TABLE FORM:
 E: Diskette
 IBM Compatible
 SYSTEM: DOS
 FastSeq Version 1.5
 ICATION DATA:
 N NUMBER: US/08/223,305C
 E: April 4, 1994
 ATION DATA:
 N NUMBER: 07/868,354
 E: April 10, 1992
 ATION DATA:
 N NUMBER: US 07/745,206
 E: 15-AUG-1991
 ATION DATA:
 N NUMBER: US 07/620,250
 E: 30-NOV-1990
 ATION DATA:
 N NUMBER: US 07/482,384
 E: 20-FEB-1990
 ATION DATA:
 N NUMBER: US 07/603,751
 E: 04-APR-1989
 ATION DATA:
 N NUMBER: WO PCT/US89/01408
 E: 04-APR-1989
 ATION DATA:
 N NUMBER: US 07/176,899
 E: 04-APR-1988
 NT INFORMATION:
 dman, Stephanie L.
 ON NUMBER: 33,779
 DOCKET NUMBER: 52516 (P519739)
 ATION INFORMATION:
 (619)238-0999
 (619)238-0062
 R SEQ ID NO: 54:
 RACTERISTICS:
 086 amino acids
 no acid
 SS: single
 linear
 E: protein
 E: internal

99.3%; Score 5559.5; DB 2; Length 1086;
 larity 99.5%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 5; Gaps 1;

AGCLLALTTLFQSLIGPSSEPPFSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
 |||||
 AGCLLALTTLFQSLIGPSSEPPFSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
 |||||
 CYQDLTYVPNNARQLVEIARIDIEKLLSNRSKALVSLAEAEKVQAAHQWREI 120
 |||||

Db 61 YEKYQDLTYVPNNARQLVEIARIDIEKLLSNRSKALVSLAEAEKVQAAHQWREI
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYOHAAVHIPTDIYEG;
 Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYOHAAVHIPTDIYEG;
 QY 181 NELNWTSSALDEVFKKREEDPSLLQVFGSATGLARYYPASPWVDSNRTPNKIDL
 Db 181 NELNWTSSALDEVFKKREEDPSLLQVFGSATGLARYYPASPWVDSNRTPNKIDL
 QY 241 RPYIQQGAASPKDMLILVDVSGVSGLTLKLRITSVSEMLETSLDDDFNVASFNI
 Db 241 RPYIQQGAASPKDMLILVDVSGVSGLTLKLRITSVSEMLETSLDDDFNVASFNI
 QY 301 VSCFQHLVOANVRNKKVLKDAVNNTAKGIDTYKKGFSFAFQOLLNINVSANCN
 Db 301 VSCFQHLVOANVRNKKVLKDAVNNTAKGIDTYKKGFSFAFQOLLNINVSANCN
 QY 361 FTDGGEERAQEI FNKYNKDKKVRFRFSVGOHNERGPIQWACENKGYIYIIPS
 Db 361 FTDGGEERAQEI FNKYNKDKKVRFRFSVGOHNERGPIQWACENKGYIYIIPS
 QY 421 INTOEYLDVLGRPMVLGADKAKOVQWNTVYLDALGLVITGLPVFNITGOFEN
 Db 421 INTOEYLDVLGRPMVLGADKAKOVQWNTVYLDALGLVITGLPVFNITGOFEN
 QY 481 NQLILGVMGVDVSLIEDIKLTPRFTLCPNGYYPADPNNGYVLLHPNLQPNPKSQ
 Db 481 NQLILGVMGVDVSLIEDIKLTPRFTLCPNGYYPADPNNGYVLLHPNLQPNPKSQ
 QY 541 DFLDLENDIKVEIRNKMIDGESGEKTRTLVKSODERYIDKGNRTYTWTPVNG
 Db 536 DFLDLENDIKVEIRNKMIDGESGEKTRTLVKSODERYIDKGNRTYTWTPVNG
 QY 601 ALVLPYTSFYIKAKLEETITQARSKKGMKDSITLKPDPNFESGYTFTIAPRDYC
 Db 596 ALVLPYTSFYIKAKLEETITQARSKKGMKDSITLKPDPNFESGYTFTIAPRDYC
 QY 661 SDNTEFLNFEFI DRKTPNNPSCNADLINRVLLDAGFTNELVQYNSKQKNIK
 Db 656 SDNTEFLNFEFI DRKTPNNPSCNADLINRVLLDAGFTNELVQYNSKQKNIK
 QY 721 FVVTGGITRVYPKEAGENQENPEYEDSFYKRSKSDNDNDNYVFTAPYFNKSGPGP
 Db 716 FVVTGGITRVYPKEAGENQENPEYEDSFYKRSKSDNDNDNYVFTAPYFNKSGPGP
 QY 781 MVSKAVEIYIQGLKLPVAVVGIKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDV
 Db 776 MVSKAVEIYIQGLKLPVAVVGIKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDV
 QY 841 LDDGGFLLMANHDDYTNQIGRFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCRPC
 Db 836 LDDGGFLLMANHDDYTNQIGRFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCRPC
 QY 901 GAGHRSAYVPSVADILQIGHWATAAASIIQQFLLSLTFFPRLLAEVEMEDDDFTI
 Db 896 GAGHRSAYVPSVADILQIGHWATAAASIIQQFLLSLTFFPRLLAEVEMEDDDFTI
 QY 961 SCITEQTQYFFDNDKSFSGVLDGNCNSRIFHGEKLMNTNLI FIMVESKGTCPCI
 Db 956 SCITEQTQYFFDNDKSFSGVLDGNCNSRIFHGEKLMNTNLI FIMVESKGTCPCI
 QY 1021 QAEQTSQGNPNCMDWKQPRYKGPVDFCDNNVLEDYTDGCGVS 1063
 Db 1016 QAEQTSQGNPNCMDWKQPRYKGPVDFCDNNVLEDYTDGCGVS 1058

RESULT 9
 US-08-455-543A-56
 ; Sequence 56, Application US/08455543A
 ; Patent No. 5792846
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael

llis, Steven
 illiams, Mark
 eldman, Daniel
 cCue, Ann
 renner, Robert
 NTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 NTION: METHODS
 UENCES: 57
 E ADDRESS:
 Brown, Martin, Haller & McClain
 60 Union Street
 Diego
 ifornia
 SA
 -2926
 ABLE FORM:
 : Diskette
 IBM Compatible
 YSTEM: DOS
 Fast-SEQ Version 1.5
 CATION DATA:
 NUMBER: US/08/455,543A
 : May 31, 1995
 TION DATA:
 NUMBER: 08/223,305
 : April 4, 1994
 TION DATA:
 NUMBER: 07/868,354
 : April 10, 1992
 TION DATA:
 NUMBER: 07/745,206
 : 15-AUG-1991
 TION DATA:
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 : 30-NOV-1990
 TION DATA:
 NUMBER: US 07/482,384
 : 20-FEB-1990
 TION DATA:
 NUMBER: US 07/603,751
 : 04-APR-1989
 TION DATA:
 NUMBER: WO PCT/US89/01408
 : 04-APR-1989
 TION DATA:
 NUMBER: US 07/176,899
 : 04-APR-1988
 T INFORMATION:
 man, Stephanie L.
 N NUMBER: 33,779
 OCKET NUMBER: 6362-52517
 TION INFORMATION:
 (619)238-0999
 (619)238-0062
 : SEQ ID NO: 56:
 : CHARACTERISTICS:
 : 84 amino acids
 : 10 acid
 : 10 single
 : linear
 : protein
 : internal

99.0%; Score 5542.5; DB 1; Length 1084;
 larity 99.2%; Pred. No. 0;
 onservative 0; Mismatches 1; Indels 7; Gaps 1;
 :CCLALTLTLFQSLILGPSSEPPPSAVTIKSWVDKMQEDLVLTAKTAGVNLVDI 60
 :CCLALTLTLFQSLILGPSSEPPPSAVTIKSWVDKMQEDLVLTAKTAGVNLVDI 60
 :QDLTYVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKQVAAHQWREDFASN 120

Db 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKQVAAHQWREI
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROI SYQHAHVHPTDIYEGE
 Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROI SYQHAHVHPTDIYEGE
 QY 181 NELNWTSALEDEVFKKREEDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLI
 Db 181 NELNWTSALEDEVFKKREEDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLI
 QY 241 RPWTIOGAASPKOMLILVDVSGSVGLTLKIRTSVSEMLETILSDDDPWNVASFNE
 Db 241 RPWTIOGAASPKOMLILVDVSGSVGLTLKIRTSVSEMLETILSDDDPWNVASFNE
 QY 301 VSCFQHLVQANVRNKKVKDAVNNITAKGITDYKKGPSFAFEQLLNYNVSRANCNI
 Db 301 VSCFQHLVQANVRNKKVKDAVNNITAKGITDYKKGPSFAFEQLLNYNVSRANCNI
 QY 361 FTGGEERAQEI FNKYNKDKKRVFRFSGVGHNYERGPIONMACENKGYIYEIPSI
 Db 361 FTGGEERAQEI FNKYNKDKKRVFRFSGVGHNYERGPIONMACENKGYIYEIPSI
 QY 421 INTOEYLDVLGRPMVLADGKAKOVQWNTNVDLDALEGLVITGTLVPVFNITQGFENI
 Db 421 INTOEYLDVLGRPMVLADGKAKOVQWNTNVDLDALEGLVITGTLVPVFNITQGFENI
 QY 481 NQLILGVMGVDVSLIEDIKLTPRTLCPNGYVFAIDPNGYVLLHPNLQPKPKSQI
 Db 481 NQLILGVMGVDVSLIEDIKLTPRTLCPNGYVFAIDPNGYVLLHPNLQPKPKSQI
 QY 541 DFLDAELENDIKVEIRNKMDIGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNG
 Db 541 DFLDAELENDIKVEIRNKMDIGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNG
 QY 601 ALVLPITYSYFYIKAKLEETITQARY-----SETLKPDPNFEESGYTIFAPRDYCI
 Db 601 ALVLPITYSYFYIKAKLEETITQARY-----SETLKPDPNFEESGYTIFAPRDYCI
 QY 661 SDNTEPELLNFNEFIDRKTNNPSCNADLINRVLLDAGFTNELVQNYWSKQKNIKI
 Db 654 SDNTEPELLNFNEFIDRKTNNPSCNADLINRVLLDAGFTNELVQNYWSKQKNIKI
 QY 721 FVITDGGITRVYVPEAGENWQENPETYEDSFYKRSLDNDNVYFTAPYFNKSGPGA
 Db 714 FVITDGGITRVYVPEAGENWQENPETYEDSFYKRSLDNDNVYFTAPYFNKSGPGA
 QY 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGVPCCKRNSDV
 Db 774 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGVPCCKRNSDV
 QY 841 LDDGGFLLMANHDDVTNQIGRFFGIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGI
 Db 834 LDDGGFLLMANHDDVTNQIGRFFGIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGI
 QY 901 GAGHRSAYVPSVADILQIGWATAAASILQOFLSLTFPRLLEAVEMEDDDFTAI
 Db 894 GAGHRSAYVPSVADILQIGWATAAASILQOFLSLTFPRLLEAVEMEDDDFTAI
 QY 961 SCITEQTQYFFDNDKSKSPGVLDCGNCRSRI FHGEKLMNTNLIFIMVESKGTCPD
 Db 954 SCITEQTQYFFDNDKSKSPGVLDCGNCRSRI FHGEKLMNTNLIFIMVESKGTCPD
 QY 1021 QABQTSQDGNPCDMVKQPRYKGPVDFDNNVLEDTDCGGVS 1063
 Db 1014 QABQTSQDGNPCDMVKQPRYKGPVDFDNNVLEDTDCGGVS 1056

RESULT 10
 US-08-223-305C-56
 ; Sequence 56, Application US/08223305C
 ; Patent No. 581824
 ; GENERAL INFORMATION:

arpold, Michael
 Ellis, Steven
 Williams, Mark
 Feldman, Daniel

McCue, Ann

Krenner, Robert

INTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

INTION: METHODS

NUENCES: 57

TE ADDRESS:

Brown, Martin, Haller & McClain

60 Union Street

Diego

California

USA

1-2926

TABLE FORM:

3: Diskette

IBM Compatible

SYSTEM: DOS

FastSeq Version 1.5

(CATION DATA:

4 NUMBER: US/08/223,305C

3: April 4, 1994

ATION DATA:

4 NUMBER: 07/868,354

3: April 10, 1992

ATION DATA:

4 NUMBER: US 07/745,206

3: 15-AUG-1991

ATION DATA:

4 NUMBER: US 07/620,250

3: 30-NOV-1990

ATION DATA:

4 NUMBER: US 07/482,384

3: 20-FEB-1990

ATION DATA:

4 NUMBER: US 07/603,751

3: 04-APR-1989

ATION DATA:

4 NUMBER: WO PCT/US89/01408

3: 04-APR-1989

ATION DATA:

4 NUMBER: US 07/176,899

3: 04-APR-1988

NT INFORMATION:

dman, Stephanie L.

ON NUMBER: 33,779

DOCKET NUMBER: 52516 (P519739)

ATION INFORMATION:

(619)238-0999

R SEQ ID NO: 56:

084 amino acids

no acid

SS: single

linear

E: protein

E: internal

ilarity 99.0%; Score 5542.5; DB 2; Length 1084;

Conservative 0; Mismatches 1; Indels 7; Gaps 1;

GCLLALTLTQSLIGPSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60

GCLLALTLTQSLIGPSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60

TQDLTYVEPNARQLVEIAARDIEKLSNRKALVSLAEAKVQAHHQWREDFASN 120

TQDLTYVEPNARQLVEIAARDIEKLSNRKALVSLAEAKVQAHHQWREDFASN 120

QY 121 EVVYVNAKDDLDPEKNDSEPGSQRIPVFIEDANFGROI SYQHAAVHLPTDIYEG
 DB 121 EVVYVNAKDDLDPEKNDSEPGSQRIPVFIEDANFGROI SYQHAAVHLPTDIYEG
 QY 181 NELNWTSALEDFVKQKREDEPSLLWQVFGSATGLARYYPASVPWVNSRTPNKIDL
 DB 181 NELNWTSALEDFVKQKREDEPSLLWQVFGSATGLARYYPASVPWVNSRTPNKIDL
 QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETLSDDDDFNVASFN
 DB 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETLSDDDDFNVASFN
 QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAGITDYKKGFSFAPBOLLNLYNVRANCN
 DB 301 VSCFOHLVQANVRNKKVLKDAVNNTAGITDYKKGFSFAPBOLLNLYNVRANCN
 QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVQGHYERGPIONMACENKGYYYEIPS
 DB 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVQGHYERGPIONMACENKGYYYEIPS
 QY 421 INTQBYLDVLRPMVLGDKAKQKQVQWNTVYLDALGLVITGTLPVENITGQFEN
 DB 421 INTQBYLDVLRPMVLGDKAKQKQVQWNTVYLDALGLVITGTLPVENITGQFEN
 QY 481 NQLILGWVGVDVSLEDIKELTPRFTLCPNGYYFAIDPNGYVLLHPLNLPKNPKSQ
 DB 481 NQLILGWVGVDVSLEDIKELTPRFTLCPNGYYFAIDPNGYVLLHPLNLPKNPKSQ
 QY 541 DFDAELENDIKVEIRNKMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNG
 DB 541 DFDAELENDIKVEIRNKMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNG
 QY 601 ALVLPYISFYIKAKLEETITQARSKKGKMDSETLKPDPNFEESGVTFTAPRDYC
 DB 601 ALVLPYISFYIKAKLEETITQARSKKGKMDSETLKPDPNFEESGVTFTAPRDYC
 QY 661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKNIK
 DB 661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKNIK
 QY 721 FVVTGCGITRVYPKEAGENWQNPETYEDSFYKRSLDNDNDNYVFTAPYFNKSGPGA
 DB 721 FVVTGCGITRVYPKEAGENWQNPETYEDSFYKRSLDNDNDNYVFTAPYFNKSGPGA
 QY 781 MVSKAVEIYIQGLKLPVAVGKIDVNSWLENFTKTSIRDPCAGPVCDCCKRNSDV
 DB 781 MVSKAVEIYIQGLKLPVAVGKIDVNSWLENFTKTSIRDPCAGPVCDCCKRNSDV
 QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
 DB 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
 QY 901 GAGHSAYVPSVADIIQIGWATAAAWSIIQQFLLSLTPRLLLEAVEMEDDDFTA
 DB 901 GAGHSAYVPSVADIIQIGWATAAAWSIIQQFLLSLTPRLLLEAVEMEDDDFTA
 QY 961 SCITEQTYFFDNDSDKSPGVLDGNCRSIFHGKELMNTNLIIFIMVESKGTCPCL
 DB 961 SCITEQTYFFDNDSDKSPGVLDGNCRSIFHGKELMNTNLIIFIMVESKGTCPCL
 QY 1021 QABQTSQDGNPCDMVKQPRYKGPVDFCNVNVLEDYTDGCVS 1063
 DB 1014 QABQTSQDGNPCDMVKQPRYKGPVDFCNVNVLEDYTDGCVS 1056

RESULT 11

US-08-455-543A-53

; Sequence 53, Application US/08455543A

; Patent No. 5792846

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

RESULT 12
US-08-223-305C-53

plication US/08223305C
824

ACTION:

Harpold, Michael
Ellis, Steven
Williams, Mark
Feldman, Daniel
McCue, Ann

Brenner, Robert

ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

ENTION: METHODS

QUENCES: 57

CE ADDRESS:

Brown, Martin, Haller & McClain

660 Union Street

Diego

California

USA

1-2926

DABLE FORM:

E: Diskette

IBM Compatible

SYSTEM: DOS

FastSeq Version 1.5

ICATION DATA:

N NUMBER: US/08/223,305C

E: April 4, 1994

ACTION DATA:

N NUMBER: 07/868,354

E: April 10, 1992

ACTION DATA:

N NUMBER: US 07/745,206

E: 15-AUG-1991

ACTION DATA:

N NUMBER: US 07/620,250

E: 30-NOV-1990

ACTION DATA:

N NUMBER: US 07/482,384

E: 20-FEB-1990

ACTION DATA:

N NUMBER: US 07/603,751

E: 04-APR-1989

ACTION DATA:

N NUMBER: WO PCT/US89/01408

E: 04-APR-1989

ACTION DATA:

N NUMBER: US 07/176,899

E: 04-APR-1988

NT INFORMATION:

dman, Stephanie L.

ON NUMBER: 33,779

DOCKET NUMBER: 52516 (P519739)

ACTION INFORMATION:

(619)238-0999

(619)238-0062

R SEQ ID NO: 53:

ACTERISTICS:

103 amino acids

no acid

SS: single

linear

E: protein

E: internal

E:

98.6%; Score 5523; DB 2; Length 1103;

larity 97.5%; Pred.No. 0;

Conservative 0; Mismatches 1; Indels 26; Gaps 2;

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AGCLLALTTLFQSLIGSSSEPPFPSPAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

|||||

61 YEKYQDLTYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALAEKVKQAAHQWRE
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121 EVVYNAKDDLDPEKNDSEPGSQRIPKPVIEDANFGROIQSYQHAAVHIPTDIYEG
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181 NELNWTSSALDEVFKONREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
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181 NELNWTSSALDEVFKONREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
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241 RPWYIQGAASPDKMLILVDVSGSVGLITLKLIRTSVSEMLETLSDDDFVNVSFPN
|||
241 RPWYIQGAASPDKMLILVDVSGSVGLITLKLIRTSVSEMLETLSDDDFVNVSFPN
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301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNVNVRANCN
|||
301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNVNVRANCN
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361 FTDGGERAQEIENKYNKDKKVRVFRFSGQHNYERGPQWMAKCNKGYIYEIPE
|||
361 FTDGGERAQEIENKYNKDKKVRVFRFSGQHNYERGPQWMAKCNKGYIYEIPE
|||
421 INTQEYLDVLGRPMVLADKAKOVNTNVLDALEGLVITGTLPVNITGQFEN
|||
421 INTQEYLDVLGRPMVLADKAKOVNTNVLDALEGLVITGTLPVNITGQFEN
|||
481 NQLILGVMGVDSLEDIKRLTPRTLCPNGYYFAIDPNGVYLLHPNLQPK-
|||
481 NQLILGVMGVDSLEDIKRLTPRTLCPNGYYFAIDPNGVYLLHPNLQPKIGVGC
|||
531 -----NPKSQBPVTLDFDLAELENDIKVEIRNMIDGESGEKTFRLVKSC
|||
541 LRKRRPNIQPKSQBPVTLDFDLAELENDIKVEIRNMIDGESGEKTFRLVKSC
|||
582 DKGNRVTYTPVNGTDYSLALVLPYSPYYIKAKLETITQASKKGKMDSETI
|||
601 DKGNRVTYTPVNGTDYSLALVLPYSPYYIKAKLETITQARY-----SETI
|||
642 EESGYTFIAPRDYCNLDKISDNNTFLLNFEFIDRKTNNPNSCNADLINRVLLI
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654 EESGYTFIAPRDYCNLDKISDNNTFLLNFEFIDRKTNNPNSCNADLINRVLLI
|||
702 ELVQNYWSKQNIKGVKARFVVDGGITRVYPKEAGENWQENPETYEDSYKRSI
|||
714 ELVQNYWSKQNIKGVKARFVVDGGITRVYPKEAGENWQENPETYEDSYKRSI
|||
762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKI
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774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKI
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822 CAGPVCDCCKNSDVMDCVILDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVN
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834 CAGPVCDCCKNSDVMDCVILDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVN
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882 FNKSVDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAASWILQOFLLE
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942 LLEAVEMEDDDFTASLSKQSCITEQTYFPDNDKSPSGVLDGNCNCSRIIFHGEKI
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1014 IFIMVESKGTCPDTRLLIOAEQTSQGNPCDMVKQPRYKGPDPVCFDNNVLEDY
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1062 VS 1063
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1074 VS 1075
|||

RE
US

plication US/08455543A
346

ATION:

Harold, Michael
Ellis, Steven
Williams, Mark
Feldman, Daniel
McCue, Ann

Brenner, Robert

ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

ENTION: METHODS

QUENCES: 57

CE ADDRESS:

Brown, Martin, Haller & McClain

560 Union Street

Diego

lifornia

USA

1-2926

DABLE FORM:

3: Diskette

IBM Compatible

SYSTEM: DOS

FastSeq Version 1.5

ICATION DATA:

1 NUMBER: US/08/455,543A

3: May 31, 1995

ATION DATA:

1 NUMBER: 08/223,305

3: April 4, 1994

ATION DATA:

1 NUMBER: 07/868,354

3: April 10, 1992

ATION DATA:

1 NUMBER: US 07/745,206

3: 15-AUG-1991

ATION DATA:

1 NUMBER: US 07/620,250

3: 30-NOV-1990

ATION DATA:

1 NUMBER: US 07/482,384

3: 20-FEB-1990

ATION DATA:

1 NUMBER: US 07/603,751

3: 04-APR-1989

ATION DATA:

1 NUMBER: WO PCT/US89/01408

3: 04-APR-1989

ATION DATA:

1 NUMBER: US 07/176,899

3: 04-APR-1988

IT INFORMATION:

man, Stephanie L.

AN NUMBER: 33,779

OCKET NUMBER: 6362-52517

ATION INFORMATION:

(619)238-0999

(619)238-0062

SEQ ID NO: 55:

ACTERISTICS:

179 amino acids

10 acid

IS: single

linear

protein

internal

98.3%; Score 5503; DB 1; Length 1079;

arity 98.8%; Pred.No. 0;

conservative 0; Mismatches 1; Indels 12; Gaps 2;

1	MAAGCLLALTLTLFQSLILGPSSEPPSAVTIKSWVDMQEDLVTLAKTASGVN	QY
1	MAAGCLLALTLTLFQSLILGPSSEPPSAVTIKSWVDMQEDLVTLAKTASGVN	Db
61	YEKYQDLTYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAKVQAAHORE	QY
61	YEKYQDLTYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAKVQAAHORE	Db
121	EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEG	QY
121	EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEG	Db
181	NELNWTLSALDEVFKKREEDPSLLMQVFGSATGLARYYPASPMVDNSRTPNKIDL	QY
181	NELNWTLSALDEVFKKREEDPSLLMQVFGSATGLARYYPASPMVDNSRTPNKIDL	Db
241	RPWYIQGAASPDKMLILVDVSGVSGLTILKLRISVSSEMLETSLDDDFNVASFN	QY
241	RPWYIQGAASPDKMLILVDVSGVSGLTILKLRISVSSEMLETSLDDDFNVASFN	Db
301	VSCFOHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSAFEPQLLNYSRANCN	QY
301	VSCFOHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSAFEPQLLNYSRANCN	Db
361	FTDGGEEARAQEIFNKYNKDKKVRFRFSVQOHYERGPQIMACENKGYYYEIPS	QY
361	FTDGGEEARAQEIFNKYNKDKKVRFRFSVQOHYERGPQIMACENKGYYYEIPS	Db
421	INTQEYLDVLGRPMVLGADKAKQVQNTVYLDLALGLVITGTLPVFNITGQFEN	QY
421	INTQEYLDVLGRPMVLGADKAKQVQNTVYLDLALGLVITGTLPVFNITGQFEN	Db
481	NQLILGVMGVDVSLIEDIKELTFRFTLCPNGYYFAIDPNCYVLLHPLNLPKPSQ	QY
481	NQLILGVMGVDVSLIEDIKELTFRFTLCPNGYYFAIDPNCYVLLHPLNLPKPSQ	Db
541	DFDLAELENDIKVEIRNNKMIDGSEKTPRTLKVSQDERYIDKGNRTYTWTPVNG	QY
536	DFDLAELENDIKVEIRNNKMIDGSEKTPRTLKVSQDERYIDKGNRTYTWTPVNG	Db
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781	MVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDP CAGPVCDCRNSDVI	QY
769	MVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDP CAGPVCDCRNSDVI	Db
841	LDDGGFLMANHDDVTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGI	QY
829	LDDGGFLMANHDDVTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGI	Db
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889	GAGHSAYVPSVADILQIGWATAAANSILOQFLSLTFPRLLEAVEMEDDDFTAI	Db
961	SCITEQTQYFFDNDNSKSPSGVLDGNCNSRI FHGEKLMNTNLI FIMVSKGTGCPD:	QY
949	SCITEQTQYFFDNDNSKSPSGVLDGNCNSRI FHGEKLMNTNLI FIMVSKGTGCPD:	Db
1021	QAEQTSQDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDCCGVS 1063	QY
1009	QAEQTSQDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDCCGVS 1051	Db

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us-10-090-827-15.ral

plication US/08223305C
824
ATTION:
Harbold, Michael
Ellis, Steven
Williams, Mark
Feldman, Daniel
McCue, Ann
Brenner, Robert
ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ENTION: METHODS
QUENCES: 57
CE ADDRESS:
Brown, Martin, Haller & McClain
660 Union Street
Diego
lifornia
USA
1-2926
DABLE FORM:
E: Diskette
IBM Compatible
SYSTEM: DOS
FastSeq Version 1.5
ICATION DATA:
N NUMBER: US/08/223,305C
E: April 4, 1994
ATION DATA:
N NUMBER: 07/868,354
E: April 10, 1992
ATION DATA:
N NUMBER: US 07/745,206
E: 15-AUG-1991
ATION DATA:
N NUMBER: US 07/620,250
E: 30-NOV-1990
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N NUMBER: US 07/482,384
E: 20-FEB-1990
ATION DATA:
N NUMBER: US 07/603,751
E: 04-APR-1989
ATION DATA:
N NUMBER: WO PCT/US89/01408
E: 04-APR-1989
ATION DATA:
N NUMBER: US 07/176,899
E: 04-APR-1988
NT INFORMATION:
dman, Stephanie L.
ON NUMBER: 33,779
DOCKET NUMBER: 52516 (P519739)
ATION INFORMATION:
(619)238-0999
(619)238-0062
R SEQ ID NO: 55:
PACTERISTICS:
079 amino acids
no acid
SS: single
linear
E: protein
E: internal
98.3%; Score 5503; DB 2; Length 1079;
larity 98.8%; Pred. No. 0;
Conservative 0; Mismatches 1; Indels 12; Gaps 2;
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61	YEKYQDLYTVENPNARQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHORE	Db
121	EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEG	Qy
121	EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEG	Db
181	NELNWTSALEDVFKKREEDPSLLMQVFGSATGLARYYPASPMVDSNRSPNKIDL	Qy
181	NELNWTSALEDVFKKREEDPSLLMQVFGSATGLARYYPASPMVDSNRSPNKIDL	Db
241	RPWYIQAASPKDMLILVDVSGVSLTLKLRISVSEMLETLSDDDDFNVASFN	Qy
241	RPWYIQAASPKDMLILVDVSGVSLTLKLRISVSEMLETLSDDDDFNVASFN	Db
301	VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYSRANCN	Qy
301	VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYSRANCN	Db
361	FTDGEERAQEIENKYNKDKKVRVPSVGOHNYERGPIONMACENKGYIYEIPS	Qy
361	FTDGEERAQEIENKYNKDKKVRVPSVGOHNYERGPIONMACENKGYIYEIPS	Db
421	INTQEVLDVLRPMVLGADKAKOVMTNVYLDALGLVITGLTPVFNITGQFEN	Qy
421	INTQEVLDVLRPMVLGADKAKOVMTNVYLDALGLVITGLTPVFNITGQFEN	Db
481	NQILGVMGVDVSLSDIKRLTPRFTLCPNGYYPADIPNGVYLLHPLNLPKPKSC	Qy
481	NQILGVMGVDVSLSDIKRLTPRFTLCPNGYYPADIPNGVYLLHPLNLPKPKSC	Db
541	DFLDAELENDIKVIRKMKIDGESGKTFRLVKSDODERYIDKGNRTYTWTPVNG	Qy
536	DFLDAELENDIKVIRKMKIDGESGKTFRLVKSDODERYIDKGNRTYTWTPVNG	Db
601	ALVLPYTSFYIYKALEETITQARSKKGMKDSKTLKPDNFEESSGYTFTIAPRDC	Qy
596	ALVLPYTSFYIYKALEETITQARY-----SETLKPDNFEESSGYTFTIAPRDC	Db
661	SDNTEFLNPNFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYFWSQKNIK	Qy
649	SDNTEFLNPNFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYFWSQKNIK	Db
721	FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGGCP	Qy
709	FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGGCP	Db
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769	MVSKAVEIYIQGKLLKPAVVVGIKIDVNSWIENFTKTSIRDPACAGPVCDCRNSDV	Db
841	LDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG	Qy
829	LDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG	Db
901	GAGHRSAYVPSVADIIQIGHWATAAASIIQQFLSLTFPRLLLEAVEMEDDDFTA	Qy
889	GAGHRSAYVPSVADIIQIGHWATAAASIIQQFLSLTFPRLLLEAVEMEDDDFTA	Db
961	SCITEQTQYFFDNDKSKPSGVLDCGNCRSIFHGEKLMNTNLIIFIMVESKGTCPCL	Qy
949	SCITEQTQYFFDNDKSKPSGVLDCGNCRSIFHGEKLMNTNLIIFIMVESKGTCPCL	Db
1021	QASQTSQGNPCDMVKQPRYKGPVCFDNNVLEDYTDGGSVS 1063	Qy
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RESULT 15

07:56:52 2004

us-10-090-827-14.ra1

GenCore version 5.1.1.6
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in search, using sw model

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10-090-827-14

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h: 0

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/cgn2_6/prodata/1/1aa/6A_COMB.pep:*

/cgn2_6/prodata/1/1aa/6B_COMB.pep:*

/cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*

/cgn2_6/prodata/1/1aa/backfiles1.pep:*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

Query	Length	DB	ID	Description
10.0	1091	1	US-07-745-206A-25	Sequence 25, Appl
10.0	1091	1	US-08-455-543A-52	Sequence 52, Appl
10.0	1091	2	US-08-223-305C-52	Sequence 52, Appl
10.0	1091	2	US-08-311-363-25	Sequence 25, Appl
9.9	1091	3	US-08-713-118-4	Sequence 4, Appl
9.9	1091	3	US-09-452-007-4	Sequence 4, Appl
9.3	1086	1	US-08-455-543A-54	Sequence 54, Appl
9.3	1086	2	US-08-223-305C-54	Sequence 54, Appl
9.0	1084	1	US-08-455-543A-56	Sequence 56, Appl
9.0	1084	2	US-08-223-305C-56	Sequence 56, Appl
8.6	1103	1	US-08-455-543A-53	Sequence 53, Appl
8.6	1103	2	US-08-223-305C-53	Sequence 53, Appl
8.2	1079	1	US-08-455-543A-55	Sequence 55, Appl
8.2	1079	2	US-08-223-305C-55	Sequence 55, Appl
6.1	1106	1	US-08-435-675B-5	Sequence 5, Appl
5.7	1106	1	US-08-336-257A-8	Sequence 8, Appl
1.5	1086	6	5386025-8	Patent No. 5386025
13.4	1145	4	US-09-470-443-2	Sequence 2, Appl
13.4	1145	4	US-09-470-443-4	Sequence 4, Appl
13.0	1076	4	US-09-470-443-6	Sequence 6, Appl
17.4	508	1	US-08-435-675B-6	Sequence 6, Appl
3.3	885	3	US-09-074-579-5	Sequence 5, Appl
3.3	885	3	US-09-388-774-5	Sequence 5, Appl
2.9	946	3	US-09-074-579-3	Sequence 3, Appl
2.9	946	3	US-09-388-774-3	Sequence 3, Appl
2.9	894	4	US-09-071-035-248	Sequence 248, App
2.9	962	4	US-09-071-035-246	Sequence 246, App

28	158.5	2.9	962	4	US-09-071-035-250	Sequence
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31	158.5	2.9	962	4	US-09-071-035-474	Sequence
32	158.5	2.9	962	4	US-09-071-035-478	Sequence
33	154.5	2.8	946	4	US-09-546-153-1	Sequence
34	154	2.8	903	1	US-08-021-601-12	Sequence
35	154	2.8	903	1	US-08-082-849B-12	Sequence
36	154	2.8	903	5	PCT-US94-01624-12	Sequence
37	152.5	2.8	789	1	US-08-471-033-32	Sequence
38	152.5	2.8	789	2	US-08-471-044-32	Sequence
39	152.5	2.8	789	2	US-08-463-483A-32	Sequence
40	152.5	2.8	789	2	US-08-471-046A-32	Sequence
41	152.5	2.8	789	2	US-08-470-566B-32	Sequence
42	152.5	2.8	789	2	US-08-838-219B-4	Sequence
43	152.5	2.8	789	2	US-08-469-334-32	Sequence
44	152.5	2.8	789	3	US-09-300-529-32	Sequence
45	152.5	2.8	789	3	US-09-233-336A-4	Sequence

ALIGNMENTS

RESULT 1
US-07-745-206A-25
Sequence 25, Application US/07745206A
Patent No. 5429971

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: Fitch, Even, Tabin & Flannery
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07745,206A
FILING DATE: 19910815
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 51504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-745-206A-25

Query Match 100.0%; Score 5443; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0;

QY 1 MAAGCLLALTTLFQSLIGPSSEPPSPFSAVTKISWVDKMQEDLVTLAKTAGVNM
DB 1 MAAGCLLALTTLFQSLIGPSSEPPSPFSAVTKISWVDKMQEDLVTLAKTAGVNM

GENERAL INFORMATION:
 APPLICANT: Harpold, Michael
 APPLICANT: Ellis, Steven
 APPLICANT: Williams, Mark
 APPLICANT: Feldman, Daniel
 APPLICANT: McCue, Ann
 APPLICANT: Brenner, Robert
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 TITLE OF INVENTION: METHODS
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/455,543A
 FILING DATE: May 31, 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/223,305
 FILING DATE: April 4, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/868,354
 FILING DATE: April 10, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/745,206
 FILING DATE: 15-AUG-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/620,250
 FILING DATE: 30-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/482,384
 FILING DATE: 20-FEB-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/603,751
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US89/01408
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/176,899
 FILING DATE: 04-APR-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-52517
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619)238-0999
 TELEFAX: (619)238-0062
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1091 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-455-543A-52

Query Match 100.0%; Score 5443; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0;

QY	1	MAAGCLLALTLTLFQSL	IGPSS	EEPP	PPSA	VTIK	SWDK	MQED	LVTL	LAKT	ASGV
Db	1	MAAGCLLALTLTLFQSL <th>IGPSS</th> <th>EEPP</th> <th>PPSA</th> <th>VTIK</th> <th>SWDK</th> <th>MQED</th> <th>LVTL</th> <th>LAKT</th> <th>ASGV</th>	IGPSS	EEPP	PPSA	VTIK	SWDK	MQED	LVTL	LAKT	ASGV


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QTSQGNPCDMVK 1036

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plication US/08311363

958

ATION:

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APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
METHODS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-311-363-25

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Query Match 100.0%; Score 5443; DB 2; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1036; Conservative 0; Mismatches 0; Indels 0;

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DB 61 YEKYQDLYTVPEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHWR
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DB 181 NELNWTLSALDEVFKKNEEDPSLLWQVFGSGLTGLARYYPASPVVDNSRTNPKIDL
QY 241 RPYIYQGAASPKDMLILVDVSGSVGLTLKLIRTSVSEMLETSLDDDFVNVASFN
DB 241 RPYIYQGAASPKDMLILVDVSGSVGLTLKLIRTSVSEMLETSLDDDFVNVASFN
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DB 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAPEQLLNYSRANCN
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07:56:52 2004

us-10-090-827-14.ra1

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Db KFLMANHDDYTNQIGRFGEIDPSLMHNLNIVSYAFNKSVDYQSVCEPGAAPKQ 900
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ication US/08713118
36
TION:
ranco, Rodrigo
un Chen, Ai Ru
uey, David J.
TION: NUCLEIC ACID ENCODING HUMAN NEURONAL
JENCES: 6
E ADDRESS:
Hamilton, Brook, Smith & Reynolds, P.C.
o Militia Drive
ngton
ISA
-4799
ABLE FORM:
: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patent In Release #1.0, Version #1.30
ICATION DATA:
I NUMBER: US/08/713,118
I: 16-SEP-1996
ION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Mata, Elizabeth W.
REGISTRATION NUMBER: 38,236
REFERENCE/DOCKET NUMBER: ACC96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-713-118-4
Query Match 99.9%; Score 5439; DB 3; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 1; Indels 0;
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Db 1 MAAGCLLALTTLFQSLILIGSPSSPEPPPSAVTIKSWVDKMQEDLVTLAKTASGVN
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Db 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHOMREI
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Db 121 EVVYNAXDDLDPEKNDSEPGSQRIPKFVIEDANFGROI SYOHAHVHPTDIYEG
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Db 181 NELNWTSAALDEVFKKNREEDPSLLMQVFGSATGLARYYPASVPWVNSRTPNKIDL
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Db 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRITSVSEMLETLSDDDFVNVSFNI
QY 301 VSCFOHLVQANVRNKKVLDANNITAKGITDYKKGFSFAPELLNLYNVSRAVNCNI
Db 301 VSCFOHLVQANVRNKKVLDANNITAKGITDYKKGFSFAPELLNLYNVSRAVNCNI
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Db 361 FTDGGEERAQELFNKYNDKKVRVFRFVSGQHYERGPQIMMACENKGYIYIIPS.
QY 421 INTQBYLDVLRPMVLADGKAKQVQWNTVYLDALGLVITGLPVFNITGQFENI
Db 421 INTQBYLDVLRPMVLADGKAKQVQWNTVYLDALGLVITGLPVFNITGQFENI
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Db 481 NQLILGVMGVDVSLSDIKRLTPRFTLCPNGYFAIDPNGYVLLHNPQLPNKPSQI
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Db 541 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRTYTWTVPNG
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Db 721 FVVTDDGITRVYPKAGENQWNPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAI
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 QTSQGNPCDMVK 1036
 Publication US/09452007
 485
 ATION:
 Franco, Rodrigo
 Sun Chen, Ai Ru
 Suey, David J.
 ENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
 ENTION: CALCIUM CHANNEL SUBUNITS
 QUENCES: 6
 CE ADDRESS:
 Hamilton, Brook, Smith & Reynolds, P.C.
 700 Militia Drive
 ington
 USA
 3-4799
 DABLE FORM:
 B: Floppy disk
 IBM PC compatible
 SYSTEM: PC-DOS/MS-DOS
 Patent in Release #1.0, Version #1.30
 ICATION DATA:
 N NUMBER: US/09/452.007
 E:
 TION:
 ATION DATA:
 N NUMBER: US/08/713.118
 E: 16-SEP-1996
 NT INFORMATION:
 a, Elizabeth W.
 ON NUMBER: 38.236
 DOCKET NUMBER: ACC96-01
 ATION INFORMATION:
 617-861-6240
 617-861-9540
 R SEQ ID NO: 4:
 RACTERISTICS:
 091 amino acids
 no acid
 linear
 E: protein
 99.9%; Score 5439; DB 3; Length 1091;
 larity 99.9%; Pred. No. 0;
 Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Qy 1021 QABQTSQGNPCDMVK 1036
 Db 1021 QABQTSQGNPCDMVK 1036

RESULT 7
 US-08-455-543A-54
 ; Sequence 54, Application US/084555543A
 ; Patent No. 5792846
 ; GENERAL INFORMATION:

Harold, Michael
 Ellis, Steven
 Williams, Mark
 Feldman, Daniel
 McCue, Ann
 Brenner, Robert
 ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ENTION: METHODS
 UENCES: 57
 E ADDRESS:

Brown, Martin, Haller & McClain

560 Union Street

Diego

California

USA

1-2926

CABLE FORM:

3: Diskette

IBM Compatible

SYSTEM: DOS

FastSeq Version 1.5

ICATION DATA:

NUMBER: US/08/455,543A

3: May 31, 1995

ATION DATA:

NUMBER: 08/223,305

3: April 4, 1994

ATION DATA:

NUMBER: 07/868,354

3: April 10, 1992

ATION DATA:

NUMBER: US 07/745,206

3: 15-AUG-1991

ATION DATA:

NUMBER: US 07/620,250

3: 30-NOV-1990

ATION DATA:

NUMBER: US 07/482,384

3: 20-FEB-1990

ATION DATA:

NUMBER: US 07/603,751

3: 04-APR-1989

ATION DATA:

NUMBER: WO PCT/US89/01408

3: 04-APR-1989

ATION DATA:

NUMBER: US 07/176,899

3: 04-APR-1988

IT INFORMATION:

Inman, Stephanie L.

IN NUMBER: 33,779

OCKET NUMBER: 6362-52517

ATION INFORMATION:

(619)238-0999

(619)238-0062

SEQ ID NO: 54:

ACTERISTICS:

86 amino acids

no acid

IS: single

linear

protein

internal

99.3%; Score 5403.5; DB 1; Length 1086;

arity 99.5%; Pred.No. 0;

Conservative 0; Mismatches 0; Indels 5; Gaps 1;

ICLLALTLTLFQSLILGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGSVNQLVDI 60

ICLLALTLTLFQSLILGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGSVNQLVDI 60

QY 61 YEKYQDLTYTVEPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHORE
 Db 61 YEKYQDLTYTVEPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHORE
 QY 121 EYVYNAKDDLDPEKNDSEPGSRIPKPVIEDANFGROI SYQHAAVHIPTDIYEG
 Db 121 EYVYNAKDDLDPEKNDSEPGSRIPKPVIEDANFGROI SYQHAAVHIPTDIYEG
 QY 181 NELNWTSSALDEVFKKRRBEDPSLLMQVFGSATGLARYYPASPWVNSRTPNKIDL
 Db 181 NELNWTSSALDEVFKKRRBEDPSLLMQVFGSATGLARYYPASPWVNSRTPNKIDL
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTILKLRITSVSEMLETLSDDDFVNVSFN
 Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTILKLRITSVSEMLETLSDDDFVNVSFN
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGSPAFQOLLNRYNSRANCN
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGSPAFQOLLNRYNSRANCN
 QY 361 FTDGGEERAQEI FNKYNKDKKVRVFRFSGQHNBERGPIQWMACENKGYYYIPIS
 Db 361 FTDGGEERAQEI FNKYNKDKKVRVFRFSGQHNBERGPIQWMACENKGYYYIPIS
 QY 421 INTQEYLDVLRPMVLADGKAKQVQWNTVYLDLLELGLVITGTLPVFNITGQFEN
 Db 421 INTQEYLDVLRPMVLADGKAKQVQWNTVYLDLLELGLVITGTLPVFNITGQFEN
 QY 481 NQLILGWVGVDVSLIEDIKELTPRFTLCPNGYYFAIDPNGYVLLHNPLOKPKSQ
 Db 481 NQLILGWVGVDVSLIEDIKELTPRFTLCPNGYYFAIDPNGYVLLHNPLOKPKSQ
 QY 541 DFLDAELNDIKVEIRNKMIDGESSEKTPRTLVKQDERYIDKGNRTYTWTPVNG
 Db 536 DFLDAELNDIKVEIRNKMIDGESSEKTPRTLVKQDERYIDKGNRTYTWTPVNG
 QY 601 ALVLTYSFYIYKAKLEETITQARSKKGMKDSITLKPDPNFESGYTFTAPRDYC
 Db 596 ALVLTYSFYIYKAKLEETITQARSKKGMKDSITLKPDPNFESGYTFTAPRDYC
 QY 661 SDNTEFLNLFNEFIDRKTNNPNSCNADLINRVLADAGFTNELVQVNSKQKNIK
 Db 656 SDNTEFLNLFNEFIDRKTNNPNSCNADLINRVLADAGFTNELVQVNSKQKNIK
 QY 721 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
 Db 716 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
 QY 781 MYSKAVEIYIQGLLKPAVVGIKIDVNSWIENFTKTSIRDP CAGPVCDCKRNSDV
 Db 776 MYSKAVEIYIQGLLKPAVVGIKIDVNSWIENFTKTSIRDP CAGPVCDCKRNSDV
 QY 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMHVLNIVYAFNKSYDYSVCEPG
 Db 836 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMHVLNIVYAFNKSYDYSVCEPG
 QY 901 GAGHSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLEAEMEDDDFTAI
 Db 896 GAGHSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLEAEMEDDDFTAI
 QY 961 SCITEQTQYFFDNDKSGFVLDGNCNCSRI FHGEKLMNTNLIFIMVESKGTCPD
 Db 956 SCITEQTQYFFDNDKSGFVLDGNCNCSRI FHGEKLMNTNLIFIMVESKGTCPD
 QY 1021 QABQTSQDGNPCDMVK 1036
 Db 1016 QABQTSQDGNPCDMVK 1031

RESULT 8

US-08-223-305C-54

; Sequence 54; Application US/08223305C

; Patent No. 5851824

ATION: Harpold, Michael
Ellis, Steven
Williams, Mark
Feldman, Daniel
McCue, Ann
Brenner, Robert
ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ENTION: METHODS
QUENCES: 57
ICE ADDRESS:
Brown, Martin, Haller & McClain
660 Union Street
Diego
California
USA
1-2926
TABLE FORM:
E: Diskette
IBM Compatible
SYSTEM: DOS
FastSEQ Version 1.5
ICATION DATA:
N NUMBER: US/08/223,305C
E: April 4, 1994
ATION DATA:
N NUMBER: 07/868,354
E: April 10, 1992
ATION DATA:
N NUMBER: US 07/745,206
E: 15-AUG-1991
ATION DATA:
N NUMBER: US 07/620,250
E: 30-NOV-1990
ATION DATA:
N NUMBER: US 07/482,384
E: 20-FEB-1990
ATION DATA:
N NUMBER: US 07/603,751
E: 04-APR-1989
ATION DATA:
N NUMBER: WO PCT/US89/01408
E: 04-APR-1989
ATION DATA:
N NUMBER: US 07/176,899
E: 04-APR-1988
NT INFORMATION:
dman, Stephanie L.
ON NUMBER: 33,779
DOCKET NUMBER: 52516 (P519739)
ATION INFORMATION:
(619)238-0999
R SEQ ID NO: 54:
ACTERISTICS:
086 amino acids
no acid
SS: single
linear
E: protein
E: internal

99.3%; Score 5403.5; DB 2; Length 1086;
ilarity 99.5%; Pred. NO. 0;
Conservative 0; Mismatches 0; Indels 5; Gaps 1;

GLIALTLTLFQSLIGSSSEPPPSAVTIKSWDMQEDLVTLAKTASGYNQLVDI 60
GLIALTLTLFQSLIGSSSEPPPSAVTIKSWDMQEDLVTLAKTASGYNQLVDI 60
YQDLYTVPNNARQVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHQRW 120

Db 61 YEKYQDLYTVPNNARQVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHQRW
Qy 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHTPTDIYE
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHTPTDIYE
Qy 181 NELNWTSADEVFPKQNEEDPSLLMQVFGSATGLARYYPASPMVDNSRTNPKIDI
Db 181 NELNWTSADEVFPKQNEEDPSLLMQVFGSATGLARYYPASPMVDNSRTNPKIDI
Qy 241 RPWYIQGAASPQKMLILVDVSGSVSLGLTKLIRTSVSEMLETSLDDDPVNVASPT
Db 241 RPWYIQGAASPQKMLILVDVSGSVSLGLTKLIRTSVSEMLETSLDDDPVNVASPT
Qy 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNTNVSRANC
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNTNVSRANC
Qy 361 FTGGEERAQEIENKYNKDKKVRVFRFSVQGHNYERGPIONMACENKGYTYEIP
Db 361 FTGGEERAQEIENKYNKDKKVRVFRFSVQGHNYERGPIONMACENKGYTYEIP
Qy 421 INTOEYLDVLGRPMVLADGKAKOVQNTNVLDALELGLVITGLPVFNITGQPEI
Db 421 INTOEYLDVLGRPMVLADGKAKOVQNTNVLDALELGLVITGLPVFNITGQPEI
Qy 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYYPFAIDPENGYYLLHPNLQPKNPKS
Db 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYYPFAIDPENGYYLLHPNLQPKNPKS
Qy 541 DFLDAELENDIKVEIRNKMIDGSGSEKTFRTLKVSQDERVIDKGNRTYTTVPNK
Db 536 DFLDAELENDIKVEIRNKMIDGSGSEKTFRTLKVSQDERVIDKGNRTYTTVPNK
Qy 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSKTLKPDNFESGYTFIAPRDY
Db 596 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSKTLKPDNFESGYTFIAPRDY
Qy 661 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSKQKNII
Db 656 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSKQKNII
Qy 721 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPG
Db 716 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPG
Qy 781 MVSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPACAPVCDCKRNSD
Db 776 MVSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPACAPVCDCKRNSD
Qy 841 LDDGGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPC
Db 836 LDDGGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPC
Qy 901 GAGHRSAYVESVADILQIGWNATAAASWILQOFLLSLTFPRLLAEVEMEDDDFTF
Db 896 GAGHRSAYVESVADILQIGWNATAAASWILQOFLLSLTFPRLLAEVEMEDDDFTF
Qy 961 SCITEQTQYFFDNDKSKFSVGLDCGNCRI FHGKLMNTNLIFIMVESKGTCPCI
Db 956 SCITEQTQYFFDNDKSKFSVGLDCGNCRI FHGKLMNTNLIFIMVESKGTCPCI
Qy 1021 QABQTSQGNPCDMVK 1036
Db 1016 QABQTSQGNPCDMVK 1031

RESULT 9
US-08-455-543A-56
; Sequence 56, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael

Ellis, Steven
Williams, Mark
Feldman, Daniel
McCue, Ann
Brenner, Robert
ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ENTION: METHODS
SEQUENCES: 57

DE ADDRESS:
Brown, Martin, Haller & McClain
560 Union Street
San Diego
California
USA

1-2926

TABLE FORM:

3: Diskette

IBM Compatible

SYSTEM: DOS

FastSEQ Version 1.5

ICATION DATA:

1 NUMBER: US/08/455,543A

3: May 31, 1995

ATION DATA:

1 NUMBER: 08/223,305

3: April 4, 1994

ATION DATA:

1 NUMBER: 07/868,354

3: April 10, 1992

ATION DATA:

1 NUMBER: US 07/745,206

3: 15-AUG-1991

ATION DATA:

1 NUMBER: US 07/620,250

3: 30-NOV-1990

ATION DATA:

1 NUMBER: US 07/482,384

3: 20-FEB-1990

ATION DATA:

1 NUMBER: US 07/603,751

3: 04-APR-1989

ATION DATA:

1 NUMBER: WO PCT/US89/01408

3: 04-APR-1989

ATION DATA:

1 NUMBER: US 07/176,899

3: 04-APR-1988

IT INFORMATION:

Inman, Stephanie L.

IN NUMBER: 33,779

DOCKET NUMBER: 6362-52517

ATION INFORMATION:

(619)238-0999

(619)238-0062

SEQU ID NO: 56:

ACTERISTICS:

84 amino acids

10 acid

IS: single

linear

protein

internal

99.0%; Score 5386.5; DB 1; Length 1084;

arity 99.2%; Pred. No. 0;

Conservative 0; Mismatches 1; Indels 7; Gaps 1;

3:LLALLTLTLFQSLIGPSEEPFPPSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60

3:LLALLTLTLFQSLIGPSEEPFPPSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60

3:LLALLTLTLFQSLIGPSEEPFPPSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60

3:LLALLTLTLFQSLIGPSEEPFPPSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60

3:LLALLTLTLFQSLIGPSEEPFPPSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60

3:LLALLTLTLFQSLIGPSEEPFPPSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60

3:LLALLTLTLFQSLIGPSEEPFPPSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60

3:LLALLTLTLFQSLIGPSEEPFPPSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60

3:LLALLTLTLFQSLIGPSEEPFPPSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60

3:LLALLTLTLFQSLIGPSEEPFPPSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60

61 YEKYQDLYTVEPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHOWRE
121 EYVYTNAXDLDPEKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEG
121 EYVYTNAXDLDPEKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEG
181 NELNMTSALDVPKKNREEDPSLLMQVFGSATGLARYYPASPVWDSRTPNKIDL
181 NELNMTSALDVPKKNREEDPSLLMQVFGSATGLARYYPASPVWDSRTPNKIDL
241 RPYWYQGAASPKOMLILVDVSGSVGLTLKLTSTVSEMLETLSDDDFVNVSFN
241 RPYWYQGAASPKOMLILVDVSGSVGLTLKLTSTVSEMLETLSDDDFVNVSFN
301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFQOLLNYSRANCN
301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFQOLLNYSRANCN
361 FTDGGEERAQEIIPNKYNKDKKVRFRFSVGOHNYERGPIONMACENKGYIYIIPS
361 FTDGGEERAQEIIPNKYNKDKKVRFRFSVGOHNYERGPIONMACENKGYIYIIPS
421 INTQSYLDVILGRPMVLADGKAKQVONTNYYLDLALGLVITGTLPVFNITGQFEN
421 INTQSYLDVILGRPMVLADGKAKQVONTNYYLDLALGLVITGTLPVFNITGQFEN
481 NQLILGVMGVDVSLIEDIKLTPRFTLCPNGYFAIDPNGYVLLHPLNLPKNPKSQ
481 NQLILGVMGVDVSLIEDIKLTPRFTLCPNGYFAIDPNGYVLLHPLNLPKNPKSQ
541 DFLDAELENDAI KVEIRNKMIDGESGEKTPRTLKVSQDERYIDKGNRTYTWTPVNG
541 DFLDAELENDAI KVEIRNKMIDGESGEKTPRTLKVSQDERYIDKGNRTYTWTPVNG
601 ALVLPITYSPYIYKAKLEETITQARSKKKKKMDSETILKPDNPEESGYTTPAPRDYC
601 ALVLPITYSPYIYKAKLEETITQARSKKKKKMDSETILKPDNPEESGYTTPAPRDYC
661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVONYWSKQKNIK
661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVONYWSKQKNIK
654 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVONYWSKQKNIK
654 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVONYWSKQKNIK
721 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
721 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
714 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
714 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGVCDCKRNSDV
781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGVCDCKRNSDV
774 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGVCDCKRNSDV
774 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGVCDCKRNSDV
841 LDDGGFLMANHDDVTNIOIGREFGIDPDLMRHLVNI SVYAFNKSVDYQSVCEPG
841 LDDGGFLMANHDDVTNIOIGREFGIDPDLMRHLVNI SVYAFNKSVDYQSVCEPG
834 LDDGGFLMANHDDVTNIOIGREFGIDPDLMRHLVNI SVYAFNKSVDYQSVCEPG
834 LDDGGFLMANHDDVTNIOIGREFGIDPDLMRHLVNI SVYAFNKSVDYQSVCEPG
901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPPRLLEAVEMEDDDFTA
901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPPRLLEAVEMEDDDFTA
894 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPPRLLEAVEMEDDDFTA
894 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPPRLLEAVEMEDDDFTA
961 SCITETQYFFDNDKSPSGVLDCCGCSRI FHGEKLMNTNLI FIMVESKGTGCPD
961 SCITETQYFFDNDKSPSGVLDCCGCSRI FHGEKLMNTNLI FIMVESKGTGCPD
954 SCITETQYFFDNDKSPSGVLDCCGCSRI FHGEKLMNTNLI FIMVESKGTGCPD
954 SCITETQYFFDNDKSPSGVLDCCGCSRI FHGEKLMNTNLI FIMVESKGTGCPD
1021 QAEQTSQDGNPCDMVK 1036
1021 QAEQTSQDGNPCDMVK 1036
1014 QAEQTSQDGNPCDMVK 1029
1014 QAEQTSQDGNPCDMVK 1029

RESULT 10

US-08-223-305C-56

; Sequence 56, Application US/08223305C

; Patent No. 5851824

; GENERAL INFORMATION:

QY	121	EVVYTNAXDDLDPEKNDSEPGSQR	KPVFI	EDANFGRQISYQHAHV	PTDIYE
Db	121	EVVYTNAXDDLDPEKNDSEPGSQR	KPVFI	EDANFGRQISYQHAHV	PTDIYE
QY	181	NELNWTALSDEVFKKREEDPSLL	WQVFGSATGLARYYP	SPWPWDNSRTPNKDI	
Db	181	NELNWTALSDEVFKKREEDPSLL	WQVFGSATGLARYYP	SPWPWDNSRTPNKDI	
QY	241	RPWYIQGAASPKDMLILVDVSGS	VSGLT	KLIRTSVSEMLETLSDDDFVN	VASF
Db	241	RPWYIQGAASPKDMLILVDVSGS	VSGLT	KLIRTSVSEMLETLSDDDFVN	VASF
QY	301	VSCFOHILVOANVRNKKVLKDA	VNNITAKGITDYKKGFSFA	FEQLLNTNVSRNCI	
Db	301	VSCFOHILVOANVRNKKVLKDA	VNNITAKGITDYKKGFSFA	FEQLLNTNVSRNCI	

301	VSCFHLVQAVRKNKVKJAVNKLIAKGLIDYANGSFAPFQKQUNINVSQR	
QY	FTDGGERAQEIFNKYNKDKKVRFRPSVGQHYERGP IQMMAENKGYIYEIP	361
Db	FTDGGERAQEIFNKYNKDKKVRFRPSVGQHYERGP IQMMAENKGYIYEIP	361
QY	INTQYLDVLGRPMVLADGKAKQVMTNVLDALELGLVITGTLVPVNI	421
Db	INTQYLDVLGRPMVLADGKAKQVMTNVLDALELGLVITGTPVNI	421

Accession	Protein	Gene	Species	Length	Score	E-value	Ident	Positives	Negatives
481	QY	NQIILGVMGVDVSLSDIKRLTPRTFLCPNGYYFAIDPNGYVYLHPNLPQKNPKS(Arabidopsis thaliana	100	100	0.0	100	100	0
481	Db	NQIILGVMGVDVSLSDIKRLTPRTFLCPNGYYFAIDPNGYVYLHPNLPQKNPKS(Arabidopsis thaliana	100	100	0.0	100	100	0
541	QY	DFDLAELENDIKVETIRNMIDGEGSEKTRFLVKSQDERYIDKGNRYTWTTPVNI	Arabidopsis thaliana	100	100	0.0	100	100	0

	Dd	541	DFDLAELNDIKVEIRNMIDGESGEKFTFLVXSQERYLDKGNRTYTPVN
	Qy	601	ALVLPTGYFYIKAKLEETITQAARSKKGKMDSLTKPDNPFESGYTFLAPRDY
	Dd	601	AIVLPVTFYVIKAKLEETITQARY-----STLKPDNPFESGYTFLAPRDY

Qy	661	SDNTEFLINFEFDTRKTPNPNCSNADLNRVLDDAGFTNELVQYWSKQKII
Db	654	SDNTEFLINFEFDTRKTPNPNCSNADLNRVLDDAGFTNELVQYWSKQKII
	701	SRNTEFLINFEFDTRKTPNPNCSNADLNRVLDDAGFTNELVQYWSKQKII

Db	714	FVVTGGITRVYPKEAGENQENPETYEDSFYKGLSLDNDNVVFTAPYFNKSGPG
Qy	781	MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACAGPVCCKENSD

Qy	841	LDGGFLMANHDDYTNQIGRFGEIDPSLMRHLVNISSVAFNKSVDYQSYCEPK
Db	834	LDGGFLMANHDDYTNQIGRFGEIDPSLMRHLVNISSVAFNKSVDYQSYCEPK

502	QY	SCIT	TCQY	FFND	SKFS	GVGL	DCGC	SRIF	PHGE	KL	MNTN	LILF	FMV	SKGT	CP	CP
894	Db	GAGH	SAV	PSV	AD	TLQI	GW	ATA	AA	SS	ILQ	FL	SL	TF	PP	RL
961	QY	SCIT	TCQY	FFND	SKFS	GVGL	DCGC	SRIF	PHGE	KL	MNTN	LILF	FMV	SKGT	CP	CP
954	Db	SCIT	TCQY	FFND	SKFS	GVGL	DCGC	SRIF	PHGE	KL	MNTN	LILF	FMV	SKGT	CP	CP

Qy	1021	QAEQISDGGNEFCMVK	1030
Dd	1014	QAEQTSDDGPNPCDMVK	1029

SECRET - STANDING TAPES ONLY

RESULT 11
US-08-455-543A-53
; Sequence 53, Application US/08455543A
; Patent No. 5792846

; FAcENL NO. 5792848
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven
 ;

Williams, Mark
Feldman, Daniel
McCue, Ann
Brenner, Robert
ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ENTION: METHODS

SOURCES: 57

CE ADDRESS:

Brown, Martin, Haller & McClain

560 Union Street

Diego

California

USA

1-2926

CABLE FORM:

3: Diskette

IBM Compatible

SYSTEM: DOS

FastSeq Version 1.5

ICATION DATA:

NUMBER: US/08/455,543A

3: May 31, 1995

ATION DATA:

NUMBER: 08/223,305

3: April 4, 1994

ATION DATA:

NUMBER: 07/869,354

3: April 10, 1992

ATION DATA:

NUMBER: US 07/745,206

3: 15-AUG-1991

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NUMBER: US 07/620,250

3: 30-NOV-1990

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NUMBER: US 07/482,384

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ATION DATA:

NUMBER: WO PCT/US89/01408

3: 04-APR-1989

ATION DATA:

NUMBER: US 07/176,899

3: 04-APR-1988

AT INFORMATION:

man, Stephanie L.

IN NUMBER: 33,779

OCKET NUMBER: 6362-52517

ATION INFORMATION:

(619)238-0999

(619)238-0062

SEQ ID NO: 53:

ACTERISTICS:

103 amino acids

to acid

IS: single

linear

3: protein

3: internal

98.6%; Score 5367; DB 1; Length 1103;

arity 97.4%; Pred. No. 0;

Conservative 0; Mismatches 1; Indels 26; Gaps 2;

XCLLATLTLFQSLIGPSSEFPFSAVTKSWVDKMQEDLVTLAKTAGVNLVDI 60

XCLLATLTLFQSLIGPSSEFPFSAVTKSWVDKMQEDLVTLAKTAGVNLVDI 60

QDLTYEPNNARQLVEIARADIEKLSNRKALVSLALEAEKVQAAHQRWRE 120

61 YEKYQDLYTVEPNNARQLVEIARADIEKLSNRKALVSLALEAEKVQAAHQRWRE
121 EVVYNAKDDLDPEKNDSEPGSORIKPVFTEDANFGROIYQHAHVHIPTDIYEG
121 EVVYNAKDDLDPEKNDSEPGSORIKPVFTEDANFGROIYQHAHVHIPTDIYEG
181 NELNWTSALEDEVFKKREEDPSLLMQVFGSATGLARYYPASPMVDNSRTPNKIDI
181 NELNWTSALEDEVFKKREEDPSLLMQVFGSATGLARYYPASPMVDNSRTPNKIDI
241 RPWYIQGAASPDKMLILVDVSGVSLGLTKLIRTSVSEMLETSDDDFVNVAFFN
241 RPWYIQGAASPDKMLILVDVSGVSLGLTKLIRTSVSEMLETSDDDFVNVAFFN
301 VSCFQHLVQANVRNKKVLDVANNITAKGTDYKKGPSFAFEOLLNVRNANCN
301 VSCFQHLVQANVRNKKVLDVANNITAKGTDYKKGPSFAFEOLLNVRNANCN
361 FTDGGERAQEI FNKYNKDKKVRVFRFSGQHNYERGP IQMACENKGYIYEIPS
361 FTDGGERAQEI FNKYNKDKKVRVFRFSGQHNYERGP IQMACENKGYIYEIPS
421 INTQEVLDVLRPMVLGADKAKQVQNTVYLDALGLVITGTLPVFNITQGFEN
421 INTQEVLDVLRPMVLGADKAKQVQNTVYLDALGLVITGTLPVFNITQGFEN
481 NOLILGVMGVDSLEDIKELTTPRFTLCPNGYYFAIDPNGVYLLHPLNLPKPGVG
481 NOLILGVMGVDSLEDIKELTTPRFTLCPNGYYFAIDPNGVYLLHPLNLPKPGVG
531 -----NPKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGKTFRTLKVSQ
541 LRKRENIQNPKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGKTFRTLKVSQ
582 DKGNRTYTWTPVNGTDYSLALVLPYTSFYIYKALEETITQARKKGGKMDSETL
601 DKGNRTYTWTPVNGTDYSLALVLPYTSFYIYKALEETITQARKKGGKMDSETL
642 EESGYTFIAPRDYCNLDKISDNNTFELNFEFIDRKTNNPNSCNADLINRVLLD
654 EESGYTFIAPRDYCNLDKISDNNTFELNFEFIDRKTNNPNSCNADLINRVLLD
702 ELVQNTWSKQKNI KGVKARFVVTGDTITRVYKPEAGENMQENPETYEDSFYKRS
714 ELVQNTWSKQKNI KGVKARFVVTGDTITRVYKPEAGENMQENPETYEDSFYKRS
762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKT
774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKT
822 CAGPVCDCRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVN
834 CAGPVCDCRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVN
882 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGHWATAAAWSILQQFLLS
894 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGHWATAAAWSILQQFLLS
942 LLEAVEMEDDDFTASLSKQSCITEQTOYFFDNDSKSFSGVLDCGNCRIFFHGEKLI
954 LLEAVEMEDDDFTASLSKQSCITEQTOYFFDNDSKSFSGVLDCGNCRIFFHGEKLI
1002 IFIMVESKGTCTCDTRLIIQAEQTSDDGNPCDMVK 1036
1014 IFIMVESKGTCTCDTRLIIQAEQTSDDGNPCDMVK 1048

RESULT 12

US-08-223-305C-53

; Sequence 53, Application US/08223305C

; Patent No. 5851824

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

Ellis, Steven
Williams, Mark
Feldman, Daniel
McCue, Ann

Bremer, Robert
ENTON: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ENTON: METHODS

SEQUENCES: 57

ICE ADDRESS:

Brown, Martin, Haller & McClain
660 Union Street
San Diego
California
USA

1-2926

DABLE FORM:

E: Diskette

IBM Compatible

SYSTEM: DOS

FastSeq Version 1.5

ICATION DATA:

N NUMBER: US/08/223,305C

E: April 4, 1994

ATION DATA:

N NUMBER: 07/868,354

E: April 10, 1992

ATION DATA:

N NUMBER: US 07/745,206

E: 15-AUG-1991

ATION DATA:

N NUMBER: US 07/620,250

E: 30-NOV-1990

ATION DATA:

N NUMBER: US 07/482,384

E: 20-FEB-1990

ATION DATA:

N NUMBER: US 07/603,751

E: 04-APR-1989

ATION DATA:

N NUMBER: WO PCT/US89/01408

E: 04-APR-1989

ATION DATA:

N NUMBER: US 07/176,899

E: 04-APR-1988

NT INFORMATION:

ON NUMBER: 33,779

DOCKET NUMBER: 52516 (P519739)

ATION INFORMATION:

(619)238-0999

AR SEQ ID NO: 53:

103 amino acids

no acid

SS: single

linear

E: protein

E: internal

98.6%; Score 5367; DB 2; Length 1103;

ilarity 97.4%; Pred. No. 0;

Conservative 0; Mismatches 1; Indels 26; Gaps 2;

IGCLALTTLTQSLIGSSSEPPPSATYIKSWDKMQEDLVTLAKTASGYNQLVDI 60

IGCLALTTLTQSLIGSSSEPPPSATYIKSWDKMQEDLVTLAKTASGYNQLVDI 60

YQDLYTVEPNARQLVEIAARDIEKLLNSRKALVSLALEAKVQAHHQWREDFASN 120

YQDLYTVEPNARQLVEIAARDIEKLLNSRKALVSLALEAKVQAHHQWREDFASN 120

121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYK
121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYK
181 NELNWTSSALDEVFKQREEDPSLLWQVFGSATGLARYYPASPPWVDSNRTNPKIDI
181 NELNWTSSALDEVFKQREEDPSLLWQVFGSATGLARYYPASPPWVDSNRTNPKIDI
241 RPWYIOGAASPDKMLILVDVSGSVGLTLKLRITSVSEMLETLSDDDFVNVASF
241 RPWYIOGAASPDKMLILVDVSGSVGLTLKLRITSVSEMLETLSDDDFVNVASF
301 VSCFQHLVQANVRNKKVLDANNITAKGITDYKKGSPFAFEQLLNTNVRANC
301 VSCFQHLVQANVRNKKVLDANNITAKGITDYKKGSPFAFEQLLNTNVRANC
361 FTGGERAQRIFNKYNKKKVEFRSPVCOHNYERGPIONMACENKGYIYEIPE
361 FTGGERAQRIFNKYNKKKVEFRSPVCOHNYERGPIONMACENKGYIYEIPE
421 INTQEVLDVLRPMVLGADKAKQVQNTNVLDALEGLVITGTLPVFNITQGFEN
421 INTQEVLDVLRPMVLGADKAKQVQNTNVLDALEGLVITGTLPVFNITQGFEN
481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYYPADPNVGLLHPNLQPK-----
481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYYPADPNVGLLHPNLQPKIGVC
531 -----NPKSQEPVTLPLDAELENDIKVIRNKKMIDGESSEKTRTLVKS
541 LRKRRPNIQPKSQEPVTLPLDAELENDIKVIRNKKMIDGESSEKTRTLVKS
582 DKGNTYTWTFVNGTDYSLALVLTPTSYFYIKAKLBETITQARSKKGMKMDSETI
601 DKGNTYTWTFVNGTDYSLALVLTPTSYFYIKAKLBETITQARY-----SETI
642 EBSGYTFIAPRDYCNLDKISDNNTEFLNNEFIDRKTNNPSCNADLINRVLLI
654 EBSGYTFIAPRDYCNLDKISDNNTEFLNNEFIDRKTNNPSCNADLINRVLLI
702 ELVQYWSKOKNKGKVKARFVWTDGGITRVYPKEAGENMOENPETYEDSFYKRSI
714 ELVQYWSKOKNKGKVKARFVWTDGGITRVYPKEAGENMOENPETYEDSFYKRSI
762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKI
774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKI
822 CAGPVCCKRNSVDMOCVILDDGGFLMANHDDYTNOIGRPFGEIDPSLMRHLV
834 CAGPVCCKRNSVDMOCVILDDGGFLMANHDDYTNOIGRPFGEIDPSLMRHLV
882 FNKSYDYQSVCEPGAAPKQAGHRSVAVPSVADILQIGWATAAASILQOFLLE
894 FNKSYDYQSVCEPGAAPKQAGHRSVAVPSVADILQIGWATAAASILQOFLLE
942 LLEAVEMEDDDFTASLSKQSCITEQTYQFPDNDKSKFSGLDCGNCRIIFHGEKI
954 LLEAVEMEDDDFTASLSKQSCITEQTYQFPDNDKSKFSGLDCGNCRIIFHGEKI
1002 IFIMVESKGTCPDTRLLIOAQTSDGNPCDMVK 1036
1014 IFIMVESKGTCPDTRLLIOAQTSDGNPCDMVK 1048

RESULT 13

US-08-455-543A-55

; Sequence 55, Application US/08455543A

; Patent No. 5792846

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

feldman, Daniel
 leCue, Ann
 renner, Robert
 NTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 NTION: METHODS

REFERENCES: 57

ADDRESS:
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ISA

--2926

ABLE FORM:

;; Diskette

IBM Compatible

SYSTEM: DOS

FastSEQ Version 1.5

CATION DATA:

I NUMBER: US/08/455,543A

;; May 31, 1995

ATION DATA:

I NUMBER: 08/223,305

;; April 4, 1994

ATION DATA:

I NUMBER: 07/868,354

;; April 10, 1992

ATION DATA:

I NUMBER: US 07/745,206

;; 15-AUG-1991

ATION DATA:

I NUMBER: US 07/620,250

;; 30-NOV-1990

ATION DATA:

I NUMBER: US 07/482,384

;; 20-FEB-1990

ATION DATA:

I NUMBER: US 07/603,751

;; 04-APR-1989

ATION DATA:

I NUMBER: WO PCT/US89/01408

;; 04-APR-1989

ATION DATA:

I NUMBER: US 07/176,899

;; 04-APR-1988

IT INFORMATION:

man, Stephanie L.

AN NUMBER: 33,779

CKET NUMBER: 6362-52517

ATION INFORMATION:

(619)238-0999

(619)238-0062

SEQ ID NO: 55:

ACTERISTICS:

79 amino acids

to acid

IS: single

linear

protein

internal

98.2%; Score 5347; DB 1; Length 1079;

arity 98.7%; Pred. No. 0;

conservative 0; Mismatches 1; Indels 12; Gaps 2;

3CLLALTLTLFQSLILGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGNQLVDI 60

3CLLALTLTLFQSLILGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGNQLVDI 60

QDLTYVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHHWRDFASN 120

QDLTYVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHHWRDFASN 120

QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAAVHIPTDIYEG
 Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAAVHIPTDIYEG
 QY 181 NELNWTISALDEVFKKREDEPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
 Db 181 NELNWTISALDEVFKKREDEPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTLKLRISVSEMLETLSDDDFVNVASFN
 Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTLKLRISVSEMLETLSDDDFVNVASFN
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFPELLNYYNVRANCN
 Db 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFPELLNYYNVRANCN
 QY 361 FTDGGERAQAEIFNKYNKDKKRVFRFVSQGHYERGPIONMACENKGYIYIIPS
 Db 361 FTDGGERAQAEIFNKYNKDKKRVFRFVSQGHYERGPIONMACENKGYIYIIPS
 QY 421 INTOEYLDVLGRPMVLADGKAKQVQWNTVNYLDALGLVITGLPVFNITGQFEN
 Db 421 INTOEYLDVLGRPMVLADGKAKQVQWNTVNYLDALGLVITGLPVFNITGQFEN
 QY 481 NQLILGVMGVDVSLIEDIKELTPRFTLCPNGYYFAIDPNGYVLLHHPNLQPKSQ
 Db 481 NQLILGVMGVDVSLIEDIKELTPRFTLCPNGYYFAIDPNGYVLLHHPNLQPKSQ
 QY 541 DELDAELENDAKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRTYTWTPVNG
 Db 541 DELDAELENDAKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRTYTWTPVNG
 QY 596 ALVLTYSFYIYIKAKLEETITQARY-----SETLKPDNFESGYTFIAPDYC
 Db 596 ALVLTYSFYIYIKAKLEETITQARY-----SETLKPDNFESGYTFIAPDYC
 QY 661 SDNTEFLNLFNEFDTRKTPNNPSCNADLINRVLLDAGFTNELVQYWSKQKNIK
 Db 649 SDNTEFLNLFNEFDTRKTPNNPSCNADLINRVLLDAGFTNELVQYWSKQKNIK
 QY 721 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
 Db 709 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
 QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWNIENFTKTSIRDPCAGPVCDCRNSDVI
 Db 769 MYSKAVEIYIQGLKLPVAVGKIDVNSWNIENFTKTSIRDPCAGPVCDCRNSDVI
 QY 841 LDDGGFLMANHDDYTNQIGRPFGEIDPSLMHRLVNI SVYAFNKSVDYQSVCBPG
 Db 829 LDDGGFLMANHDDYTNQIGRPFGEIDPSLMHRLVNI SVYAFNKSVDYQSVCBPG
 QY 901 GAGHSAYVPSVADILQIGWATAAASLQOQFLSLSTFPRLLEAEMEDDDFTA
 Db 889 GAGHSAYVPSVADILQIGWATAAASLQOQFLSLSTFPRLLEAEMEDDDFTA
 QY 961 SCITEQTQYFFDNDKSPSGVLDCCGCSRIFFHGEKLMNTNLIIFIMVESKGTCPD
 Db 949 SCITEQTQYFFDNDKSPSGVLDCCGCSRIFFHGEKLMNTNLIIFIMVESKGTCPD
 QY 1021 QABQTSDBGPNCDMVK 1036
 Db 1009 QABQTSDBGPNCDMVK 1024

RESULT 14

US-08-223-305C-55

; Sequence 55, Application US/08223305C

; Patent No. 5851824

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

121 EVVYTNAKODLPKNDSEPSGRQIKPVFTIEDANFGRCISYCHAAVHPITDIYEC
181 NELNWTLSALDEVFKQNEEDPSLLMQVFGSATGLARYYPASPWVDNSRTEPKNDI
181 NELNWTLSALDEVFKQNEEDPSLLMQVFGSATGLARYYPASPWVDNSRTEPKNDI

241 RPWYIQAASPKDMLILDVSGSVSGITLKLIRTSVSEMLETLLSDDDFVNVSFNF

301 VSCFQHLVOANVRNKKULKDAVNNTAKGITDYKKGFSPAQQLINYNVSRANCO

361 PTDGGERAQEIVFNKYNKKDKKVRVERSVGQHNVERGPIQWMA CENKGGYVEIPDS
361 PTDGGERAQEIVFNKYNKKDKKVRVERSVGQHNVERGPIQWMA CENKGGYVEIPDS

421 INTQEVLDVIGRPMVLADGKAKQVQVNNVYLDALEIGLVITGTLVPVFNITGQFEN
421 INTQEVLDVIGRPMVLADGKAKQVQVNNVYLDALEIGLVITGTLVPVFNITGQFEN
421 INTQEVLDVIGRPMVLADGKAKQVQVNNVYLDALEIGLVITGTLVPVFNITGQFEN
421 INTQEVLDVIGRPMVLADGKAKQVQVNNVYLDALEIGLVITGTLVPVFNITGQFEN

481 NQLILGVMGVDVSLDIKRLTPRETLCPNGYYFAIDPNGVYLLHPNLQPKPKSC
481 NQLILGVMGVDVSLDIKRLTPRETLCPNGYYFAIDPNGVYLLHPNLQPKPKSC

541 DFLDAELNDI KVEIRNKWIDGESGKTRTL VKSQDERVIDKGNRTTWTTPNG
536 DFLDAELNDI KVEIRNKWIDGESGKTRTL VKSQDERVIDKGNRTTWTTPNG

601 ALVLPTYSFVYIKAKLEETITQARSKGKMDSETLKPDNFEESCYTFIAPRDYC
596 ALVLPTYSFVYIKAKLEETITQAPV-----SMTLKPDNFEESCYTTFIAPRDYC

661 SDNTEPLINPNEIDRKTNNPSCHADLINRVLLDAGFTNELQNYWWSKQKNIK
540 SDNTEPTLNAPETDRTDNDPSCHADINVDI DAGEFNEI QNYWWSKQKNIK
530 ADVEFTICIIIAAGAGMEIIIIQKQK QIADIKDNI ELUQIIIFIRKNDI

005 SJANNLEFLEHNFNEFLDKRALFAMFSSKADULLINKVJLDJDFINLVQVQIMWKAQVLL
721 FVWTDGGITRVYVPEAGENQWNPETEDSFVKRSLDNDNVVTFAPYFNKSGPGA
000 FVWTDGGITRVYVPEAGENQWNPETEDSFVKRSLDNDNVVTFAPYFNKSGPGA
000 FVWTDGGITRVYVPEAGENQWNPETEDSFVKRSLDNDNVVTFAPYFNKSGPGA

709 FVVDGGLLRVIPABAGENQWNEFEYEDSTINRSJLUNDUNIVFAPFITNKSJGFG
781 MYSKAVEIYIQGLLKPAVGIKIDVNSWIENFTTISRDPAGVCDCCKRNSDV
782 YAGSQTTHVCGHLYKQIMVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV

769 MVSRAVEIYIQGKLLKPAAVGIKIDVNSWIEFTKITSIRDFCAGEPVCDUCKRNSD
841 LDDGFLLMANHDDYTQIGRFGEIDPSLMRHVLNIVSYAFNKSYDYQSVCBPE

829 LDDGGFLLMANHDDYTNQIGRFEGEIDPSPLEMKHLNVSIAFNAKSYDYQSVCFFP
901 GAGHRSAYVPVSADILQIGWNATAAWSILIQOFLLSLTFPRLLSAVERNEDDDTFA

889 GAGHRSAYPEVSADILIGWWTATAAAWSILCOOLFLLSLTFPLLEAAVEMEDDDDFIT
961 SCITEQTQVFNDKSPGVLDGCGNSRIFHGEKLMNTNLIFIMVESKGTCPD

949 SCITTEQYFFPNDSDSKSPGVLDGCGNSRIIPHGEKLLMNTNLIFLMVESKGTGCPCL
1021 QAEQTS DGNPCDMVK 1036

1009 QAEQTS DGNPCDMVK 1024

675B-5
e 5, Application US/08435675B
No. 5710250
L INFORMATION:

ICANT: Ellis, Steven Bradley
ICANT: Williams, Mark E.
ICANT: Harpold, Michael Miller
ICANT: Schwartz, Arnold

121 EVVYTNAKODLPKNDSEPSGRQIKPVFTIEDANFGRCISYCHAAVHPITDIYEC
181 NELNWTLSALDEVFKQNEEDPSLLMQVFGSATGLARYYPASPWVDNSRTEPKNDI
181 NELNWTLSALDEVFKQNEEDPSLLMQVFGSATGLARYYPASPWVDNSRTEPKNDI

241 RPWYIQAASPKDMLILDVSGSVSGITLKLIRTSVSEMLETLLSDDDFVNVSFNF

301 VSCFQHLVOANVRNKKULKDAVNNTAKGITDYKKGFSPAQQLINYNVSRANCO

361 PTDGGERAQEIVFNKYNKKQKVVRFPSVGHNYERGPQIOMMACENKGGYVEYTPS
361 PTDGGERAQEIVFNKYNKKQKVVRFPSVGHNYERGPQIOMMACENKGGYVEYTPS

421 INTQEVLDVIGRPMVLADGKAKQVQVNNVYLDALEIGLVITGTLVPVFNITGQFEN
421 INTQEVLDVIGRPMVLADGKAKQVQVNNVYLDALEIGLVITGTLVPVFNITGQFEN
421 INTQEVLDVIGRPMVLADGKAKQVQVNNVYLDALEIGLVITGTLVPVFNITGQFEN
421 INTQEVLDVIGRPMVLADGKAKQVQVNNVYLDALEIGLVITGTLVPVFNITGQFEN

481 NQLILGVMGVDVSLDIKRLTPRETLCPNGYYFAIDPNGVYLLHPNLQPKPKSC
481 NQLILGVMGVDVSLDIKRLTPRETLCPNGYYFAIDPNGVYLLHPNLQPKPKSC

541 DFLDAELNDI KVEIRNKWIDGESGKTRTL VKSQDERVIDKGNRTTWTTPVNG
536 DFLDAELNDI KVEIRNKWIDGESGKTRTL VKSQDERVIDKGNRTTWTTPVNG

601 ALVLPTYSFVYIKAKLEETITQARSKGKMDSETLKPDNFEESCYTFIAPRDYC
596 ALVLPTYSFVYIKAKLEETITQAPV-----SMTLKPDNFEESCYTTFIAPRDYC

661 SDNTEPLINPNEIDRKTNNPSCHADLINRVLLDAGFTNELQNYWWSKQKNIK
540 SDNTEPTLNAPETDRTDNDPSCHADINVDI DAGEFNEI QNYWWSKQKNIK
530 ADVEFTICIIIAAGAGMEIIIIQKQK QIADIKDNI ELUQIIIFIRKNDI

005 SJANNLEFLEHNFNEFLDKRALFAMFSSKADULLINKVJLDJDFINLVQVQIMWKAQVLL
721 FVWTDGGITRVYVPEAGENQWNPETEDSFVKRSLDNDNVVTFAPYFNKSGPGA
000 FVWTDGGITRVYVPEAGENQWNPETEDSFVKRSLDNDNVVTFAPYFNKSGPGA
000 FVWTDGGITRVYVPEAGENQWNPETEDSFVKRSLDNDNVVTFAPYFNKSGPGA

709 FVVDGGLLRVIPABAGENQWNEFEYDSTINRSJLUNDUNIVFAPAFINWSGFGF
781 MYSKAVEIYIQGLLKPAVGIKIDVNSWIENFTTISRDPAGVCDCCKRNSDV
782 YAGSQTHTVTCCTHKKQIMVAVGVIRVQVNVNNTNNVTGDTGQITVYCVGTWTHCH

769 MVSRAVEIYIQGKLLKPAAVGIKIDVNSWIEFTKITSIRDFCAGEPVCDUCKRNSD
841 LDDGFLLMANHDDYTQIGRFGEIDPSLMRHVLNIVSYAFNKSYDYQSVCBPE

829 LDDGGFLLMANHDDYTNQIGRFEGEIDPSPLEMKHLNVSVAFNKSYDYQSVCFFP
901 GAGHRSAYPSPSADILQIGWNATAAWSILIQOFLLSLTFPRLLSAVERNEDDDTFA

889 GAGHRSAYPEVSADILIGWWTATAAAWSILCOQFLLSLTFPLLEAAVEMEDDDDFIT
961 SCITEQTQVFFNDNDSKPSGVLDGCGNSRIFHGEKLMNTNLIFIMVESKGTCPCD

949 SCITTEQYFFPNDSDSKSPGVLDGCGNSRIIPHGEKLLMNTNLIFLMVESKGTGCPCL
1021 QAEQTS DGNPCDMVK 1036

1009 QAEQTS DGNPCDMVK 1024

675B-5
e 5, Application US/08435675B
No. 5710250
L INFORMATION:

ICANT: Ellis, Steven Bradley
ICANT: Williams, Mark E.
ICANT: Harpold, Michael Miller
ICANT: Schwartz, Arnold

07:56:52 2004

us-10-090-827-14.ra1

remner, Robert
NATION: CALCIUM CHANNEL COMPOSITIONS AND METHODS

ENCES: 6

E ADDRESS:

Brown, Martin, Haller & McClain
60 Union Street
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-2926

ABLE FORM:

: Diskette

IBM Compatible

SYSTEM: DOS

FastSEQ Version 1.5

CATION DATA:

NUMBER: US/08/435,675B

: 05-MAY-1995

TON: 435

TION DATA:

NUMBER: US 08/314,083

: 28-SEP-1994

NUMBER: US 07/914,231

: 13-JUL-1992

NUMBER: US 07/603,751

: 08-NOV-1990

IT INFORMATION:

man, Stephanie L

AN NUMBER: 33,779

CKET NUMBER: 6362-53193

TION INFORMATION:

619-238-0999

:19-238-0062

SEQ ID NO: 5:

ACTERISTICS:

.06 amino acids

io acid

IS: single

linear

: protein

: internal

: internal

: internal

: internal

: internal

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Db 361 MLFTDGGEEAQAEIFAKYNDKVKRVFTFSVGQHYNDRGPQWMAKCNKGYEII
QY 419 IRIHQEYLDVLRPMWLAGKAKQVQWTVYLDLDELGLVITGLPVENITGQFI
Db 421 IRIHQEYLDVLRPMWLAGKAKQVQWTVYLDLDELGLVITGLPVENITGQFI
QY 479 LKNQILGVMGVDVSLIEDIKELTPRFTLCPNGYYPADPNGYVLLHPLNLPK---
Db 481 LKNQILGVMGVDVSLIEDIKELTPRFTLCPNGYYPADPNGYVLLHPLNLPKPIG
QY 531 -----NPKSQEPTVLDLDAELENDIKVEIRNKMIDGESGEXTFRTLVK
Db 541 INLRKRENVQPKSQEPTVLDLDAELENDIKVEIRNKMIDGESGEXTFRTLVK
QY 580 YIDKGNRTYTWTPVNGTDY-SLALVLPYFYIKAKLEETITQARSKKGMKOSI
Db 601 YIDKGNRTYTWTPVNGTDYSSALVLPYFYIKAKLEETITQARY-----SI
QY 639 DNFEESGYTFIAPRDYCNLDKISDNNTFLLNFNEFIDRKTNNPNSCNADLINRV
Db 654 DNFEESGYTFIAPRDYCSDLKPSDNNTFLLNFNEFIDRKTNNPNSCNTDLINRV
QY 699 FTNELVQNYWSKQNIKGKARFVVDGGITRVYVYKKEAGENWQENPETEYDSFYKI
Db 714 FTNELVQNYWSKQNIKGKARFVVDGGITRVYVYKKEAGENWQENPETEYDSFYKI
QY 759 DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKAPVAVVGIIKIDVNSWIENF
Db 774 DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKAPVAVVGIIKIDVNSWIENF
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Db 834 RDPGAGPVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPDLMRHI
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Job time : 21.6157 secs

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arity 94.8%; Pred. No. 0;
conservative 14; Mismatches 12; Indels 29; Gaps 4;
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GenCore version 5.1.1.6
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in search, using sw model

February 20, 2004, 16:53:09 ; Search time 17.3096 Seconds
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2488.357 Million cell updates/sec

10-090-827-13

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top 10.0 , Gapext 0.5

8717 seqs, 42310858 residues

ts satisfying chosen parameters: 328717

gth: 0

gth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Issued Patents AA:*

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the number of results predicted by chance to have a
or than or equal to the score of the result being printed,
red by analysis of the total score distribution.

SUMMARIES

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10.0	1091	1	US-08-455-543A-52	Sequence 52, Appl
10.0	1091	1	US-08-223-305C-52	Sequence 52, Appl
10.0	1091	2	US-08-311-363-25	Sequence 25, Appl
10.0	1091	3	US-08-713-118-4	Sequence 4, Appl
10.0	1091	3	US-09-452-007-4	Sequence 4, Appl
10.0	1091	3	US-08-455-543A-54	Sequence 54, Appl
10.0	1091	2	US-08-223-305C-54	Sequence 54, Appl
10.0	1091	1	US-08-455-543A-56	Sequence 56, Appl
10.0	1091	2	US-08-223-305C-56	Sequence 56, Appl
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10.0	1091	2	US-08-223-305C-53	Sequence 53, Appl
10.0	1091	1	US-08-455-543A-55	Sequence 55, Appl
10.0	1091	2	US-08-223-305C-55	Sequence 55, Appl
10.0	1091	1	US-08-435-675B-5	Sequence 5, Appl
10.0	1091	6	US-08-336-257A-8	Sequence 8, Appl
10.0	1091	6	5386025-8	Patent No. 5386025
10.0	1091	4	US-09-470-443-2	Sequence 2, Appl
10.0	1091	4	US-09-470-443-4	Sequence 4, Appl
10.0	1091	4	US-09-470-443-6	Sequence 6, Appl
10.0	1091	3	US-08-435-675B-6	Sequence 6, Appl
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10.0	1091	3	US-09-388-774-5	Sequence 5, Appl
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ALIGNMENTS

RESULT 1
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Sequence 25, Application US/07745206A
Patent No. 5429921

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: McCue, Ann

APPLICANT: Feldman, Daniel

TITLE OF INVENTION: Human Calcium Channel Compositions and

TITLE OF INVENTION: Methods

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESS: Fitch, Even, Tabin & Flannery

STREET: 135 S. LaSalle

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07745,206A

FILING DATE: 19910815

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Feder, Scott B

REFERENCE/DOCKET NUMBER: 51504

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-372-7842

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 1091 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-745-206A-25

Query Match 100.0%; Score 5346; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0;

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DB 1 MAAGCLLALTTLFQSLIGPSSEPPFSAVITIKSWDKMOEDLVTLAKTAGVNN

[illegible]

Application IIS/08455543A

846
ATTENTION:
Harpold, Michael
Ellis, Steven
Williams, Mark

APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-52

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44 arpol, Michael
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49 renner, Robert

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TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/223,305C
 FILING DATE: April 4, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/868,354
 FILING DATE: April 10, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/745,206
 FILING DATE: 15-AUG-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/620,250
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 FILING DATE: 20-FEB-1990
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 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US89/01408
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/176,899
 FILING DATE: 04-APR-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 52516 (P519739)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619)238-0999
 TELEFAX: (619)238-0062
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1091 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-223-305C-52

Query Match 100.0%; Score 5346; DB 2; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; C

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ATION:

Harpold, Michael

Ellis, Steven

Williams, Mark

Feldman, Daniel

McCue, Ann

Brenner, Robert

ENTION: Human Calcium Channel Compositions and

ENTION: Methods

QUENCES: 32

CE ADDRESS:

Brown, Martin, Haller & McClain

660 Union Street

CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/311,363
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/745,206
 FILING DATE: 15-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-51506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 238-0999
 TELEFAX: (619) 238-0062
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1091 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-311-363-25

Query Match 100.0%; Score 5346; DB 2; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1018; Conservative 0; Mismatches 0; Indels 0;

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 DB 421 INTQEYLDVLRPMVLADGAKQVQWNTVYLDALGLVITGLPVFNITGQFEN
 QY 481 NQLILGVMGVDSLEDIKELTPRTFLCPNGYYPFADIPNGVYLLHPLNLPKPKSQ
 DB 481 NQLILGVMGVDSLEDIKELTPRTFLCPNGYYPFADIPNGVYLLHPLNLPKPKSQ
 QY 541 DFLLDAELENDDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNG
 DB 541 DFLLDAELENDDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNG

PTYSFYIKAKLEETITQARSKGKMKDSETLKPDNFESGYTFIAPRDYCNLKI 660
 TEFLLNFNEFDRTKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
 TEFLLNFNEFDRTKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
 DGGITRVVPKEAGENWQENPETYEDSFYKRSILDNDNVYFTAPYFNKSPGAYESGI 780
 DGGITRVVPKEAGENWQENPETYEDSFYKRSILDNDNVYFTAPYFNKSPGAYESGI 780
 AVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDP CAGPVCDCRNSDVMDCVI 840
 AVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDP CAGPVCDCRNSDVMDCVI 840
 QFLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEGAPKQ 900
 QFLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEGAPKQ 900
 RSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLLEAVEMEDDDFTASLSQ 960
 RSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLLEAVEMEDDDFTASLSQ 960
 EQTYFFDNDKSPSGVLDGNCRSRIFHGKLMNTNLIFIMVESKGTCPCDTRL 1018
 EQTYFFDNDKSPSGVLDGNCRSRIFHGKLMNTNLIFIMVESKGTCPCDTRL 1018

ication US/08713118

36

tion:

Farago, Rodrigo

un Chen, Ai Ru

uey, David J.

NTION: NUCLEIC ACID ENCODING HUMAN NEURONAL

NTION: CALCIUM CHANNEL SUBUNITS

UENCES: 6

E ADDRESS:

Hamilton, Brook, Smith & Reynolds, P.C.

o Militia Drive

ngton

SA

-4799

ABLE FORM:

: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.30

CATION DATA:

NUMBER: US/08/713,118

: 16-SEP-1996

ION: 435

T INFORMATION:

, Elizabeth W.

N NUMBER: 38,236

CKET NUMBER: ACC96-01

TION INFORMATION:

617-861-6240

17-861-9540

: SEQ ID NO: 4:

ACTERISTICS:

91 amino acids

o acid

linear

: protein

99.9%; Score 5342; DB 3; Length 1091;

Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1017; Conservative 0; Mismatches 1; Indels 0;
 QY 1 MAAGCLLALTTLTLPSSLIGSSSEPPSPSAVTIKSMVDKMOEDLVTLAKTAGSVN
 Db 1 MAAGCLLALTTLTLPSSLIGSSSEPPSPSAVTIKSMVDKMOEDLVTLAKTAGSVN
 QY 61 YEKYQDLTVTPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREI
 Db 61 YEKYQDLTVTPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREI
 QY 121 EYVYNKADLDLDPKNDSEPGSQRIKPVFIEDANFGROI SYOHAHVHIPTDIYEG:
 Db 121 EYVYNKADLDLDPKNDSEPGSQRIKPVFIEDANFGROI SYOHAHVHIPTDIYEG:
 QY 181 NELNWTSSALDEVFKKNREEDPSLLWQVFGSATGLARYYPASVPVDSNRTPNKIDL
 Db 181 NELNWTSSALDEVFKKNREEDPSLLWQVFGSATGLARYYPASVPVDSNRTPNKIDL
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETLSDDDFVNVASFNI
 Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETLSDDDFVNVASFNI
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGIITDYKKGFSFAFEQLLNYNVSRANCNI
 Db 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGIITDYKKGFSFAFEQLLNYNVSRANCNI
 QY 361 PTDGGEERAQELFNKYNDKKVRVFRFSVGOHNYERGPIOMMACENKGYTYEIPS:
 Db 361 PTDGGEERAQELFNKYNDKKVRVFRFSVGOHNYERGPIOMMACENKGYTYEIPS:
 QY 421 INTQBYLDVLGRPMVLADGKAKQVOMTNVYLDALGLVITGTLPVFNITQGFENI
 Db 421 INTQBYLDVLGRPMVLADGKAKQVOMTNVYLDALGLVITGTLPVFNITQGFENI
 QY 481 NQLILGVNGVDVSLIEDIKRLTPRFLCPNGYFFAIDPNGYVLLHNPLOPKPKPSQI
 Db 481 NQLILGVNGVDVSLIEDIKRLTPRFLCPNGYFFAIDPNGYVLLHNPLOPKPKPSQI
 QY 541 DFLDAELENIDKVRIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTWTPVNG
 Db 541 DFLDAELENIDKVRIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTWTPVNG
 QY 601 ALVLPTYSFYIYAKLEETITQARSKGKMKDSETLKPDNFESGYTFIAPRDYCI
 Db 601 ALVLPTYSFYIYAKLEETITQARSKGKMKDSETLKPDNFESGYTFIAPRDYCI
 QY 661 SDNNTFELINFNEDRTKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIK
 Db 661 SDNNTFELINFNEDRTKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIK
 QY 721 FVWTDGGITRVVPKEAGENWQENPETYEDSFYKRSILDNDNVYFTAPYFNKSPGPGAI
 Db 721 FVWTDGGITRVVPKEAGENWQENPETYEDSFYKRSILDNDNVYFTAPYFNKSPGPGAI
 QY 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDP CAGPVCDCRNSDVA
 Db 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDP CAGPVCDCRNSDVA
 QY 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGI
 Db 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGI
 QY 901 GAGRSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLLEAVEMEDDDFTAS
 Db 901 GAGRSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLLEAVEMEDDDFTAS
 QY 961 SCITEQTYQYFFDNDKSPSGVLDGNCRSRIFHGKLMNTNLIFIMVESKGTCPCDI
 Db 961 SCITEQTYQYFFDNDKSPSGVLDGNCRSRIFHGKLMNTNLIFIMVESKGTCPCDI

RESULT 6

361	Db	FTDGEERAQELFNKYNKDKKRVFRFSVQGHNTERGFIQWACENKGYITELP
421	Qy	INTQBYLDVLGRPMVLADGAKAQVQWNTNVYLDALDELGLVITGLPVENITGQFEN
421	Db	INTQBYLDVLGRPMVLADGAKAQVQWNTNVYLDALDELGLVITGLPVENITGQFEN
481	Qy	NQLILGWGVDSVLEDKELTPRFTLCPNGYYFAIDPNGYVLLHPNLQPNKPSX
481	Db	NQLILGWGVDSVLEDKELTPRFTLCPNGYYFAIDPNGYVLLHPNLQPNKPSX
541	Qy	DFDLAELENDIKVIRNKMIDGESGKXFTRLVKSQDERVIDKGNRTYTWTPVNG
541	Db	DFDLAELENDIKVIRNKMIDGESGKXFTRLVKSQDERVIDKGNRTYTWTPVNG
601	Qy	ALVLPYTSFYIYKAKLBETITQARSKKGKMKOSETLKPDPNFESGYTFFIAPDYC
601	Db	ALVLPYTSFYIYKAKLBETITQARSKKGKMKOSETLKPDPNFESGYTFFIAPDYC
661	Qy	SDNNTFFLLNFEFIDRKTNNPCSNADLINRVLLDAGFTNELVQNVYMSKQKIK
661	Db	SDNNTFFLLNFEFIDRKTNNPCSNADLINRVLLDAGFTNELVQNVYMSKQKIK
721	Qy	FVWTDGGITRVYPKEAGENQWENETVEDSPYKBSLNDNDNVFTAPYFNKSGPGF
721	Db	FVWTDGGITRVYPKEAGENQWENETVEDSPYKBSLNDNDNVFTAPYFNKSGPGF
781	Qy	MYSKAVEIYIYGKLLKPAVGIKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDV
781	Db	MYSKAVEIYIYGKLLKPAVGIKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDV
841	Qy	LDDGGFLMAHNDHYTNOIGRPFGEIDPSLMRHLVNI SVTAFNKS YDYQSVCEPC
841	Db	LDDGGFLMAHNDHYTNOIGRPFGEIDPSLMRHLVNI SVTAFNKS YDYQSVCEPC
901	Qy	GAGHRSAYVPSVADILQIGWATAAAWSILQOFLLSLTFPRLLAEAVEMDDDFTF
901	Db	GAGHRSAYVPSVADILQIGWATAAAWSILQOFLLSLTFPRLLAEAVEMDDDFTF
961	Qy	SCITITQOTQYFPDNDKSPSGVDCNGCSIRIPHGBKLMNTNLI FIMVSKSGTCPCI
961	Db	SCITITQOTQYFPDNDKSPSGVDCNGCSIRIPHGBKLMNTNLI FIMVSKSGTCPCI

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1  RESULT 7
2  US-08-455-543A-54
3  ; Sequence 54, Application US/08455543A
4  ; Patent No. 5792846
5  ;
6  ; GENERAL INFORMATION:
7  ;
8  ; APPLICANT: Harpold, Michael
9  ; APPLICANT: Ellis, Steven
10 ; APPLICANT: Williams, Mark
11 ; APPLICANT: Feldman, Daniel
12 ; APPLICANT: McCue, Ann
13 ; APPLICANT: Brenner, Robert
14 ;
15 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
16 ; TITLE OF SEQUENCES: METHODS
17 ; NUMBER OF SEQUENCES: 57
18 ;
19 ; CORRESPONDENCE ADDRESS:
20 ; ADDRESS: Brown, Martin, Haller & McClain
21 ; STREET: 1660 Union Street
22 ; CITY: San Diego
23 ; STATE: California
24 ; COUNTRY: USA
25 ;
26 ; ZIP: 92101-2926
27 ;
28 ; COMPUTER READABLE FORM:
29 ; MEDIUM TYPE: Diskette
30 ; COMPUTER: IBM Compatible
31 ; OPERATING SYSTEM: DOS
32 ; SOFTWARE: FastSEQ Version 1.5
33 ;
34 ; CURRENT APPLICATION DATA:
35 ; APPLICATION NUMBER: US/08/455.543A
36 ; FILING DATE: May 31, 1995

```

TION DATA:
 : NUMBER: 08/223,305
 : April 4, 1994
 TION DATA:
 : NUMBER: 07/868,354
 : April 10, 1992
 TION DATA:
 : NUMBER: US 07/745,206
 : 15-AUG-1991
 TION DATA:
 : NUMBER: US 07/620,250
 : 30-NOV-1990
 TION DATA:
 : NUMBER: US 07/482,384
 : 20-FEB-1990
 TION DATA:
 : NUMBER: US 07/603,751
 : 04-APR-1989
 TION DATA:
 : NUMBER: WO PCT/US89/01408
 : 04-APR-1989
 TION DATA:
 : NUMBER: US 07/176,899
 : 04-APR-1988
 TION DATA:
 : INFORMATION:
 : Inventor: Lman, Stephanie L.
 : IN NUMBER: 33,779
 : SOCKET NUMBER: 6362-52517
 : TION INFORMATION:
 : (619)238-0999
 : 619)238-0062
 : SEQ ID NO: 54:
 : 86 amino acids
 : co acid
 : S: single
 : linear
 : : protein
 : : internal

99.3%; Score 5306.5; DB 1; Length 1086;
 arity 99.5%; Pred. No. 0;
 conservative 0; Mismatches 0; Indels 5; Gaps 1;
 KLLALTLTFLSLLIGPSSSEPPFSAVTKSWDKQEDLVLTAKTASGVNQLVDI 60
 KLLALTLTFLSLLIGPSSSEPPFSAVTKSWDKQEDLVLTAKTASGVNQLVDI 60
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 QDLYTVEPNARQLVEIAARDIEKLLSNRKALVSLALEAEKVQAAHQWREDFASN 120
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 WTSALDEVPKKNREDDPILLMQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240
 TQGAASPKDMLILVDVSGVSLTLKLRITSVSEMLETLSDDDFVNVAASFNSNAQD 300
 TQGAASPKDMLILVDVSGVSLTLKLRITSVSEMLETLSDDDFVNVAASFNSNAQD 300
 QHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAPQLLNYNVSRANCKNIIML 360
 QHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAPQLLNYNVSRANCKNIIML 360
 XGERAQEIPFNKYDKKVRFRFVSQGNRYERGPIQWMAKNGKYYEIPISGIR 420
 XGERAQEIPFNKYDKKVRFRFVSQGNRYERGPIQWMAKNGKYYEIPISGIR 420

QY 421 INTQYLDVLGRPMVLADGKAKQVOMTVNVDLDAELGLVITGTLFVFNITQGFEN
 DB 421 INTQYLDVLGRPMVLADGKAKQVOMTVNVDLDAELGLVITGTLFVFNITQGFEN
 QY 481 NQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPLNLPKPKSQ
 DB 481 NQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPLNLPKPKSQ
 QY 541 DFLDAELENDIKVEIRNMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNG
 DB 536 DFLDAELENDIKVEIRNMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNG
 QY 601 ALVLPYSFYIKAKLEETITQARKSKGKMKDSETLKPDNFEESGYTFIAPRDYCI
 DB 596 ALVLPYSFYIKAKLEETITQARKSKGKMKDSETLKPDNFEESGYTFIAPRDYCI
 QY 661 SDNTEFLINFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQNKIK
 DB 656 SDNTEFLINFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQNKIK
 QY 721 FVTDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGA
 DB 716 FVTDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGA
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVI
 DB 776 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVI
 QY 841 LDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLNIVSYAFNKSVDYQSVCEPG
 DB 836 LDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLNIVSYAFNKSVDYQSVCEPG
 QY 901 GAGHSAYVPSVADILQIGWATAAAMSILOQFLSLTFPRLLLEAVEMEDDDFTAI
 DB 896 GAGHSAYVPSVADILQIGWATAAAMSILOQFLSLTFPRLLLEAVEMEDDDFTAI
 QY 961 SCITEQTYFFDNDKSPSGVLDCGNCRSRIFHGEKLMNTNLIFIMVESKGTGCPD
 DB 956 SCITEQTYFFDNDKSPSGVLDCGNCRSRIFHGEKLMNTNLIFIMVESKGTGCPD

RESULT 8

US-08-223-305C-54
 ; Sequence 54, Application US/08223305C
 ; Patent No. 5851824
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven
 ; APPLICANT: Williams, Mark
 ; APPLICANT: Feldman, Daniel
 ; APPLICANT: McCue, Ann
 ; APPLICANT: Brenner, Robert
 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/223,305C
 ; FILING DATE: April 4, 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/868,354
 ; FILING DATE: April 10, 1992

ATION DATA: US 07/745,206
N NUMBER: 15-AUG-1991
ATION DATA: US 07/620,250
N NUMBER: 30-NOV-1990
ATION DATA: US 07/482,384
N NUMBER: 20-FEB-1990
ATION DATA: US 07/603,751
N NUMBER: 04-APR-1989
ATION DATA: WO PCT/US89/01408
N NUMBER: 04-APR-1989
ATION DATA: US 07/176,899
N NUMBER: 04-APR-1988
NT INFORMATION:
dman, Stephanie L.
ON NUMBER: 33,779
DOCKET NUMBER: 52516 (P519739)
ATION INFORMATION:
(619)238-0999
R SEQ ID NO: 54:
RACTERISTICS:
086 amino acids
no acid
SS: single
linear
E: protein
E: internal

99.3%; Score 5306.5; DB 2; Length 1086;

larity 99.5%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 5; Gaps 1;
GCLLALTLTFLQSLIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
GCLLALTLTFLQSLIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
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YNNAKDDLDPKNDSEPGSQRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEGSTIVL 180
YNNAKDDLDPKNDSEPGSQRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEGSTIVL 180
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NWTSALEDEVFKKNEEDPSLLQWVFGSATGLARYYPASPMVDNSRTNPKIDLYDVR 240
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YIQGAASPDKMLIIVDVSQSGVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
FOHLVQANVRNKKVLDVANNITAKGIIIDYKKGFSFAFEQLNNTVNSRANCKLIIML 360
FOHLVQANVRNKKVLDVANNITAKGIIIDYKKGFSFAFEQLNNTVNSRANCKLIIML 360
GGEERAQEIFNKYKNDKKVRFVRSVQGHNYERGPQIOMMACENKGYIYEIPSIGAIR 420
GGEERAQEIFNKYKNDKKVRFVRSVQGHNYERGPQIOMMACENKGYIYEIPSIGAIR 420
QEYLDVLRGPMVLADGAKAQVQWNTVYLDALDELGLVITGTLPVNTITQGFENKTNLK 480
QEYLDVLRGPMVLADGAKAQVQWNTVYLDALDELGLVITGTLPVNTITQGFENKTNLK 480
ILGVMGVDVSLEDIKRLTPRTFLCPNGYFAIDPENGYYLLHPNLQPK-- 540

Db 481 NQLILGVMGVDVSLEDIKRLTPRTFLCPNGYFAIDPENGYYLLHPNLQPK-----
Qy 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLKVKSDQDERVIDKGNRTYTWTPVAK
Db 536 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLKVKSDQDERVIDKGNRTYTWTPVAK
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Db 596 ALVLPTYSFYIYIKAKLEBETITQARSKKGKMDSETLKPDPFESGYTFIAPROY(
Qy 661 SDNNTFELNPFNEFIDRKTNNPNSCNADLNRLVLLDAGFTNELLVQNYWSKQKNI
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Qy 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSNDNDNYVFTAPYFNKSGPGF
Db 716 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSNDNDNYVFTAPYFNKSGPGF
Qy 781 MVSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPCAGPVCDCCKRNSDY
Db 776 MVSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPCAGPVCDCCKRNSDY
Qy 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPC
Db 836 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPC
Qy 901 GAGHRSAYVPSVADIIQIGWATAAASWIIQQFLLSLTFFPRLLAEVEMEDDDFTF
Db 896 GAGHRSAYVPSVADIIQIGWATAAASWIIQQFLLSLTFFPRLLAEVEMEDDDFTF
Qy 961 SCITEQTYEFDNDSDSKSPSGVLDGCGNCSRFHGEKLMNTNLIIFIMVBSKGTCPCI
Db 956 SCITEQTYEFDNDSDSKSPSGVLDGCGNCSRFHGEKLMNTNLIIFIMVBSKGTCPCI

RESULT 9

US-08-455-543A-56
; Sequence 56, Appellence US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991

TION DATA:
NUMBER: US 07/620,250
: 30-NOV-1990
TION DATA:
NUMBER: US 07/482,384
: 20-FEB-1990
TION DATA:
NUMBER: US 07/603,751
: 04-APR-1989
TION DATA:
NUMBER: WO PCT/US89/01408
: 04-APR-1989
TION DATA:
NUMBER: US 07/176,899
: 04-APR-1988
T INFORMATION:
man, Stephanie L.
N NUMBER: 33,779
CKET NUMBER: 6362-52517
TION INFORMATION:
(619)238-0999
619)238-0062
SEQ ID NO: 56:
ACTERISTICS:
84 amino acids
o acid
S: single
linear
: protein
: internal

98.9%; Score 5289.5; DB 1; Length 1084;

arity 99.2%; Pred. No. 0;
onservative 0; Mismatches 1; Indels 7; Gaps 1;
CLLALTTLFSLTIGPSSPPFSAVTKSWDKMQEDLVLTAKTAGSVNQLVDI 60
CLLALTTLFSLTIGPSSPPFSAVTKSWDKMQEDLVLTAKTAGSVNQLVDI 60
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QDLVTEPNNAQLVEIAARDIEKLLSNRKALVSLAEAEKVQAAHQRWDFASN 120
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YNAKDDLPKNDSPGSRQIKPVFIEDANFGRLSYOHAHVHPTDIYEGSTIVL 180
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QGEERAQEIFNKYNDKKVRVFRFSVQGHNYERGPIQWMAKNGYIYIPSGAIR 420
EYLDVGLRPMVLGAKQVQWNTVYLDALGLVITGTLVFNITGOFENKTNLK 480
EYLDVGLRPMVLGAKQVQWNTVYLDALGLVITGTLVFNITGOFENKTNLK 480
LGVMGVDSLEDIKELTFRFTLCPNGYFAIDPNGYVLLHNPQKNPKSPEPTVL 540
LGVMGVDSLEDIKELTFRFTLCPNGYFAIDPNGYVLLHNPQKNPKSPEPTVL 540
VARELNDIKVEIRNKMIDGESGEKTFRTLVKSDQERYIDKGNRTYTWTVPNGTDYSL 600

Db 541 DFLDAELNDIKVEIRNKMIDGESGEKTFRTLVKSDQERYIDKGNRTYTWTVPNGT
QY 601 ALVLPYTSFYIYKAKLBETITQARSKKGMKEDSETLAKPDNFEESGYTFIAPRDYCI
Db 601 ALVLPYTSFYIYKAKLBETITQARY-----SETLAKPDNFEESGYTFIAPRDYCI
QY 661 SDNTEFLNENEFIDRKTNNPSCNADLINRVLLDAGFTNELVQNYWSKQKNIK
Db 654 SDNTEFLNENEFIDRKTNNPSCNADLINRVLLDAGFTNELVQNYWSKQKNIK
QY 721 FVVDGGITRVYPKEAGENWOENPETYEDSFYKSLDNDNVVFTAPYFNKSGPGA
Db 714 FVVDGGITRVYPKEAGENWOENPETYEDSFYKSLDNDNVVFTAPYFNKSGPGA
QY 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGPVCDCCKNSDV
Db 774 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGPVCDCCKNSDV
QY 841 LDDGGFLMANHDDVTNQIGRFFGGEIDPRLMRHLVNIISVYAFNKSVDYQSVCEPG
Db 834 LDDGGFLMANHDDVTNQIGRFFGGEIDPRLMRHLVNIISVYAFNKSVDYQSVCEPG
QY 901 GAGHSAYVPSVADILQIGMWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTAK
Db 894 GAGHSAYVPSVADILQIGMWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTAK
QY 961 SCITEQTYFFDNDKSPSGVLDGNCNRSIFHGEKLMNTNLIIFIMVESKGTCPCD
Db 954 SCITEQTYFFDNDKSPSGVLDGNCNRSIFHGEKLMNTNLIIFIMVESKGTCPCD

RESULT 10

US-08-223-305C-56
; Sequence 56, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990

ATION DATA:
 1 NUMBER: US 07/603,751
 2: 04-APR-1989
 ATION DATA:
 1 NUMBER: WO PCT/US89/01408
 2: 04-APR-1989
 ATION DATA:
 1 NUMBER: US 07/176,899
 2: 04-APR-1988
 3: 04-APR-1988
 4: man, Stephanie L.
 5: JACKET NUMBER: 52516 (P519739)
 6: ATION INFORMATION:
 7: (619)238-0999
 8: (619)238-0062
 9: 1 SEQ ID NO: 56:
 10: 184 amino acids
 11: 10 acid
 12: 1S: single
 13: linear
 14: 1: protein
 15: 3: internal

98.9%; Score 5289.5; DB 2; Length 1084;

Identity 99.2%; Pred. No. 0;
 Conservative 0; Mismatches 1; Indels 7; Gaps 1;

3CLLALTLTFLQSLLIGPSSEPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
 3CLLALTLTFLQSLLIGPSSEPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
 YQDLYTVEPNNAQLVEIARDIEKLNSKALVSLALEAEKVQAAHOREPASN 120
 YQDLYTVEPNNAQLVEIARDIEKLNSKALVSLALEAEKVQAAHOREPASN 120
 YNAKODLDEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
 YNAKODLDEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
 NWTSSALDEVFKQNEEDPSLLWQVFGSATGLARYYPASVPWVDSRTPNKIDLYDVR 240
 NWTSSALDEVFKQNEEDPSLLWQVFGSATGLARYYPASVPWVDSRTPNKIDLYDVR 240
 YIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300
 YIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300
 FOHLVQANVRNKKVLDKAVNNITAKGIDTYKKGFSPAFEQLLNYSRANCKIIML 360
 FOHLVQANVRNKKVLDKAVNNITAKGIDTYKKGFSPAFEQLLNYSRANCKIIML 360
 3GEERAQEIENKYNKDKKVRFRPSVQCHNYERGPIQWMAKENGYYEIPSTGAI 420
 3GEERAQEIENKYNKDKKVRFRPSVQCHNYERGPIQWMAKENGYYEIPSTGAI 420
 QEYLDVIGRPMVLADGKAKQVMTNVVLDLLEGLVITGTLVPVNTGQENKTNLK 480
 QEYLDVIGRPMVLADGKAKQVMTNVVLDLLEGLVITGTLVPVNTGQENKTNLK 480
 ILGVMGVDSVLEDKRLTPRTFLCPNGYFPAIDPENGVLHLPNLPKNPKSQBPVTL 540
 ILGVMGVDSVLEDKRLTPRTFLCPNGYFPAIDPENGVLHLPNLPKNPKSQBPVTL 540
 DAELNDIKVEIRNMIDGSEGEKFTPLVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
 DAELNDIKVEIRNMIDGSEGEKFTPLVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
 LPTYSFYIKAKLETITQARSKKGMKDSSETLKPDPNFESGYTFIAPRYCNDLKI 660
 LPTYSFYIKAKLETITQARY-----SETLKPDPNFESGYTFIAPRYCNDLKI 653

661 SDNTEFLINFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQVNSKQKNIK
 654 SDNTEFLINFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQVNSKQKNIK
 721 FVTDGGITRVVPKEAGNWNQENPETYEDSFYKRSIDNDNNYFTTAPYFNKSGPGA
 714 FVTDGGITRVVPKEAGNWNQENPETYEDSFYKRSIDNDNNYFTTAPYFNKSGPGA
 781 MYSKAVEIYIQGLKLPKPAVVGKIDVNSWNIENFTKTSIRDPKAGPVCDCRNSDV
 774 MYSKAVEIYIQGLKLPKPAVVGKIDVNSWNIENFTKTSIRDPKAGPVCDCRNSDV
 841 LDDGGFLLMANHDDVTNQIGREFGHEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
 834 LDDGGFLLMANHDDVTNQIGREFGHEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
 901 GAGHSAYVPSVADILQIGWATAAASILQOFLISLTPRLLLEAVEMEDDDPTA
 894 GAGHSAYVPSVADILQIGWATAAASILQOFLISLTPRLLLEAVEMEDDDPTA
 961 SCITOTQYFFDNDKSPGVLDCGNCRSIFHGEKLMNTNLIFIMVESKGTCPCD
 954 SCITOTQYFFDNDKSPGVLDCGNCRSIFHGEKLMNTNLIFIMVESKGTCPCD
 RESULT 11
 US-08-455-543A-53
 : Sequence 53, Application US/08455543A
 : Patent No. 5792846
 : GENERAL INFORMATION:
 : APPLICANT: Harpold, Michael
 : APPLICANT: Ellis, Steven
 : APPLICANT: Williams, Mark
 : APPLICANT: Feldman, Daniel
 : APPLICANT: McCue, Ann
 : APPLICANT: Brenner, Robert
 : TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 : TITLE OF INVENTION: METHODS
 : NUMBER OF SEQUENCES: 57
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Brown, Martin, Haller & McClain
 : STREET: 1660 Union Street
 : CITY: San Diego
 : STATE: California
 : COUNTRY: USA
 : ZIP: 92101-2926
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FastSEQ Version 1.5
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/455,543A
 : FILING DATE: May 31, 1995
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/223,305
 : FILING DATE: April 4, 1994
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/868,354
 : FILING DATE: April 10, 1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/745,206
 : FILING DATE: 15-AUG-1991
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/620,250
 : FILING DATE: 30-NOV-1990
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/482,384
 : FILING DATE: 20-FEB-1990
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/603,751
 : FILING DATE: 04-APR-1989

TION DATA:
NUMBER: WO PCT/US89/01408
: 04-APR-1989

TION DATA:
NUMBER: US 07/176,899
: 04-APR-1988

T INFORMATION:
man, Stephanie L.
N NUMBER: 33,779
CKET NUMBER: 6362-52517
TION INFORMATION:
(619)238-0999

SEQ ID NO: 53:

ACTERISTICS:

03 amino acids

o acid

S: single

linear

: protein

: internal

98.6%; Score 5270; DB 1; Length 1103;

arity 97.4%; Fred. No. 0;

onservative 0; Mismatches 1; Indels 26; Gaps 2;

CLLALTTLFQSLIGSPSEPPPSAVTIKSWDKQEDLVTLAKTAGVGNQLVDI 60

CLLALTTLFQSLIGSPSEPPPSAVTIKSWDKQEDLVTLAKTAGVGNQLVDI 60

QDLTVTPNNARQVLVEIARIEKLSNRKALVSLALEAEKQAAHQWRDPASN 120

QDLTVTPNNARQVLVEIARIEKLSNRKALVSLALEAEKQAAHQWRDPASN 120

YNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROI SYOHAHVHPTDIYEGSTIVL 180

YNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROI SYOHAHVHPTDIYEGSTIVL 180

WTSALDEVKKNRDEPSLLQVFGSATGLARYYPASVWVNSRTPNKIDLYDVR 240

WTSALDEVKKNRDEPSLLQVFGSATGLARYYPASVWVNSRTPNKIDLYDVR 240

IQGAASPKOMLILVDVSGSVSGLTLKLRTSVSEMLETLSDDDFVNVA SFNSAOD 300

IQGAASPKOMLILVDVSGSVSGLTLKLRTSVSEMLETLSDDDFVNVA SFNSAOD 300

QHLVQANVRNKKVLKDAVNNITAKGITDYKKGSPFAPEQLLNYNVSRANCKIIML 360

QHLVQANVRNKKVLKDAVNNITAKGITDYKKGSPFAPEQLLNYNVSRANCKIIML 360

GEERAQEIFNKNYKDKKVRVRFVSGQHYERGPQIWMACENKGYIYEIPSIGAIR 420

GEERAQEIFNKNYKDKKVRVRFVSGQHYERGPQIWMACENKGYIYEIPSIGAIR 420

EYLDVLRPMVLADGKAKQVQWNTVYLDALBLGLVITGTLVPVNIQTGFENKTNLK 480

EYLDVLRPMVLADGKAKQVQWNTVYLDALBLGLVITGTLVPVNIQTGFENKTNLK 480

LGVMGVDSLEDDIKRLTPRFTLCPNGYVFAIDPNGYVLLHPNLOPK----- 530

LGVMGVDSLEDDIKRLTPRFTLCPNGYVFAIDPNGYVLLHPNLOPK----- 530

-----NPKSQBPVTLDFDLAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYI 581

RPNIQNPQSQBPVTLDFDLAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYI 600

RTYTWTPVNGTYSALVLPYTSFYFIKAKLEETITQARSKGKQKMOSETLKPONF 641

RTYTWTPVNGTYSALVLPYTSFYFIKAKLEETITQARSKGKQKMOSETLKPONF 653

XTFTAPRDYCNLDKISDNNTTEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGTIN 701

Db 654 BSGYTFIAPRDYCNLDKISDNNTTEFLNFNEFIDRKTTPNPNPCNADLINRVLLD
QY 702 ELVQNYMSKQKNIKGVKARFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLL
Db 714 ELVQNYMSKQKNIKGVKARFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLL
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLLKPAAVVGKIDVNSWIENFTKTS
Db 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLLKPAAVVGKIDVNSWIENFTKTS
QY 822 CAGPVCCCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPRLMRHLVNI
Db 834 CAGPVCCCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPRLMRHLVNI
QY 882 FNKSYDYQSVCEPGAAPKQAGAGHRSAYVPSVADILQIGMWATAAAWSTLQOFLLSI
Db 894 FNKSYDYQSVCEPGAAPKQAGAGHRSAYVPSVADILQIGMWATAAAWSTLQOFLLSI
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFNDSDSKSPSGVLDGNCNCRIFHGEKLA
Db 954 LLEAVEMEDDDFTASLSKQSCITEQTQYFFNDSDSKSPSGVLDGNCNCRIFHGEKLA
QY 1002 IFIMVESKGTCPCDTRL 1018
Db 1014 IFIMVESKGTCPCDTRL 1030

RESULT 12

US-08-223-305C-53

; Sequence 53: Application US/08223305C

; Patent No. 5851824

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/223,305C

; FILING DATE: April 4, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/868,354

; FILING DATE: April 10, 1992

; APPLICATION DATA:

; APPLICATION NUMBER: US 07/745,206

; FILING DATE: 15-AUG-1991

; APPLICATION DATA:

; APPLICATION NUMBER: US 07/620,250

; FILING DATE: 30-NOV-1990

; APPLICATION DATA:

; APPLICATION NUMBER: US 07/482,384

; FILING DATE: 20-FEB-1990

; APPLICATION DATA:

; APPLICATION NUMBER: US 07/603,751

; FILING DATE: 04-APR-1989

; APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US89/01408

QY	702	ELVQYWSKQNIIGVKARFVVTDDGGITRVYPKEAGENQWENPETVEDSFYKRSI
DB	714	ELVQYWSKQNIIGVKARFVVTDDGGITRVYPKEAGENQWENPETVEDSFYKRSI
QY	762	VFTAPYFNKSPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKT
DB	774	VFTAPYFNKSPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKT
QY	822	CAGPVCDCRNSDVMDCVILDDGGFLMANHDDYTQIGRPFGEIDPISLMRHLVN
DB	834	CAGPVCDCRNSDVMDCVILDDGGFLMANHDDYTQIGRPFGEIDPISLMRHLVN
QY	882	FNKSYDYQSVCEPGAAPKQAGHRSAVPSVADILQIGMWATAAAWSILQQFLLS
DB	894	FNKSYDYQSVCEPGAAPKQAGHRSAVPSVADILQIGMWATAAAWSILQQFLLS
QY	942	LLEAVEMEDDDFTASLSKQSCITTEQTOYFPDNDKSFSGVLDCGNCRSRIFHGEKLI
DB	954	LLEAVEMEDDDFTASLSKQSCITTEQTOYFPDNDKSFSGVLDCGNCRSRIFHGEKLI
QY	1002	IFIMVSKGTCPCDTRL 1018
DB	1014	IFIMVSKGTCPCDTRL 1030
RESULT 13		
US-08-455-543A-55		
Sequence 55, Application US/08455543A		
Patent No. 5792846		
GENERAL INFORMATION:		
APPLICANT: Harpold, Michael		
APPLICANT: Ellis, Steven		
APPLICANT: Williams, Mark		
APPLICANT: Feldman, Daniel		
APPLICANT: McCue, Ann		
APPLICANT: Brenner, Robert		
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND		
TITLE OF INVENTION: METHODS		
NUMBER OF SEQUENCES: 57		
CORRESPONDENCE ADDRESS:		
ADDRESSEE: Brown, Martin, Haller & McClain		
STREET: 1660 Union Street		
CITY: San Diego		
STATE: California		
COUNTRY: USA		
ZIP: 92101-2926		
COMPUTER READABLE FORM:		
MEDIUM TYPE: Diskette		
COMPUTER: IBM Compatible		
OPERATING SYSTEM: DOS		
SOFTWARE: FastSeq Version 1.5		
CURRENT APPLICATION DATA:		
APPLICATION NUMBER: US/08/455,543A		
FILING DATE: May 31, 1995		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER: 08/223,305		
FILING DATE: April 4, 1994		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER: 07/868,354		
FILING DATE: April 10, 1992		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER: US 07/745,206		
FILING DATE: 15-AUG-1991		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER: US 07/620,250		
FILING DATE: 30-NOV-1990		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER: US 07/482,384		
FILING DATE: 20-FEB-1990		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER: US 07/603,751		
FILING DATE: 04-APR-1989		
PRIOR APPLICATION DATA:		

NUMBER: WO PCT/US89/01408
: 04-APR-1989
TION DATA:
NUMBER: US 07/176,899
: 04-APR-1988
T INFORMATION:
man, Stephanie L.
N NUMBER: 33,779
CKET NUMBER: 6362-52517
TION INFORMATION:
(619)238-0999
619)238-0062
SEQ ID NO: 55:
ACTERISTICS:
79 amino acids
o acid
S: single
linear
: protein
: internal

98.2%; Score 5250; DB 1; Length 1079;
arity 98.7%; Pred. No. 0;
onservative 0; Mismatches 1; Indels 12; Gaps 2;
ICLLALTILFSLITGPSEPPFSAVTKSWVDKQEDLVTLAKTASGVNQLVDI 60
ICLLALTILFSLITGPSEPPFSAVTKSWVDKQEDLVTLAKTASGVNQLVDI 60
QDLYTVEPNNAQQLVEIARDIEKLLNSRKALVSLAEAKVQAAHQWRDPASN 120
QDLYTVEPNNAQQLVEIARDIEKLLNSRKALVSLAEAKVQAAHQWRDPASN 120
YNAKDDLOPEKNDSEPGRIKPVFIEDANFGRLSYQHAHVHPTDIYEGSTIVL 180
YNAKDDLOPEKNDSEPGRIKPVFIEDANFGRLSYQHAHVHPTDIYEGSTIVL 180
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WTSALDEYFKKREDDPSLLWQVFGSATGLARYYPASVPWDSNRTPNKIDLYDVR 240
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TQGAASPDKMLILVDVSGSVGLTLKLRISVSEMLETLSDDDFVNVSFNSNAQD 300
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XGEERAQEIFNKYKDKKVRVFRFSVQGHNYERGPQWMACENKGYIYIPISGAI 420
YELDLGRPMVLADKAKOVQNTVYLDALGLVITGTLPVNITGOFENKTNLK 480
YELDLGRPMVLADKAKOVQNTVYLDALGLVITGTLPVNITGOFENKTNLK 480
LQVGMGVDSLEDIKLTLPRTLCPNGYYPALDPNGVYLLHPLNLPKNPKSEPVTL 540
LQVGMGVDSLEDIKLTLPRTLCPNGYYPALDPNGVYLLHPLNLPKNPKSEPVTL 540
DALENDIKVEIRNKMIDGSGEKTFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600
DALENDIKVEIRNKMIDGSGEKTFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 595
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LPTYSFYIYKAKLEETITQARY-----SETLKPNPFESGYTFTIAPRYCNDLKI 648
VTEFLNPFNEFIDRKTNNPNSCNADLINRVLDAGFTNELVQYWSKQNKIKGVKAR 720
VTEFLNPFNEFIDRKTNNPNSCNADLINRVLDAGFTNELVQYWSKQNKIKGVKAR 708

721 FVTDGGITRVYPKEAGENWQENPETYEDSFYKSLDNDNVTFTAPYFNKSPGGA'
Db
709 FVTDGGITRVYPKEAGENWQENPETYEDSFYKSLDNDNVTFTAPYFNKSPGGA'
Qy
781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCCKRNSDV
Db
769 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCCKRNSDV
Qy
841 LDDGGFLMANHDDYTNOIGRFFGFEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGI
Db
829 LDDGGFLMANHDDYTNOIGRFFGFEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGI
Qy
901 GAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVEMEDDDFTAI
Db
889 GAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVEMEDDDFTAI
Qy
961 SCITTEOTQYFFDNDKSPFSGVLDGNCNCSRI FHGEKLMNTNLI FIMVESKGTGCPDY
Db
949 SCITTEOTQYFFDNDKSPFSGVLDGNCNCSRI FHGEKLMNTNLI FIMVESKGTGCPDY

RESULT 14
US-08-223-305C-55
; Sequence 55, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:

dman, Stephanie L.
ON NUMBER: 33,779
DOCKET NUMBER: 52516 (P519739)
ATION INFORMATION:
(619)238-0999
(619)238-0062

R SEQ ID NO: 55:
079 amino acids

no acid
SS: single

linear
E: protein

E: internal

larity 98.2%; Score 5250; DB 2; Length 1079;

Conservative 0; Mismatches 1; Indels 12; Gaps 2;

GCLLALTLTQLSLIGSPSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60

GCLLALTLTQLSLIGSPSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60

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YNNAKDLDPEKNDESPGQRIKPVFIEDANFGQISYQHAHVHPTDIYEGSTIVL 180

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Qy 841 LDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPK
Db 829 LDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPK
Qy 901 GAGHSAYVPSVADIIQIGWATAAAMSIIQQFLLSLTFFPRLLLEAVEMEDDDFTF
Db 889 GAGHSAYVPSVADIIQIGWATAAAMSIIQQFLLSLTFFPRLLLEAVEMEDDDFTF
Qy 961 SCITEQTYFFDNDSDSKSPSGVLDGCGNSRIFPHGEKLMNTNLIIFIMVESKGTCPCI
Db 949 SCITEQTYFFDNDSDSKSPSGVLDGCGNSRIFPHGEKLMNTNLIIFIMVESKGTCPCI

RESULT 15

US-08-435-675B-5

; Sequence 5, Application US/08435675B

; Patent No. 5710250

; GENERAL INFORMATION:

; APPLICANT: Ellis, Steven Bradley

; APPLICANT: Williams, Mark E.

; APPLICANT: Harpold, Michael Miller

; APPLICANT: Schwartz, Arnold

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: CALCITUM CHANNEL COMPOSITIONS AND METHODS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/435,675B

; FILING DATE: 05-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/314,083

; FILING DATE: 28-SEP-1994

; APPLICATION NUMBER: US 07/914,231

; FILING DATE: 13-JUL-1992

; APPLICATION NUMBER: US 07/603,751

; FILING DATE: 08-NOV-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Seidman, Stephanie L

; REGISTRATION NUMBER: 33,779

; REFERENCE/DOCKET NUMBER: 6362-53193

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-238-0999

; TELEFAX: 619-238-0062

; TELEX:

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1106 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

US-08-435-675B-5

Query Match 96.1%; Score 5137.5; DB 1; Length 1106;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 986; Conservative 13; Mismatches 12; Indels 29;

us-10-090-827-13.ra

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 :KYQDLYTVEPNNAQQLVEI AARDIEKLLNSRKALVRLALEAEKVQAAHQRDEPA 120
 :VYVNAKODLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTI 178
 :VYVNAKODLDPEKNDSEPGSQRIKPVFIEDANFRQVSYQHAHVHIPTDIYEGSTI 180
 :L N W T S A L D Y F V K N R E E D S L L W Q V G S A T G L A R Y Y P A S P W D N S R T P N K L D L Y D V 238
 :L N W T S A L D Y F V K N R E E D S L L W Q V G S A T G L A R Y Y P A S P W D N S R T P N K L D L Y D V 240
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 :CFQHLVQANVRNKKVYLKDAVNNTAKGIITDYKKGPSFAPEQLLNTVNSRANCNKII 358
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 :TQEYLDVLGRPMVLADGKAKQVOMTVNYLDALBELGLVITGTLPVENITQGFENKTN 478
 :TQEYLDVLGRPMVLADGKAKQVOMTVNYLDALBELGLVITGTLPVENITQGFENKTN 480
 :LILGWGMDVSLDEIKRLTPRFTLPCNGYYFAIDPNGVYLLHPNLQPK----- 530
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 :-----NPKSQBPVTLDFDLAELENDIKVEIRNRMDIGSESEKTFRTLKVSQDER 579
 :KRPNVQNPKSQBPVTLDFDLAELENDIKVEIRNRMDIGSESEKTFRTLKVSQDER 600
 :GNRTYTWTVPNGTGY--SLALVLPYTSFYIYKAKLBETITQARSKGKMOBETLKP 638
 :GNRTYTWTVPNGTGYSSALVLPYTSFYIYKAKIBETITQARY-----SETLKP 653
 :ESGYTFIAPRDYCNDLKI SDNNTPELLNPEFIDRKTNNPNSCNADLINRVLLDAG 698
 :ESGYTFIAPREDYCSDLKPSDNNTPELLNPEFIDRKTNNPNSCNTDLINRVLLDAG 713
 :LVQNYNSKQKNIKGVTARFVTTDGGITRVYPKEAGENWOENPETVEBSFYKRSLDN 758
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 :FIMVESKGTCPCDTRL 1018
 :FIMVESKGTCPCDTRL 1033

GenCore version 5.1.6
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in search, using sw model

bruary 20, 2004, 16:51:31 ; Search time 36.5788 Seconds
(without alignments)
7181.696 Million cell updates/sec

3-10-090-827-13

346

MAAGCLLALTLFLQSLIG.....TNLIFIMVSKGTCPDTRL 1018

OSUMG2

ipop 10.0 , Gapext 0.5

30525 seqs, 258052604 residues

its satisfying chosen parameters: 830525

lght: 0

lght: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

3PREMBL 23:*

: sp_archaea.*

: sp_bacteria.*

: sp_fungi.*

: sp_human.*

: sp_invertebrate.*

: sp_mammal.*

: sp_mhc.*

: sp_organelle.*

: sp_phase.*

: sp_plant.*

: sp_rodent.*

: sp_virus.*

: sp_vertebrate.*

: sp_unclassified.*

: sp_rvirus.*

: sp_bacteriap.*

: sp_archaeap.*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

Entry	Length	DB	ID	Description
19.4	1110	4	Q9UIU0	Q9uiuo homo sapien
18.9	1091	6	O77773	O77773 sus scrofa
17.3	1091	11	Q9ERS3	Q9ers3 rattus norv
16.2	1084	11	Q8CFG7	Q8cfg7 rattus norv
16.0	1103	11	Q8B532	Q8b532 mus musculu
15.5	1079	11	Q8VHS9	Q8vhs9 rattus norv
16.8	745	4	Q9UDQ3	Q9udq3 homo sapien
14.2	1150	4	Q9NY47	Q9ny47 homo sapien
14.0	1157	11	Q8CFG6	Q8cfg6 rattus norv
13.9	1156	11	Q9EQG2	Q9eqg2 mus musculu
13.7	1143	4	Q9NY48	Q9ny48 homo sapien
13.7	1145	4	Q9Y268	Q9y268 homo sapien
13.7	1148	11	Q8C8R8	Q8c8r8 mus musculu
13.5	1098	11	Q8CHE9	Q8che9 mus musculu
13.5	1084	11	Q920H6	Q920h6 mus musculu
13.3	1076	4	Q9UEW0	Q9uew0 homo sapien

17	2682	50.2	975	4	Q9NSA6	Q9nsa6 hom
18	1090	20.4	1085	11	Q8CFG5	Q8cfg5 ra
19	1085	20.3	1091	11	Q9Z1L5	Q9z1l5 mu
20	1084	20.3	1091	4	Q8IZS8	Q8izs8 hom
21	1061.5	19.9	1120	4	Q8IZS9	Q8izs9 hom
22	1015	19.0	997	4	Q9NY16	Q9ny16 hom
23	1000.5	18.7	1218	5	Q9V6T7	Q9v6t7 drc
24	982.5	18.4	1170	5	Q8IP22	Q8ip22 drc
25	929.5	17.4	2190	5	Q9VJM0	Q9vjm0 drc
26	884	16.5	1255	5	Q9NKG3	Q9nkg3 dro
27	875	16.4	170	4	Q9UDL7	Q9udl7 hom
28	875	16.4	1120	5	Q9VJN7	Q9vjn7 dro
29	738.5	13.8	519	4	Q9NY18	Q9ny18 hom
30	658	12.3	317	11	Q920H5	Q920h5 mu
31	569.5	10.7	1148	5	Q17517	Q17517 cae
32	533	10.0	842	5	Q95R75	Q95r75 dro
33	526.5	9.8	394	13	Q8AVY7	Q8avy7 xe
34	514.5	9.6	104	4	Q9UD81	Q9ud81 hom
35	506	9.5	100	6	Q9GLH1	Q9glh1 bos
36	498.5	9.3	121	4	Q9UD82	Q9ud82 hom
37	482	9.0	98	4	Q9UDU5	Q9udus hom
38	465	8.7	97	4	Q9UD80	Q9ud80 hom
39	459	8.6	100	11	Q8C6Y3	Q8c6y3 mu
40	402	7.5	77	4	Q95026	Q95026 hom
41	337.5	6.3	1185	4	Q9HCJ9	Q9hcj9 hom
42	317.5	5.9	223	11	Q9R142	Q9r142 mu
43	231	4.3	978	6	Q95KE0	Q95ke0 mac
44	227	4.2	43	6	Q8HYX0	Q8hyx0 bos
45	222	4.2	1449	5	Q9V917	Q9v917 dro

ALIGNMENTS

RESULT 1

ID	Q9UIU0	PRELIMINARY;	PRT; 1110 AA.
AC	Q9UIU0;		
DT	01-MAY-2000 (TRENBLrel. 13, Created)		
DT	01-MAY-2000 (TRENBLrel. 13, Last sequence update)		
DT	01-MAY-2002 (TRENBLrel. 20, Last annotation update)		
DE	Dihydropyridine receptor alpha 2 subunit.		
GN	CACNA2D1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20005942; PubMed=10534405;		
RA	Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;		
RT	"Genomic structure and functional expression of a human alpha(2).		
RT	calcium channel subunit gene (CACNA2).";		
RL	Genomics 61:201-209(1999).		
DR	EMBL; AF083854; AAF03259.1; JOINED.		
DR	EMBL; AF083817; AAF03259.1; JOINED.		
DR	EMBL; AF083818; AAF03259.1; JOINED.		
DR	EMBL; AF083819; AAF03259.1; JOINED.		
DR	EMBL; AF083820; AAF03259.1; JOINED.		
DR	EMBL; AF083821; AAF03259.1; JOINED.		
DR	EMBL; AF083822; AAF03259.1; JOINED.		
DR	EMBL; AF083823; AAF03259.1; JOINED.		
DR	EMBL; AF083824; AAF03259.1; JOINED.		
DR	EMBL; AF083825; AAF03259.1; JOINED.		
DR	EMBL; AF083826; AAF03259.1; JOINED.		
DR	EMBL; AF083827; AAF03259.1; JOINED.		
DR	EMBL; AF083828; AAF03259.1; JOINED.		
DR	EMBL; AF083829; AAF03259.1; JOINED.		
DR	EMBL; AF083830; AAF03259.1; JOINED.		
DR	EMBL; AF083831; AAF03259.1; JOINED.		
DR	EMBL; AF083832; AAF03259.1; JOINED.		
DR	EMBL; AF083833; AAF03259.1; JOINED.		
DR	EMBL; AF083834; AAF03259.1; JOINED.		

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35; AAF03259.1; JOINED.
36; AAF03259.1; JOINED.
37; AAF03259.1; JOINED.
38; AAF03259.1; JOINED.
39; AAF03259.1; JOINED.
40; AAF03259.1; JOINED.
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42; AAF03259.1; JOINED.
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44; AAF03259.1; JOINED.
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46; AAF03259.1; JOINED.
47; AAF03259.1; JOINED.
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49; AAF03259.1; JOINED.
50; AAF03259.1; JOINED.
51; AAF03259.1; JOINED.
52; AAF03259.1; JOINED.
53; AAF03259.1; JOINED.
R004010; Cache.
R002035; VWFA_A.
3; Cache; 1.
2; vwa; 1.
27; vwa; 1.
0234; VWFA; 1.

110 AA; 125307 MW; 8358DC6AD489C074 CRC64;

larity 99.4%; Score 5312.5; DB 4; Length 1110;
larity 97.9%; Pred. No. 0;
Conservative 1; Mismatches 2; Indels 19; Gaps 1;

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GCLLALTLTLFQSLIGSSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
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NWTSALEVFKNREEDPSLLWQVFGSATGLARYYPASPWVDSNRTNPKIDLYDVR 240
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YIQGAASPKDMLILVDVSGVSGTLKILRTSVSEMLETSLDDDFVNVASFNSNAQD 300
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RRPNIQNKQSQEPVTLDFLDAELNDIKVIRNKMIDGESGKTFRTLVSQDERYI 600
NRTYTWTPVNGTDYSLALVLPITYSYFYIKAKLEETITQARSKKMKDSETLKPDNF 641

601 DKGNRITYTWTPVNGTDYSLALVLPITYSYFYIKAKLEETITQARSKKMKDSETL
642 EESGYTPIAPRDYCNDLKISDNNTFLLNFNEFDRTKTPNPNPSCNADLINRVLLI
661 EESGYTPIAPRDYCNDLKISDNNTFLLNFNEFDRTKTPNPNPSCNADLINRVLLI
702 ELQVNYWSKQKNIKGKVKARFVVDGGITRVYPKEAGENWQENPETYEDSFYKRSI
721 ELQVNYWSKQKNIKGKVKARFVVDGGITRVYPKEAGENWQENPETYEDSFYKRSI
762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKI
781 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKI
822 CAGPVCDCCKRNSDVMDCVILDDGFLLMANHHDDYTNOIGRFFGFIDESLMRHLV
841 CAGPVCDCCKRNSDVMDCVILDDGFLLMANHHDDYTNOIGRFFGFIDESLMRHLV
882 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAAMSILQOFLLE
901 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAAMSILQOFLLE
942 LLEAVEMEDDDFTASLSKQSCITEQTQYFPDNDKSKFSFSGVLDGNCRSRIFHGKI
961 LLEAVEMEDDDFTASLSKQSCITEQTQYFPDNDKSKFSFSGVLDGNCRSRIFHGKI
1002 IFIMVRSKGTCPCDTRL 1018
1021 IFIMVRSKGTCPCDTRL 1037

RESULT 2
077773 PRELIMINARY; PRT; 1091 AA.
AC 077773;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Voltage-dependent calcium channel alpha-2 delta subunit precursor.
OS Sus scrofa (Pig).
OC Mammalia; Euthalia; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=98411353; PubMed=9738015;
RA Brown J.P., Gee N.S.;
RT "Cloning and deletion mutagenesis of the alpha2 delta calcium ch
RT subunit from porcine cerebral cortex. Expression of a soluble fo
RL J. Biol. Chem. 273:25458-25465 (1998).
DR EMBL; AF07665; AAC36289.1;
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWFA_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00327; VWFA; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Signal.
FT CHAIN 1 24 POTENTIAL.
FT CHAIN 25 1091 VOLTAGE-DEPENDENT CALCIUM CHANNEL A
FT DELTA SUBUNIT.
SQ SEQUENCE 1091 AA; 123150 MW; 293DDC7BEB9EB60E CRC64;

Query Match 98.9%; Score 5388; DB 6; Length 1091;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1006; Conservative 5; Mismatches 7; Indels 0;

1 MAAGCLLALTLTLFQSLIGSSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVN

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|||||NTSEFLINFEIDRKTNPSCNTDLINRIILLDAGFTNELVQVWSKQNKIKGVKAR 720
|||||TDGGITRVYPKEAGENWQENPETEYDSFKYKSLDNDNVFTAPYFNKSGPGAYESGI 780
|||||TDGGITRVYPKEAGENWQENPETEYDSFKYKSLDNDNVFTAPYFNKSGPGAYESGI 780
|||||KAVIYIQGKLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840
|||||KAVELYIQGKLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840
|||||GGFLLMANHDDYTNQIGRFGEIDPSLMHVLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
|||||GGFLLMANHDDYTNQIGRFGEIDPSLMHVLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
|||||HRSAYVPSVADILQIGMWATAAASIIQQFLLSLTFFPRLLLEAVEMEDDDFTASLSKQ 960
|||||HRSAYVPSITDILQIGMWATAAASIIQQFLLSLTFFPRLLLEAVEMEDDDFTASLSKQ 960
|||||TEQTYQFFDNDKSPSGVLDGCGNSRIFPHGEKLANVNLIFIMVBSKGTCPDTRL 1018
|||||TEQTYQFFKNDTKSFGILLDCGNSRIFPHVEKLANVNLVFMVBSKGTCPDTRL 1018

PRELIMINARY; PRT; 1084 AA.
(TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
nel alpha-2 delta-1 subunit isoform e.
gicus (Rat).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
0116;

M N.A.
ue-Dawley; TISSUE=Heart atrium;
est P.M.;
egicus voltage-dependent calcium channel alpha-2 delta-1
m e (CACNA2D1e) mRNA.
EB-2002) to the EMBL/GenBank/DBJ databases.
76; ARO14652.1; -.
084 AA; 122711 MW; 6269E92D8F1657FF CRC64;

6.2%; Score 5141.5; DB 11; Length 1084;
larity 95.7%; Pred. No. 2.6e-313;
Conservative 21; Mismatches 16; Indels 7; Gaps 1;

3CLLALTTLTQSLILIGPSSEPPPSAVTIKSWYDKMQEDLVTLAKTAGVNLVDI 60
3CLLALTTLTQSLILIGPSSEPPPSAVTIKSWYDKMQEDLVTLAKTAGVNLVDI 60
YQDLYTVPEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
YQDLYTVPEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
YNAKDDLPEDKNDSPGSRIRKPVFTEDANFGRIQSYQAAVHIPTDIYEGSTIVL 180
YNAKDDLPEDKNDSPGSRIRKPVFTEDANFGRIQSYQAAVHIPTDIYEGSTIVL 180
WNTSALDEVFKNRDEPDLQWVFGSATGLARYYPASPVNDNRTPNKIDLYDVR 240
WNTSALDEVFKNRDEPDLQWVFGSATGLARYYPASPVNDNRTPNKIDLYDVR 240
YIGAAKPKDMLILVDVSGVSGLTIKLITPSVSEMLETLSDDDFNVVASFNSNAQ 300
YIGAAKPKDMLILVDVSGVSGLTIKLITPSVSEMLETLSDDDFNVVASFNSNAQ 300
FOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLNLYNVRANCKNIIML 360
FOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLNLYNVRANCKNIIML 360

```

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QY 361 FTGGERRAQEIENKYNKDKKVRVFSVQHNVERGPIOMMACENKGYVYEIPE
DB 361 FTGGERRAQEIENKYNKDKKVRVFSVQHNVERGPIOMMACENKGYVYEIPE
QY 421 INTQEYLDVLRPMVLGADKAKQVQWNTVYLDALGLVITGLPVFNITQGFEN
DB 421 INTQEYLDVLRPMVLGADKAKQVQWNTVYLDALGLVITGLPVFNITQGFEN
QY 481 NQILGVMGVDVSLSDIKRLTPRFTLCPNGYYPADIPNGYVLLHPNLQPKPKSC
DB 481 NQILGVMGVDVSLSDIKRLTPRFTLCPNGYYPADIPNGYVLLHPNLQPKPKSC
QY 541 DFLDAELNDIKVEIRNKMIDGESGKTPRLTVKSQDERVIDKGNRTYTWTPVNG
DB 541 DFLDAELNDIKVEIRNKMIDGESGKTPRLTVKSQDERVIDKGNRTYTWTPVNG
QY 601 ALVLPVSYFYIIKAKLEETITQARSKKMKDSEITLKPONFEESGYTFFIAPDYC
DB 601 ALVLPVSYFYIIKAKLEETITQARSKKMKDSEITLKPONFEESGYTFFIAPDYC
QY 661 SDNTEFLNFEFIDRKTNPNSCNADLINRVLLDAGFTNELVQVWSKQNKIK
DB 661 SDNTEFLNFEFIDRKTNPNSCNADLINRVLLDAGFTNELVQVWSKQNKIK
QY 721 FVVTGCGITRVYPKEAGENWQENPETEYDSFKYKSLDNDNVFTAPYFNKSGPGA
DB 721 FVVTGCGITRVYPKEAGENWQENPETEYDSFKYKSLDNDNVFTAPYFNKSGPGA
QY 781 MYSKAVEIYIQGKLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDV
DB 781 MYSKAVEIYIQGKLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDV
QY 841 LDGGFLLMANHDDYTNQIGRFGEIDPSLMHVLVNI SVYAFNKSVDYQSVCEPG
DB 841 LDGGFLLMANHDDYTNQIGRFGEIDPSLMHVLVNI SVYAFNKSVDYQSVCEPG
QY 901 GAGHSAYVPSVADILQIGMWATAAASIIQQFLLSLTFFPRLLLEAVEMEDDDFTA
DB 901 GAGHSAYVPSITDILQIGMWATAAASIIQQFLLSLTFFPRLLLEAVEMEDDDFTA
QY 961 SCITEQTYQFFDNDKSPSGVLDGCGNSRIFPHGEKLANVNLIFIMVBSKGTCPCD
DB 961 SCITEQTYQFFKNDTKSFGILLDCGNSRIFPHVEKLANVNLVFMVBSKGTCPCD

RESULT 5
O08532 PRELIMINARY; PRT; 1103 AA.
AC O08532; O08533; O08534; O08535; O08536;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta
DE subunits precursor.
GN CACNA2D1 OR CACNA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97113514; PubMed=8955374;
RA Angelotti T. Hofmann P.;
RL FEBS Lett. 397:331-337(1996).
CC -!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT R(
CC EXCITATION-CONTRACTION COUPLING.
CC -!- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBU(
CC ALPHA-1, ALPHA-2, BETA AND GAMMA.
CC -!- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULF(
CC LINKED.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

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Db	769	MVSKAVELYIQGLLKPAVGIKIDVNSWIEINFTKTSIRDP	CAGPVCDCRNSD
Qy	841	LDGCGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI	SVYAFNKSYYDYSVCEPC
Db	829	LDGCGFLLMANHDDYTNOIGRFFGEIDPSMWRHLVNI	SLVYAFNKSYYDYSVCDPC
Qy	901	GAGHSAYVPSVADTLOIGWATAAASWIILOQFLLSL	TFPRLLLEAVEMEDDDFTF
Db	889	GAGHSAYVPSITDILQIGWATAAASWIIQLLLSL	TFPRLLLEAVEMESDDFTF
Qy	961	SCITEQTQYFFDNDSKPSGVLDCGNCRSRIPHGEKLM	NMTNLFIIMVBSKGTCPCI
Db	949	SCITEQTQYFFDNDSKPSGVLDCGNCRSRIFHVEKLM	NLTNLVFIIMVBSKGTCPCI
RESULT 7			
Q9UDQ3			
IC	Q9UDQ3	PRELIMINARY;	PRT; 745 AA.
AD	Q9UDQ3;		
DT	01-WAY-2000 (TreeBLrel. 13, Created)		
DT	01-WAY-2000 (TreeBLrel. 13, Last sequence update)		
DT	01-WAR-2003 (TreeBLrel. 23, Last annotation update)		
DE	WUGSC:H DJ0560014.1 protein (Fragment).		
GN	WUGSC:H DJ0560014.1		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RX	SEQUENCE FROM N.A.		
RP	MEDLINE=99063752; PubMed=9847074;		
RP	Sulston J.E., Waterston R.;		
RT	"Toward a complete human genome sequence."		
RL	Genome Res. 8:1097-1108(1998).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RP	Mead K., Bauer C.;		
RT	"The sequence of Homo sapiens PAC clone RP4-560014."		
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RP	Waterston R.;		
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AC006145; AAD20938.1; -		
DR	InterPro; IPR004010; Cache.		
DR	InterPro; IPR002035; VWF_A.		
DR	Pfam; PF02743; Cache; 1.		
DR	Pfam; PF00092; vwa; 1.		
DR	PROSITE; PS50234; VWF_A. 1		
FT	NON_TER		
SQ	SEQUENCE 745 AA; 84396 MW; BC07B53484B71E4 CRC64;		
	Query Match 66.8%; Score 3570; DB 4; Length 745;		
	Best Local Similarity 99.7%; Pred. No. 4e-215;		
	Matches 670; Conservative 1; Mismatches 1; Indels 0;		
Qy	347	YVNSRANCKIIMLFTDGGERAQEI FNKNKDKKRVVPF	SVGQHNRYERGPIQW
Db	1	YVNSRANCKIIMLFTDGGERAQEI FNKNKDKKRVFT	FSVGQHNRYERGPIQW
Qy	407	KGYYPEIPSGAIRINTEQYLDVLGRPMVLADGKAKQ	OVWNTVYLDALLEGLVIT
Db	61	KGYYPEIPSGAIRINTEQYLDVLGRPMVLADGKAKQ	OVWNTVYLDALLEGLVIT
Qy	467	FNITQGFENKTNLKNQIILGVMGVDVLSLEDIKRL	TPRFTLCPNGYYFAIDPNGYV
Db	121	FNITQGFENKTNLKNQIILGVMGVDVLSLEDIKRL	TPRFTLCPNGYYFAIDPNGYV
Qy	527	LQPNKPSQEPVTLDFDLAELENDIKVEIRKNMIDGES	EKFTLTVKSQDERYI
Db	181	LQPNKPSQEPVTLDFDLAELENDIKVEIRKNMIDGES	EKFTLTVKSQDERYI
Qy	587	TYVTPVNGTDYSIALVLPTYSFYIKAEETITQARSK	KGKMKDSETLKPQNF

```
|||||
|TPVNGTDSLALVLPYTSFYIYKAKLEETITQARSKGKMDSETLKPDPFESGY 300
|
|APRDYCNDLKISDNNTTEFLNFNEFIDRKTNNPNSCNADLINRVLLDAGTNELVN 706
|
|APRDYCNDLKISDNNTTEFLNFNEFIDRKTNNPNSCNADLINRVLLDAGTNELVN 360
|
|QKXIKGVKARFVVTGGITRVYPKBAGENQENPETYEDSFYKSLDNDNYYFTAP 766
|
|QKXIKGVKARFVVTGGITRVYPKBAGENQENPETYEDSFYKSLDNDNYYFTAP 420
|
|GSPGAYESGIMYSKAVEIYIOGKLAKPAVVGIKIDVNSWENFTKSTEDPCAGV 826
|
|GSPGAYESGIMYSKAVEIYIOGKLAKPAVVGIKIDVNSWENFTKSTEDPCAGV 480
|
|GRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGIDPSLMHRLVNI SYAFNKSY 886
|
|GRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGIDPSLMHRLVNI SYAFNKSY 540
|
|VCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTPRLLEAV 946
|
|VCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTPRLLEAV 600
|
|DDFTASLSKQSCITQOTQYFFDNDKSGVLDGCGNCSRI FHGEKLMNTLIFIMV 1006
|
|DDFTASLSKQSCITQOTQYFFDNDKSGVLDGCGNCSRI FHGEKLMNTLIFIMV 660
|
|TCPCDTRL 1018
|
|TCPCDTRL 672
|
|
|PRELIMINARY; PRT; 1150 AA.
|
|TREMELrel. 15, Created)
|TREMELrel. 15, Last sequence update)
|TREMELrel. 23, Last annotation update)
|el, alpha 2/delta subunit 2.
|
|(Human).
|tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
|heria; Primates; Catarrhini; Hominidae; Homo.
|06;
|
|N.A.
|d;
|
|C-1999) to the EMBL/GenBank/DBJ databases.
|
|N.A.
|d;
|
|S.; Marais E., Lacinova L.;
|tribution and functional characterization of the calcium
|2delta-2 subunit.";
|R-2000) to the EMBL/GenBank/DBJ databases.
|8; CAB86193.1;
|004010; Cache.
|002035; VWF_A.
|; Cache; 1.
|; vwa; 1.
|7; VWA; 1.
|234; VWA; 1.
|50 AA; 129876 MW; 37875F687AF5E73C CRC64;
|
|54.2%; Score 2900; DB 4; Length 1150;
|arity 54.7%; Pred. No. 7.3e-173;
|onservative 164; Mismatches 273; Indels 30; Gaps 13;
|
|LTLFQSLIGSPSEPPPSAVTIKSWDKQEDLVTLAKTASGVNQLVDIYKQD 66
|
|LPLPLLAAPGASAYSFPQOHTMQHWRLEQEVGVNRIFGGVQQLREIYKDRN 103
```

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QY 67 LYTVBPNNARQOLVEIARADIEKLNSRSLVSLAEAEKVQAAHQWRBDFASNE
|
|104 LFEQENEPQKLEKVEKAGDIESILLQKQALADAAENFQKAEHWQDNKEED
|
|QY 127 AKDDL---DPEKNDSBPSQ--RIKPVFTIEDANFGRIQISYQAAVHIPTDIYEGS
|
|DB 164 AKADAEELDDPESEDYERGSKASTLRDLDFIEDPNFNKNVNSYAAVQIPTDIYKGS
|
|QY 182 ELNWTLSALDEVFKKREDEPSSLQVFGSATGLARYYPASPWVDSNRTNPKIDL
|
|DB 224 ELNWTLEALENVFWRNRQDTILLQVFGSATGVTRYIPATPW----RAPKIDL
|
|QY 242 PWYIQGAASPDKMLILVDVSGSVGLTLKLIRTSSEMLETLSDDDFVNVSFNS
|
|DB 280 PWYIQGAASPDKMWIIVDVSGSVGLTLKLIRTSSEMLETLSDDDFVNVSFNE
|
|QY 302 SCFQHLVQANVANKVLDKAVNNITAKGITYKGFSPAFBQOLLNVSBRANCK
|
|DB 340 SCFTHLVQANVANKVFKKAVQGMVAKGTYGKAGFEVAFDQOLQNSNITRANCNK
|
|QY 362 TDGGERAQEIENKYN-KDKKVRVFRFVSQGNVYRGPIQWMACENKGYIYFIPS
|
|DB 400 TDGGERVQDVFEKTNWNRTRVRFVSQGNVYRVTPLOMACANKGYIYFIPS
|
|QY 421 INTQRYLDVLRPMVLADGKAKQVQWNTVYLDALBLGLVITGTLPVFNITQFEN
|
|DB 460 INTQRYLDVLRPMVLADGKAKQVQWNTVYLDALBLGLVITGTLPVFNITQ--DG
|
|QY 481 NOLILGVMGVDSLEDIKRLPRFTLCPNGYFPAIDPNGYVLLHNLQPNPKSQ
|
|DB 518 NOLILGVMGIDVALNDIKRLTNYTLGANGYVFAIDLNGYVLLHNLKPKQTTFNR
|
|QY 541 DFLDAELNDIKVEIRNMIDGESGKTRTLVKSODERYIDKGNRTYTWTPVNG
|
|DB 578 DFLDAELNDENKEIRRSIMIDGNKGHKQIRTLVKSIDERYIDEVTRNYTWVPIS
|
|QY 601 ALVLPYTSFYIYKAKLEETITQARSKGKMDSETLKPDPFESGYTFIAPRDYCI
|
|DB 638 GLVLPYTSFYIYKAKLEETITQARSKGKMDSETLKPDPFESGYTFIAPREYCI
|
|QY 661 SDNTEFLNNEFIDRKTNNPNSCNADLINRVLLDAGTNELVQYWSKQK-NII
|
|DB 698 SDNTEFLNNEFIDRKTNNPNSCNADLINRVLLDAGTNELVQYWSKQK-NII
|
|QY 720 RRVVTDGGITRVYPKBAGENQENPETYEDSFYKSLDNDNYYFTAPYENK-SGP
|
|DB 758 VFAATDGGITRVYPKBAGENQENPETYEDSFYKSLDNDNYYFTAPYENK-SGP
|
|QY 779 ---GIMVSKAVEIYIOGKLAKPAVVGIKIDVNSWENF-----TKTISIRDP--CA
|
|DB 818 DTVGILVSTAVELSLGRRTLRPAVVGKLDLEAWAEKPKVLASNRTHQDQPKC-
|
|QY 826 -VCDCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGIDPSLMHRLVNI SV
|
|DB 877 CEMDCEVNNEDLLCVLIDDGGFLVLSNQNHQWQVGRFFSEVDANLMLALYNSF
|
|QY 885 SYDQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTPI
|
|DB 937 SYDQACAPQPPGNLGAAPRGVPTVADFLNLAWTSAANLSLFOQLLYGLIY
|
|QY 945 AVEMEDDDFTASLSKQSCITQOTQYFFDNDKSGVLDGCGNCSRI FHGEKLMNT
|
|DB 997 ADPAEAEQ-SPESTRESSCWKQOTQYFSGVNSYNAIIDGNCNCSRLFHAQRLTNT
|
|QY 1005 MVESKGTCPD 1015
|
|DB 1056 VAEKPLCSQCE 1066
|
|
|RESULT 9
|Q8CFG6
|ID Q8CFG6 PRELIMINARY; PRT; 1157 AA.
```

M O F I C M G O O N X R O J U P L K V
N D B A O O O E H H P S S S S

Q2 Q3 Q4 Q5 Q6 Q7 Q8 Q9 Q10 Q11

TYIQGAASPKOMLILVDVSGSVGLTKLRTSVSEMLETLSDDDFVNVASFNSNAQ 299
 TYIQGAASPKOMLILVDVSGSVGLTKLRTSVSEMLETLSDDDFVNVASFNSNAQ 300
 TYIQGAASPKOMLILVDVSGSVGLTKLAKTISVCEMLDTLSDDDFVNVASFNEKAQ 340
 FFOHLVQOANVRNKKVLKDAVNNITAKGITYYKGFSPAFQOLLNYNVSRANCKILM 359
 FTHLVQOANVRNKKVFKBAVQGVMAKGTGYKAGFEYAFQOLQNSNITRANCNRMIM 400
 JGGEERAQBI FKNYIN - KDKKVRVFRFSVQGHNYERGBIOWMACSNKGYVEIPSIGA 418
 JGGERVQDVVEEKYNWPNRTVRFTISVQGHNYDVFTPLQMACCNKGYFEIPSIGA 460
 TQOBYLDVLGRPMVLADGKAKQVQWNTNYYLDALGLVITGTLPVFVNITQGFENKTN 478
 TQOBYLDVLGRPMVLADGKAKQVQWNTNYYLDALGLVITGTLPVFVNITQ - DGPGE 518
 JILILGVMGVDSLEDIKLTERFTLCPNGYVYFADPNQVYLLHNPLOPKPKSOEVP 538
 JILILGVMGIDVALNDIKLTPNTLILGANGYVYFADILNGYVLLHNPLOPKPTNFEVP 578
 LDABELEDNKEEIRRSMDGDKGHQIRTLVKSLEDEYIDEVIRNVTWTFIRSTNY 638
 VLPPTYSFYIYKAKLEETITQASKKGYKMDSTLKPDPNPEESGYTPIAPRDYCNLD 658
 VLPPTYSTYYLOANRDQILQVKLPISKLDKDFELLFPSSFESEGHVPIAPREYCKOL 698
 WNTTEFLNPNFEFFIDRKTNNPNSCNADLINRVLLDAGFTWELQNYWYSKQK-NIKGV 717
 NSTEFLKDFELMEKVTFDSQCNWFLHNULDITGTQQLVERVWRDQDLNMTYSL 758
 VVTDGGITRVYPKBAGENWQENPETEYDSFYKRSLDNDNYVFTAPYFNK-SQPGAY 776
 AATDGGITRVFPENKAAEDWTENPENFNASFYRRSLDNHGYIFKPPHQDSLRLPLEL 818
 -GIMWSKAVEIYIOGKLLKPAVGVGKIDVNSWIEFN-----TKTSIRDP--CAGP- 825
 VGVLLSTAVELSLGRRTLRPAVGVGVKLDLEAWAEKFKVLASNRTHQDQPKC-GPS 877
 CDCRNSDVMDCVILDDGGFLMANHDDYTQIGRFFGGEIDPSLRHLNINISYAF 882
 MDCEVNNEDLVCVILDDGGFLVSNQNHQWQVGRFFFEVDANLMLALYNNSFYTR 937
 DYQSVCEPGAAPKXGAGHRSAYVPSVADILOIGMWATAAAMSILQQLSLSTFPRL 942
 DYQAAACAPOPPGNLGAAPRGVFEVPTIADFLNLAWMTSAAASLFLQQLLYGLYHSW 957
 EMBEDDDFTASLSKOSCITEQOYFEPDNDKSFPGLVDCGNCRSRI FHGEKLMNTNLI 1002
 PAAEG-SPETRESSCWKQTYFYFGSVNASYNAILIDCGNCSRLFHAQRLTNTNLL 1056
 ESKGTCPCD 1015
 EKPLCSQCE 1069
 RELIMINARY; PRT; 1143 AA.
 TrEMBLrel. 15, Created)
 TrEMBLrel. 15, Last sequence update)
 TrEMBLrel. 23, Last annotation update)
 el, alpha 2/delta subunit 2.
 (Human).
 tacea; Chordata; Craniata; Vertebrata; Euteleostomi;
 heria; Primates; Catarrhini; Hominidae; Homo.
 06;
 N.A.

AATDGGITRVPKKAEDWTENPEPPFNASFYRRSLDNHGVYFKPPHQDALLRPLELEN 810
 -GIMVXAVEIYIQGKLLKPAVVGKIDVANSWIENF-----TKTSIRDP--CAGP--- 825
 VGLVSTAVELSLGRRLTRPAVGVKLDLEMAEKFKVLASNRTHQDPQKCGPNSH 869
 CDCKNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNIVSYAFNK 884
 MDCEVNNEDLLCVLIDDDGFLVLSNQNHQDQVGRFFSEVDANLMLALYNNSPYTRKE 929
 DYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAAWSILQQFLSLTFPRLLIE 944
 DYQACACAPQPGNIGAAPRGVFTVADFLNLAWTSAALWSLQQFLYGLIYHSWFQ 989
 EMEDDFTASLKSQSCITEQTYFFNDKSFSGVLDGCGNCSRFHGEKLMNTNLIFI 1004
 PAEABG-SPETRESSCMKQTYVFGSVNAYNAIDCGNCSRLFAQLRTNLNLLFV 1048
 3SKGTCPCD 1015
 3KPLCSQCE 1059

PRELIMINARY; PRT; 1145 AA.

(TREMBLrel. 12, Created)
 (TREMBLrel. 12, Last sequence update)
 (TREMBLrel. 23, Last annotation update)
 protein KIAA0558.

(Human).
 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Theria; Primates; Carnivora; Hominidae; Homo.
 606;
 M N.A.

Latif F., Ding J., Lin J., Mathis M.,
 new candidate human tumor suppressor gene located in the
 cell lung cancer homozygous deletion region homologous to
 ted calcium channel alpha 2/ delta subunit.",
 CT-1998) to the EMBL/GenBank/DBJ databases.

M N.A.
 atif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,
 Johnson B., Lerman M.I.;
 2 delta subunit of the L-type voltage gated calcium
 des in the lung cancer critical region on 3p21.3.",
 AN-1998) to the EMBL/GenBank/DBJ databases.

M N.A.
 0545; PubMed=9628581;
 shikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
 of the coding sequences of unidentified human genes. IX.
 sequences of 100 new cDNA clones from brain which can
 ge proteins in vitro.",
 1-39(1998).
 09; AAC70914.1; -;
 92; AAB96913.1; -;
 30; BAA25484.1; -;
 1400; CACNA2D2.
 R004010; Cache.
 R002035; VWF_A.
 3; Cache; 1.
 2; vwa; 1.
 27; VWA; 1.
 0234; VWFA; 1.
 protein.

SQ SEQUENCE 1145 AA; 129268 MW; 9ADA4807FC70971B CRC64;
 Query Match
 Best Local Similarity 53.7%; Score 2872.5; DB 4; Length 1145;
 Matches 562; Conservative 162; Mismatches 270; Indels 37;

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 Db 44 LWLLPLPLLAAPGASAYSPQOHTMOHWRRLQEVQVDMRIFGGVQOOLREI
 QY 67 LYTVENPAROLVEIARDIEKLLSNRSKALVSLALEAEKQAAHOMREDFASN
 Db 104 LFEQVENEPQKLVKAGDIESLLDRKQVALKRLADAAEFQKAHRWQDNKEE
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 Db 164 AKAAELDDPSESDVERGSKASTLRDLFIEDPNFKNKVNSYAAVQIPTDIYK;
 QY 182 ELNWTSAIDVFKKRNREDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
 Db 224 ELNWTALENVFMRNRQDPTLLMQVFGSATGVTRYYPATPW----RAPKKIDL
 QY 242 PWYIQGAASPDMILVDVSGVSGLTCLKIRTSVSEMLETSDDDDFNVASFN;
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 Db 400 TDGGEEDVQDFEKNVNPNTVTFVSVGQHNHYDVTPLQMACANKGYEIP;
 QY 421 INTQEYLDVIGRPMVLGADKAKQVQWTVNYLDALGLGITGTLPVFNITQPEZ
 Db 460 INTQEYLDVIGRPMVLGADKAKQVQWTVNYEDALGLGVTVGTLPVFNLTQ--DC
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 Db 751 VFAATDGGITRVYPKKAEDWTENPEPPFNASFYRRSLDNHGVYFKPPHQDALLR
 QY 779 ---GIMVXAVEIYIQGKLLKPAVVGKIDVANSWIENF-----TKTSIRDP--CA
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 QY 826 -VCDCKNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNIVSY
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 (T-EMBLrel. 23, Last sequence update)
 (T-EMBLrel. 23, Last annotation update)
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 Heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1090;
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 6J; TISSUE=Retina;
 683; PubMed=12466851;
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 3; BAC31998.1; --
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 53.7%; Score 2868.5; DB 11; Length 1148;
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 QY 942 LLEAVEMEDDDFTASLSKQSCITECTQYFFDNDKSPSGVLDGNCGRIFHGEKLA
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 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
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 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
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 GN MKIAA0558.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
 RA Ohara O., Koga H.;
 RT "Prediction of the coding sequences of mouse homologues of KIAA g
 RT I. The complete nucleotide sequences of 100 mouse KIAA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clone
 RT randomly sampled from size-fractionated libraries.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB093246; BAC41430.1; --
 FT NON_TER
 SQ SEQUENCE 1098 AA; 124551 MW; 6D9581577E548720 CRC64;
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 Best Local Similarity 54.3%; Pred. No. 1.8e-170;
 Matches 556; Conservative 165; Mismatches 263; Indels 39; G
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the number of results predicted by chance to have a
 r than or equal to the score of the result being printed,
 ed by analysis of the total score distribution.

SUMMARIES

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0.0	1036	15	US-10-090-827-14	Sequence 14, Appl	
0.0	1063	15	US-10-090-827-15	Sequence 15, Appl	
0.0	1091	9	US-09-875-423-4	Sequence 4, Appl	
0.0	1091	12	US-10-162-102-17	Sequence 17, Appl	
0.0	1091	15	US-10-162-012-17	Sequence 17, Appl	
0.0	1091	15	US-10-090-827-16	Sequence 16, Appl	
9.3	1086	12	US-10-375-253-49	Sequence 49, Appl	
8.9	1084	12	US-10-375-253-53	Sequence 53, Appl	
8.9	1018	15	US-10-090-827-6	Sequence 6, Appl	
8.9	1036	15	US-10-090-827-7	Sequence 7, Appl	
8.9	1063	15	US-10-090-827-8	Sequence 8, Appl	
8.9	1069	15	US-10-090-827-9	Sequence 9, Appl	
8.9	1091	15	US-10-090-827-5	Sequence 5, Appl	
8.6	1103	12	US-10-375-253-47	Sequence 47, Appl	

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	17	5219	97.6	1091	12	US-10-375-253-20	Sequence
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	22	1085	20.3	1091	12	US-10-162-102-18	Sequence
	23	1085	20.3	1091	15	US-10-162-012-18	Sequence
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ALIGNMENTS

RESULT 1
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 ; Sequence 13, Application US/10090827
 ; Publication No. US20030073132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert
 ; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 sub
 ; TITLE OF INVENTION: binding ligands
 ; FILE REFERENCE: 179
 ; CURRENT APPLICATION NUMBER: US/10/090,827
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US/09/397,549
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 1018
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-090-827-13

Query Match 100.0%; Score 5346; DB 15; Length 1018;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; G

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EQTYFFDNDKSPGVLDCGNCRIHFHGEKLMNTNLFIMVESKGTCPDTRL 1018

lication US/10090827
US20030073132A1

er-Lambert

ION: Method for the screening of alpha 2 delta-1 subunit

ION: binding ligands

179

TION NUMBER: US/10/090,827

DATE: 2002-03-06

ON NUMBER: US/09/397,549

TE: 1999-09-16

D NOS: 21

lin Ver. 2.1

, sapiens

100.0%; Score 5346; DB 15; Length 1063;

arity 100.0%; Pred. No. 0;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-09-875-423-4

; Sequence 4, Application US/09875423

; Patent No. US20020081657A1

; GENERAL INFORMATION:

; APPLICANT: Curtis, Rory A.J.

; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL

; FILE REFERENCE: 10448-059001

; CURRENT APPLICATION NUMBER: US/09/875,423

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/209,257

; PRIOR FILING DATE: 2000-06-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 1091

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-875-423-4

Query Match 100.0%; Score 5346; DB 9; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; C

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RSAYVPSVADILQIGWATAAANSILOQFLLSLTPPRLLLEAVEMEDDDFTASLSKQ 960
RSAYVPSVADILQIGWATAAANSILOQFLLSLTPPRLLLEAVEMEDDDFTASLSKQ 960
EQTOVFFNDKSPSGVLDGNCRSRIFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018
EQTOVFFNDKSPSGVLDGNCRSRIFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018

lication US/10162012
US20030051660A1
ION:
is, Rory A.J.
os-Santiago, Inmaculada
Wei
ION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
10448-190001

ION NUMBER: US/10162,012
DATE: 2002-06-04

ON NUMBER: US 60/209,845
TE: 2000-06-06

ON NUMBER: US 09/875,321
TE: 2001-06-06

ON NUMBER: PCT/US01/18340
TE: 2001-06-06

ON NUMBER: US 60/209,257
TE: 2000-06-05

ON NUMBER: US 09/875,423
TE: 2001-06-05

ON NUMBER: PCT/US01/18398
TE: 2001-06-05

ON NUMBER: US 60/209,238
TE: 2000-06-05

ON NUMBER: US 09/875,363
TE: 2001-06-05

ON NUMBER: PCT/US01/18247
TE: 2001-06-05

ON NUMBER: US 60/227,068
TE: 2000-08-22

ON NUMBER: US 09/928,530
TE: 2001-08-13

ON NUMBER: PCT/US01/25475
TE: 2001-08-15

ON NUMBER: US 60/226,770
TE: 2000-08-21

ON NUMBER: US 09/934,421
TE: 2001-08-21

ON NUMBER: PCT/US01/26096
TE: 2001-08-21

ON NUMBER: US 60/279,281
TE: 2001-03-28

ON NUMBER: US 10/109,029
TE: 2002-03-28

ON NUMBER: PCT/US02/09728
TE: 2002-03-28

ON NUMBER: US 60/290,288
TE: 2001-05-11

ON NUMBER: US (not assigned)
TE: 2002-05-13

D NOS: 48
EQ for Windows Version 4.0

sapiens

Query Match 100.0%; Score 5346; DB 15; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0;
QY 1 MAAGCLLALTTLTFLQSLLIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGVNI
Db 1 MAAGCLLALTTLTFLQSLLIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGVNI
QY 61 YEKYQDLTVTFPNNARQIVAAARDIEKLLNSRKALVSLALEAEKVQAAHOREI
Db 61 YEKYQDLTVTFPNNARQIVAAARDIEKLLNSRKALVSLALEAEKVQAAHOREI
QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROI SYQHAHAVHIPTDIYEG
Db 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROI SYQHAHAVHIPTDIYEG
QY 181 NELNWTSAIDVFKKNREDEPSLLMQVFGSATGLARYYPASPWVDNSTRPNKIDL
Db 181 NELNWTSAIDVFKKNREDEPSLLMQVFGSATGLARYYPASPWVDNSTRPNKIDL
QY 241 RPWYIQAASPKDMLILVDVSSVSGLTCLKIRTSVSEMLETSLDDDFNVASFN
Db 241 RPWYIQAASPKDMLILVDVSSVSGLTCLKIRTSVSEMLETSLDDDFNVASFN
QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCNI
Db 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCNI
QY 361 FTDGGERAAQEIFNKYNKDKKVRPFRVSVGQHNVERGPIQWMACENKGYTYEIPS
Db 361 FTDGGERAAQEIFNKYNKDKKVRPFRVSVGQHNVERGPIQWMACENKGYTYEIPS
QY 421 INTQYLDVLGRPMVLADGKAKOVNTNVLDALEGLVITGTLPVNITQGFENI
Db 421 INTQYLDVLGRPMVLADGKAKOVNTNVLDALEGLVITGTLPVNITQGFENI
QY 481 NQLILGVNGVDVSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPNLOPKPKSQI
Db 481 NQLILGVNGVDVSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPNLOPKPKSQI
QY 541 DFLDAELENDIKVEIRNMIDGESGEKTFRTLKVSQDERYIDKGNRTYTWTVPNG
Db 541 DFLDAELENDIKVEIRNMIDGESGEKTFRTLKVSQDERYIDKGNRTYTWTVPNG
QY 601 ALVLPYTFYIKAKLEETITQARKSKGKMDSETLKPDPNFESGYTFIAPRDYCI
Db 601 ALVLPYTFYIKAKLEETITQARKSKGKMDSETLKPDPNFESGYTFIAPRDYCI
QY 661 SDNNTFEFLNFNEFIDRKTNNPSCNADLIINRVLLDAGFTNELLVQNYWSKQNIKI
Db 661 SDNNTFEFLNFNEFIDRKTNNPSCNADLIINRVLLDAGFTNELLVQNYWSKQNIKI
QY 721 FVWTDGGITRVYPKEAGENWQENPETYEDSYFKRSLDNDNVFTAPYFNKSGPGA
Db 721 FVWTDGGITRVYPKEAGENWQENPETYEDSYFKRSLDNDNVFTAPYFNKSGPGA
QY 781 MYSKAVEIYIQGKLLKPAVVGIKIDVNSWIEBNFTKTSIRDPCAGVCDCKRNSDV
Db 781 MYSKAVEIYIQGKLLKPAVVGIKIDVNSWIEBNFTKTSIRDPCAGVCDCKRNSDV
QY 841 LDDGFFLLMANHDDYTNOIGRFFGIDPSLMRHLNVSIVAFNKSVDYQSVCEPGA
Db 841 LDDGFFLLMANHDDYTNOIGRFFGIDPSLMRHLNVSIVAFNKSVDYQSVCEPGA
QY 901 GAGERSATVPSVADILQIGWATAAANSILOQFLLSLTPPRLLLEAVEMEDDDFTAS
Db 901 GAGERSATVPSVADILQIGWATAAANSILOQFLLSLTPPRLLLEAVEMEDDDFTAS
QY 961 SCITETQYQYFFDNDKSPSGVLDGNCRSRIFHGEKLMNTNLIIFIMVESKGTCPDIT
Db 961 SCITETQYQYFFDNDKSPSGVLDGNCRSRIFHGEKLMNTNLIIFIMVESKGTCPDIT

QY	721	FVYTDGGITRVYKPEAGENWQENPETYEDSFYKSLDNDNVYFTAPYFNKSGPGI	
Db	721	FVYTDGGITRVYKPEAGENWQENPETYEDSFYKSLDNDNVYFTAPYFNKSGPGI	
QY	781	MYSKAVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDI	
Db	781	MYSKAVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDI	
QY	841	LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPC	
Db	841	LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPC	
QY	901	GAGHSAYVPSVADILQIGMWATAAAMSILQQFLLSLTFPRLLAEAVEMEDDDFT7	
Db	901	GAGHSAYVPSVADILQIGMWATAAAMSILQQFLLSLTFPRLLAEAVEMEDDDFT7	
QY	961	SCITBQTOYFPFNDKSPSGVLDGNCNCSRI FHGKLMNTNLI FIMVSKGTGCPCI	
Db	961	SCITBQTOYFPFNDKSPSGVLDGNCNCSRI FHGKLMNTNLI FIMVSKGTGCPCI	
RESULT 8			
US-10-375-253-49			
; Sequence 49, Application US/10375253			
; Publication NO. US20040018510A1			
; GENERAL INFORMATION:			
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES			
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND			
; METHOD OF INVENTION: METHODS			
; FILE REFERENCE: SD9813DA			
; CURRENT APPLICATION NUMBER: US/10/375,253			
; CURRENT FILING DATE: 2003-02-27			
; PRIOR APPLICATION NUMBER: 08/450,273			
; PRIOR FILING DATE: 1995-05-25			
; PRIOR APPLICATION NUMBER: 08/404,354			
; PRIOR FILING DATE: 1995-02-15			
; PRIOR APPLICATION NUMBER: 07/914,231			
; PRIOR FILING DATE: 1992-07-13			
; PRIOR APPLICATION NUMBER: 08/314,083			
; PRIOR FILING DATE: 1994-09-28			
; PRIOR APPLICATION NUMBER: 07/914,231			
; PRIOR FILING DATE: 1992-07-13			
; PRIOR APPLICATION NUMBER: 07/603,751			
; PRIOR FILING DATE: 1990-11-09			
; PRIOR APPLICATION NUMBER: 08/290,012			
; PRIOR FILING DATE: 1994-08-11			
; PRIOR APPLICATION NUMBER: 08/149,097			
; PRIOR FILING DATE: 1993-11-05			
; PRIOR APPLICATION NUMBER: 08/105,536			
; PRIOR FILING DATE: 1993-08-11			
; PRIOR APPLICATION NUMBER: 08/149,097			
; PRIOR FILING DATE: 1993-11-05			
; Remaining Prior Application data removed - See File Wrapper or PAL			
; NUMBER OF SEQ ID NOS: 65			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 49			
; LENGTH: 1086			
; TYPE: PRT			
; ORGANISM: Human			
US-10-375-253-49			
Query Match 99.3%; Score 5306.5; DB 12; Length 1086;			
Best Local Similarity 99.5%; Pred. No. 0;			
Matches 1013; Conservative 0; Mismatches 0; Indels 5;			
QY	1	MAAGCLLALTTLTFQSLIGPSSSEPPPSAVTIKSWDKMDEDLVTLAKTAGSVN	
Db	1	MAAGCLLALTTLTFQSLIGPSSSEPPPSAVTIKSWDKMDEDLVTLAKTAGSVN	
QY	61	YERYQDLTYTPEPNARQLVFAARDIEKGLSNRSKALVSLALAEKVOAHQWRE	
Db	61	YERYQDLTYTPEPNARQLVFAARDIEKGLSNRSKALVSLALAEKVOAHQWRE	

LPVSYFYIIKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFIAPRDYCNLDKI 660
 LPVSYFYIIKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFIAPRDYCNLDKI 653
 VTSEFLNPFNFIIDRKTPNNPSCNADLLNRLVLDAGFTNELVQVWSKQKNIKGKVKAR 720
 VTSEFLNPFNFIIDRKTPNNPSCNADLLNRLVLDAGFTNELVQVWSKQKNIKGKVKAR 713
 IDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
 IDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 773
 KAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRPCAGPVCDCKRNSDVMDCVI 840
 KAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRPCAGPVCDCKRNSDVMDCVI 833
 GGFLLMANHHDDYTNOIGRFFGEIDPDLMRHLVNI SVYAFNKSVDYQSVCEPAGAPKQ 900
 GGFLLMANHHDDYTNOIGRFFGEIDPDLMRHLVNI SVYAFNKSVDYQSVCEPAGAPKQ 893
 HRSAYVPSVADIIQIGMWATAAASWSIIQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
 HRSAYVPSVADIIQIGMWATAAASWSIIQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 953
 TEQTYQYFFDNDKSKFSFGLDCGNCRSRIFHGEKLMNTNLIFIMVESKGTCPDTRL 1018
 TEQTYQYFFDNDKSKFSFGLDCGNCRSRIFHGEKLMNTNLIFIMVESKGTCPDTRL 1011

lication US/10090827

US20030073132A1

TION:

ner-Lambert

TION: Method for the screening of alpha 2 delta-1 subunit

TION: binding ligands

: 179

ATION NUMBER: US/10/090,827

DATE: 2002-03-06

ION NUMBER: US/09/397,549

ATE: 1999-09-16

ID NOS: 21

ntIn Ver. 2.1

scrofa

larity 98.9%; Score 5288; DB 15; Length 1018;

Conservative 5; Mismatches 7; Indels 0; Gaps 0;

GCLLALTLTQSLIGSSPEPPSAVTITKSWDKMOEDLVTAKTAGSNOLVDI 60
 GCLLALTLTQSLIGSSPEPPSAVTITKSWDKMOEDLVTAKTAGSNOLVDI 60
 YQDLTYVEPNARQVLVEIARDIEKLSNRSKALVSLALEAEKVQAAHQRDEFSN 120
 YQDLTYVEPNARQVLVEIARDIEKLSNRSKALVSLALEAEKVQAAHQRDEFSN 120
 YYNKADLDPEKNDSEPGSRIKPVFTEDANFGRQISYQAAHVIPTDIYEGSTIVL 180
 YYNKADLDPEKNDSEPGSRIKPVFTEDANFGRQISYQAAHVIPTDIYEGSTIVL 180
 NMTSALDEVFKKNEEPDPSLLWQVFGSATGLARYYPASPMVDNSRTNPKIDLYDVR 240
 NMTSALDEVFKKNEEPDPSLLWQVFGSATGLARYYPASPMVDNSRTNPKIDLYDVR 240
 YIQGAASPKDMLILVDYSGVSGGLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300
 YIQGAASPKDMLILVDYSGVSGGLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300

301 VSCFQHLVQANVRNKKVLKXAVNNITAKGITDYKKGFSFAFEQLLNYSRANCN
 301 VSCFQHLVQANVRNKKVLKXAVNNITAKGITDYKKGFSFAFEQLLNYSRANCN
 361 FTDGGERAQEIPFNKYNKDKKVRVFPSPVQGHYERGPQIOWMACENKGYIYEIPS
 361 FTDGGERAQEIPFNKYNKDKKVRVFPSPVQGHYERGPQIOWMACENKGYIYEIPS
 421 INTQEVLDVLGRPMVLGAKAQOVMTNVYLDALGLVITGTLPVFNITGQPEN
 421 INTQEVLDVLGRPMVLGAKAQOVMTNVYLDALGLVITGTLPVFNITGQPEN
 481 NQILGVGMGVDSLEDIKRLTPRFTLCPNGYYPAIDPNGYVLLHPLNLPKNPKSQ
 481 NQILGVGMGVDSLEDIKRLTPRFTLCPNGYYPAIDPNGYVLLHPLNLPKNPKSQ
 541 DFLDASLENDIKVETIRNKMIDGESGEKTRTLVKSOERYIDKGNRTYTWTPVNG
 541 DFLDASLENDIKVETIRNKMIDGESGEKTRTLVKSOERYIDKGNRTYTWTPVNG
 601 ALVLPYTSFYIIKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFIAPRDY
 601 ALVLPYTSFYIIKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFIAPRDY
 661 SONNTFLLNFNEFIDRKTPNNPSCNADLLNRLVLDAGFTNELVQVWSKQKNIK
 661 SONNTFLLNFNEFIDRKTPNNPSCNADLLNRLVLDAGFTNELVQVWSKQKNIK
 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGA
 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGA
 781 MYSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRPCAGPVCDCKRNSDV
 781 MYSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRPCAGPVCDCKRNSDV
 841 LDGGLFLMANHHDDYTNOIGRFFGEIDPDLMRHLVNI SVYAFNKSVDYQSVCEP
 841 LDGGLFLMANHHDDYTNOIGRFFGEIDPDLMRHLVNI SVYAFNKSVDYQSVCEP
 901 GAGHSAYVPSVADIIQIGMWATAAASWSIIQQFLLSLTFPRLLLEAVEMEDDDFT
 901 GAGHSAYVPSVADIIQIGMWATAAASWSIIQQFLLSLTFPRLLLEAVEMEDDDFT
 961 SCITEQTYQYFFDNDKSKFSFGLDCGNCRSRIFHGEKLMNTNLIFIMVESKGTCPD
 961 SCITEQTYQYFFDNDKSKFSFGLDCGNCRSRIFHGEKLMNTNLIFIMVESKGTCPD

RESULT 11

US-10-090-827-7

; Sequence 7, Application US/10090827

; Publication No. US20030073132A1

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert

; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 su

; FILE REFERENCE: 179

; CURRENT APPLICATION NUMBER: US/10/090,827

; PRIOR FILING DATE: 2002-03-06

; PRIOR APPLICATION NUMBER: US/09/397,549

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 1036

; TYPE: PR

; ORGANISM: Sus scrofa

US-10-090-827-7

Query Match

Best Local Similarity 98.9%; Score 5288; DB 15; Length 1036;

98.8%; Pred. No. 0;

TDGGITRVYPKEAGENWQENPETYEDSFYKRSNDNDNYVFTAPYFNKSGPGAYBSGI 780
 KAVEIYIOGKLLKPAVVGIGKIDVNSWIENFTKTSIRDPCAGVCDCKRNSDVMDCVI 840
 KAVEIYIOGKLLKPAVVGIGKIDVNSWIENFTKTSIRDPCAGVCDCKRNSDVMDCVI 840
 XGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPAAAPKQ 900
 XGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPAAAPKQ 900
 HRSAYVPSVADTLOIGMWATAAAWSILOQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
 HRSAYVPSIADILHIGMWATAAAWSILOQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
 TEQTOYFFDNDKSFSGVLDCGNCRSRIFHGEKLMNTNLIFIMVESKGTGCPDTRL 1018
 TEQTOYFFDNDKSFSGVLDCGNCRSRIFHGEKLMNTNLIFIMVESKGTGCPDTRL 1018
 Publication US/10090827
 US20030073132A1
 TION:
 ner-Lambert
 TION: Method for the screening of alpha 2 delta-1 subunit
 TION: binding ligands
 : 179
 ATION NUMBER: US/10/090,827
 DATE: 2002-03-06
 TON NUMBER: US/09/397,549
 DATE: 1999-09-16
 ID NOS: 21
 ntIn Ver. 2.1

: scrofa

98.9%; Score 5288; DB 15; Length 1069;
 larity 98.8%; Pred. No. 0;
 Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 GCLLALTLTLFQSLIGPSSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
 GCLLALTLTLFQSLIGPSSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
 YQDLTYVEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120
 YQDLTYVEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120
 YNNAKDDLPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPDITYEGSTIVL 180
 YNNAKDDLPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPDITYEGSTIVL 180
 NWTGALDEVFKNREEDPSLLWQVFGSATGLARYYPASWPVDNRTNPKIDLYDVR 240
 NWTGALDEVFKNREEDPSLLWQVFGSATGLARYYPASWPVDNRTNPKIDLYDVR 240
 YIOGAASPKDMLILVDVSGVSGLTCLKIRTSVSEMLETSLDDPPVNVASFNSNAQD 300
 YIOGAASPKDMLILVDVSGVSGLTCLKIRTSVSEMLETSLDDPPVNVASFNSNAQD 300
 FQHLVQANVRNKKVQDAVNNITAKGIDYKKGFSFAFEQQLLNYSRANCKNIML 360
 FQHLVQANVRNKKVQDAVNNITAKGIDYKKGFSFAFEQQLLNYSRANCKNIML 360
 GGEERAQEIFNKNKDKKVRFRFSVGOHNYTERGPIQWACENKGYIYEPSIGAIR 420
 GGEERAQEIFNKNKDKKVRFRFSVGOHNYTERGPIQWACENKGYIYEPSIGAIR 420
 QEYLDVLRPMTAGDKAKQVQWNTVNYLDALDELGLVITGTLPVNITQFENKTNLK 480

Db 421 INTQEVLDVLRPMVTLAGDKAKQVQWNTVNYLDALDELGLVITGTLPVNITQFENITQNEI
 QY 481 NQILTLGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPKPKS
 Db 481 NQILTLGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPKPKS
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERVIDKGNRTYTTWTPVNK
 Db 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERVIDKGNRTYTTWTPVNK
 QY 601 ALVLPYTSFYIYIKAKUBETITQARSKKGKMDSETLKPDPFESGYTFIAPRDY
 Db 601 ALVLPYTSFYIYIKAKUBETITQARSKKGKMDSETLKPDPFESGYTFIAPRDY
 QY 661 SDNNTEFLNFNFIDRKTNNPNSCNADLNRVLLDAGFTNELLVONTWSKQKNI
 Db 661 SDNNTEFLNFNFIDRKTNNPNSCNADLNRVLLDAGFTNELLVONTWSKQKNI
 QY 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSNDNDNYVFTAPYFNKSGPG
 Db 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSNDNDNYVFTAPYFNKSGPG
 QY 781 MVSKAIVEIYIOGKLLKPAVVGIGKIDVNSWIENFTKTSIRDPCAGVCDCKRNSD
 Db 781 MVSKAIVEIYIOGKLLKPAVVGIGKIDVNSWIENFTKTSIRDPCAGVCDCKRNSD
 QY 841 LDGGLFLMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEP
 Db 841 LDGGLFLMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEP
 QY 901 GAGHRSAYVPSVADTLOIGMWATAAAWSILOQFLLSLTFPRLLLEAVEMEDDDFTY
 Db 901 GAGHRSAYVPSIADILHIGMWATAAAWSILOQFLLSLTFPRLLLEAVEMEDDDFTY
 QY 961 SCITEQTOYFFDNDKSFSGVLDCGNCRSRIFHGEKLMNTNLIFIMVESKGTGCPCI
 Db 961 SCITEQTOYFFDNDKSFSGVLDCGNCRSRIFHGEKLMNTNLIFIMVESKGTGCPCI

RESULT 14

US-10-090-827-5
 ; Sequence 5, Application US/10090827
 ; Publication No. US20030073132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert
 ; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 su
 ; FILE REFERENCE: 179
 ; CURRENT APPLICATION NUMBER: US/10/090,827
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US/09/397,549
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 1091
 ; TYPE: PRT
 ; ORGANISM: Sus scrofa
 US-10-090-827-5

Query Match 98.9%; Score 5288; DB 15; Length 1091;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 1006; Conservative 5; Mismatches 7; Indels 0;

QY 1 MAAGCCLALTLTLFQSLIGPSSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVN
 Db 1 MAAGCCLALTLTLFQSLIGPSSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVN
 QY 61 YEKYQDLTYVEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHQRW
 Db 61 YEKYQDLTYVEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHQRW

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|||||
VRYTTPVNGTDYSLALVLPYTFYFKAKLEETITQARY-----SETLAPDNF 653
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3YTFIAPRDYCNDLKISDNNEFLNNEFIDRKTNNPSCNADLINRVLLDAGFTN 713
QNTWSKOKNIGVKARFVVTDDGGITRVYPKEAGENMOENPETVEDSFYKRSLDNDNY 761
QNTWSKOKNIGVKARFVVTDDGGITRVYPKEAGENMOENPETVEDSFYKRSLDNDNY 773
APYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP 821
APYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP 833
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PVCDCRNSDVMDCVILDDGGFLLMANHDDYTQIGRFFGCEIDPISLMRHLVNI SVYA 893
3YDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAWSILQQFLLSLTFPR 941
3YDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAWSILQQFLLSLTFPR 953
AVEMEDDDFTASLSKSCITEQYQYFFDNDKSFSGVLDGCGCSRIFPHGEKLMNTNL 1001
AVEMEDDDFTASLSKSCITEQYQYFFDNDKSFSGVLDGCGCSRIFPHGEKLMNTNL 1013
AVESKGTCPDTRL 1018
AVESKGTCPDTRL 1030

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in search, using sw model

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46
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3308 segs, 9616862 residues

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gth: 0

gth: 2000000000

imum Match 0%

aximum Match 100%

isting first 45 summaries

TR 76:*

pir1:*

pir2:*

pir3:*

pir4:*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

ery	rch	Length	DB	ID	Description
0.0	1091	2	JH0565		calcium channel al
6.2	1091	2	A4147		calcium channel pr
6.0	1106	1	CHBA2		calcium channel pr
0.3	1091	2	T30256		calcium channel al
1.4	734	2	S44617		C50C3.11 protein -
0.7	1148	2	T18770		probable calcium c
3.7	1450	2	C86880		hypothetical prote
3.6	886	2	S54355		inter-alpha-trypsi
3.5	885	2	S30350		inter-alpha-trypsi
3.3	1819	2	D97033		uncharacterized pr
3.1	889	2	JC5576		inter-alpha-trypsi
3.0	2706	2	T28155		variant-specific s
3.0	1984	2	A44396		P-type cation tran
2.9	575	2	D64998		hypothetical prote
2.9	918	2	E90542		lipoprotein (impor
2.9	680	2	A97331		membrane associat
2.9	1516	2	E71619		RA2 endonuclease
2.9	2364	2	I40884		cytotoxin L - C10s
2.9	946	1	IYH02		inter-alpha-trypsi
2.9	1315	2	T28679		fibrinogen-binding
2.9	932	2	JC5953		inter-alpha-inhibi
2.8	1291	2	S46431		botulinum neurotox
2.8	1291	2	A97777		botulinum neurotox
2.8	420	2	S76691		hypothetical prote
2.8	1426	2	A99580		hypothetical prote
2.8	921	2	JC4625		inter-alpha-trypsi
2.8	1385	2	D98824		hypothetical prote
2.8	654	2	A69656		methyl-accepting c
2.8	1027	2	B90527		atp-binding protei

30	149	2.8	459	2	F64688	proteinase
31	149	2.8	930	2	JX0368	inter-alpha
32	148.5	2.8	2401	2	T28676	rhoptyr pr
33	148	2.8	964	2	S28855	DNA-direct
34	146.5	2.7	1285	2	B72420	hypothetic
35	146	2.7	688	2	D96930	methyl-acc
36	146	2.7	4688	2	F82885	hypothetic
37	145.5	2.7	676	2	T47637	hypothetic
38	145.5	2.7	689	2	F84811	probable r
39	145.5	2.7	1237	2	AC1583	internalin
40	145.5	2.7	2013	2	AD1129	probable p
41	145.5	2.7	3216	2	C90538	hypothetic
42	145.5	2.7	5005	2	F82884	hypothetic
43	144	2.7	1087	1	S41797	cellulose
44	144	2.7	1091	2	S33850	fibronectin
45	143.5	2.7	1252	2	H97178	ATP-depend

ALIGNMENTS

RESULT 1

JH0565
calcium channel alpha-2b chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug
C:Accession: JH0565
R:Williams, M. F., Feldman, D. H.; McCue, A. F.; Brenner, R.; Velicelebi,

Neuron 8, 71-84, 1992
A:Title: Structure and functional expression of alphas, alpha2, and b

A:Reference number: JH0564; MUID:92110010; PMID:1309651

A:Accession: JH0565

A:Molecule type: mRNA

A:Residues: 1-1091 <WIL>

A:Cross-references: GB:M76559; NID:gl79761; PIDN:AAA51903.1; PID:gl797

A:Experimental source: Basal ganglia

A:Note: Several conflicts are found between GenBank submission, author

C:Comment: This protein is a subunit of the voltage dependent calcium

C:Superfamily: calcium channel alpha-2 chain

C:Keywords: glycoprotein; phosphoprotein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-1067/Product: calcium channel alpha-2b chain #status predicted <

F:32.268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (b

F:91.142,250,625,817/Binding site: phosphate (Ser) (covalent) (b

F:92.136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/

F:501/Binding site: phosphate (Thr) (covalent) #status predicted

F:833/Binding site: phosphate (Ser) (covalent) (b

Query Match 100.0%; Score 5346; DB 2; Length 1091;

Best Local Similarity 100.0%; Pred. No. 1.6e-313;

Matches 1018; Conservative 0; Mismatches 0; Indels 0; G

Qy 1 MAAGCLALTLTLPQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVC

Db 1 MAAGCLALTLTLPQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVC

Qy 61 YEKQDLYTFEPNARQLVEIARDIEKLSNRSKALVSLALEAEKVQAQAHQWREC

Db 61 YEKQDLYTFEPNARQLVEIARDIEKLSNRSKALVSLALEAEKVQAQAHQWREC

Qy 121 EVVYNAKDDLDPKNDSEFGSQRIKPVFIEDANFGRIQISYQHAHVHPTDIYEGS

Db 121 EVVYNAKDDLDPKNDSEFGSQRIKPVFIEDANFGRIQISYQHAHVHPTDIYEGS

Qy 181 NELNWTALDEVPKNEEDPSLLWQVFGSATGLARYTPASPWNDSRTPNKIDLY

Db 181 NELNWTALDEVPKNEEDPSLLWQVFGSATGLARYTPASPWNDSRTPNKIDLY

Qy 241 RPWYIQGAASPKDMLILVDVSGVSGVGLTKLIRTSVSEMLETISDDDFVNVASFNS

Db 241 RPWYIQGAASPKDMLILVDVSGVSGVGLTKLIRTSVSEMLETISDDDFVNVASFNS

Qy 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFEQLLNYNVSRANCNK

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GGEEAQAQEIFNKYNKDKKVRFRFSVGGQHNTERGPIOMMACENKGYIYEIPSIGAIR 420
QYELDLVGRPMVLADGKAKQVQNTNVIYLDALDELGLVITGTLPVNIITGQFENKTNLK 480
QYELDLVGRPMVLADGKAKQVQNTNVIYLDALDELGLVITGTLPVNIITGQFENKTNLK 480
ILVGMGVDSLEDKRLTPRTFLCPNGYFPAIDPNVGVYLLHPNLQPKNPKSOEPVTL 540
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DAELNDIKVEIRNKMIDGESGKTRFLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
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NTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELLVONVWSKQNIKGVKAR 720
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TDGGITRVPYKEAGENQENPETYEDSFYKRSLDNDNVTTPYFYNKSGFGAYESGI 780
KAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
KAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
GGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNISVYAFNKSXDYQSVCEPAGAPKQ 900
GGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNISVYAFNKSXDYQSVCEPAGAPKQ 900
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HRSAYVPSVADILQIGMWATAAAMSILQOFLSLTFFPRLLEAVEMEDDDFTASLSKQ 960
TEQTYFFDNDKSKFSFGLDCGNCRIFFHGEKLMNTNLIIFIMVESKGTCCDTRL 1018
TEQTYFFDNDKSKFSFGLDCGNCRIFFHGEKLMNTNLIIFIMVESKGTCCDTRL 1018

rotein alpha-2 chain precursor - rat
: dihydropyridine-sensitive L-type
m channel alpha-2 chain
norvegicus (Norway rat)
34 #sequence_revision 27-Jun-1994 #text_change 20-Aug-1999
47
H.; Lee, P.; King, R.G.; Chin, H.
Sci. U.S.A. 89, 3251-3255, 1992
1 expresses an alternatively spliced form of the dihydropyridine-sensit
c: A44147; MUID:92228762; PMID:1314383
47
lary
RNA
l <KIM>
3: GB:M86621; NID:G203954; PIDN:AAA41088.1; PID:G203955
cium channel alpha-2 chain
m; glycoprotein; ion channel; transmembrane protein
larity 95.8%; Score 5145; DB 2; Length 1091;
Conservative 22; Mismatches 19; Indels 2; Gaps 2;
3CLLALTLTLFQSLILGPSSEEPFPPSVTIKSWVDKMQEDLVTLAKTASGVNLVDI 60

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61 YEKYQDLYTVPEPNARQLVEIAARDTEKLSNRSKALVRLAMEAKVQAAHQRRI
121 EVVYNAKODLDPEKNDSPEGSQRIKPVFTEDANFGRIQISYQHAHVHIPTDIYEC
121 EVVYNAKODLDPERNESESGSQRIKPVFTEDANFGRIQISYQHAHVHIPTDIYEC
181 NELNWTSSALDEVFKORREDEPSLLMQVFGSATGLARYYPASPWVDSRTPNKIDI
181 NELNWTSSALDEVFKORREDEPTLLWQVF-AAARLARYYPASPWVDSRTPNKIDI
241 RPWYIQGAASPKDMLILVDVSGSVSGTGLKIRTSVSEMLETLSDDDFVNVSFN
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300 VSCFQHLVQANVRNKKVLDKAVNNITAKGITYDYKKGFTFAFEQLLNVNVSANCK
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360 FTDGGERAQEIIFNKNKDKKVRFRFSVGGQHNTERGPIOMMACENKGYIYEIPSE
421 INTQBYLDVLGRPMVLADGKAKQVQNTNVIYLDALDELGLVITGTLPVNIITGQFEN
420 INTQBYLDVLGRPMVLADGKAKQVQNTNVIYLDALDELGLVITGTLPVNIITGQFEN
481 NQILGVGMGVDSLEDKRLTPRTFLCPNGYFPAIDPNVGVYLLHPNLQPKNPKSQ
480 NQILGVGMGVDSLEDKRLTPRTFLCPNGYFPAIDPNVGVYLLHPNLQPKNPKSQ
541 DFDAELNDIKVEIRNKMIDGESGKTRFLVKSQDERYIDKGNRTYTWTPVNG
540 DFDAELNDIKVEIRNKMIDGESGKTRFLVKSQDERYIDKGNRTYTWTPVNG
600 LALVLPTYFYIYKAKLETTIQAARSKKGMKDSITLKPDPNFEESGYTFIAPRDY
600 LALVLPTYFYIYKAKLETTIQAARSKKGMKDSITLKPDPNFEESGYTFIAPRDY
660 ISDNNTFELNFEIDRKTNNPNSCNADLINRVLLDAGFTNELLVONVWSKQNI
660 PSNNTFELNFEIDRKTNNPNSCNADLINRVLLDAGFTNELLVONVWSKQNI
720 RFVWTDGGITRVPYKEAGENQENPETYEDSFYKRSLDNDNVTTPYFYNKSGPG
720 RFVWTDGGITRVPYKEAGENQENPETYEDSFYKRSLDNDNVTTPYFYNKSGPG
780 IMVSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSD
780 IMVSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSD
840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNISVYAFNKSXDYQSVCEP
840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNISVYAFNKSXDYQSVCEP
900 QGAGHRSAYVPSVADILQIGMWATAAAMSILQOFLSLTFFPRLLEAVEMEDDDFT.
900 QGAGHRSAYVPSITDILQIGMWATAAAMSILQOFLSLTFFPRLLEAVEMEDDDFT.
960 QSCITEQTYFFDNDKSKFSFGLDCGNCRIFFHGEKLMNTNLIIFIMVESKGTCCPCI
960 QSCITEQTYFFDNDKSKFSFGLDCGNCRIFFHGEKLMNTNLIIFIMVESKGTCCPCI

```

RESULT 3

CHRA2

calcium channel protein alpha-2 chain precursor - rabbit

N:Alternate names: dihydropyridine-binding protein, 140K

C:Species: Oryctolagus cuniculus (domestic rabbit)

92 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
 79; A39518; A33409
 Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell
 -1664, 1988
 and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of
 r: S10579; MUID:88336904; PMID:2458626
 79
 mRNA
 5 <ELL>
 6
 9: EMBL:M21948; NID:g164762; PIDN:AAA81562.1; PID:g164763
 06-Lys, and deletion of 620-Ser were also found
 6, A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P.
 6, 3287-3293, 1991
 al characterization of the dihydropyridine-sensitive calcium channel al
 r: A39518; MUID:91131638; PMID:1847144
 18
 protein
 73 <JAV>
 1 and identical molecular weights (17K) following deglycosylation
 Hawkes, M.J.; Brush, K.; Cook, R.
 7820-7828, 1989
 composition of the purified dihydropyridine binding protein from skelet
 c: A33409; MUID:90122765; PMID:2558713
 39
 lary
 protein
 'S', 46-47 <HAM>
 calcium channel alpha-2 chain
 m; disulfide bond; glycoprotein; ion channel; membrane protein; phosph
 mal sequence #status predicted <SIG>
 calcium channel alpha-2 chain #status predicted <MAT>
 150,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding site:
 96.0%; Score 5132.5; DB 1; Length 1106;
 arity 94.7%; Pred.No. 1.1e-300;
 conservative 14; Mismatches 12; Indels 29; Gaps 4;
 3
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 RPLAWTLTLQAWLILIGPSSSEPPSPSAVTKSWDKMQEDLVTLAKTASGVNQLV 60
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 KYQDLTYTEPNARQIVELIARDIEKLSNRSKALVSLALEAEKVAQAQHWREDA 120
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 DGEERAQEI FAKYNDKKVRFPFSVQGHNYERQPIQWACENKGYIYEIPSIGA 420
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 TQEYLDVLRPWLADGAKQVQWNTNVDLALGLVITGTLVPNITGQENKTN 480
 LILGVMGVDSLEDIKRLTPRFTLCPNGYYPFAIDPNGVYLLHPNLPKPK----- 530
 LILGVMGVDSLEDIKRLTPRFTLCPNGYYPFAIDPNGVYLLHPNLPKPKIGVGPT 540

QY 531 -----NPKSQPVTLDFLDALENDIKVEIRNKMIDGESGEKTERTLVR
 Db 541 INLRKRPVQPKSPVTLDFLDALENDIKVEIRNKMIDGESGEKTERTLVR
 QY 580 YIDKGNRTYTWTPVNGTDY-SLALVLPYTSFYIYKAKLEETITQARSKKGKMDK
 Db 601 YIDKGNRTYTWTPVNGTDYSSALVLPYTSFYIYKAKLEETITQARY-----S
 QY 639 DNFEESGYTFIAPRDYCNLDKISDNNTEFLNPNFIDRKTNNPNSCNADLINRV
 Db 654 DNFEESGYTFIAPRDYCNLDKISDNNTEFLNPNFIDRKTNNPNSCNADLINRV
 QY 699 FTNELVQNTWSKQNIKGVAKRVVTDGGITRVVYKAEAGNENPETVEDSFYK
 Db 714 FTNELVQNTWSKQNIKGVAKRVVTDGGITRVVYKAEAGNENPETVEDSFYK
 QY 759 DNVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENF
 Db 774 DNVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENF
 QY 819 RDCAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTQIGRFFGEIDPDLMRH
 Db 834 RDCAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTQIGRFFGEIDPDLMRH
 QY 879 VYAFNKSVDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGHWATAAASIIQQF
 Db 894 VYAFNKSVDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGHWATAAASIIQQF
 QY 939 FPRLEAVEMEDDDFTASLSKQSCITEQYQYFDDNDSKFSVGLDCGNCRIFFHG
 Db 954 FPRLEAVEMEDDDFTASLSKQSCITEQYQYFDDNDSKFSVGLDCGNCRIFFHV
 QY 999 TWLIFIMVSKGTCPCDTRL 1018
 Db 1014 TWLIFIMVSKGTCPCDTRL 1033
 RESULT 4
 T30256
 calcium channel alpha-2-delta-C chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Ju
 C:Accession: T30256
 R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, P.
 J. Neurosci. 19; 648-691, 1999
 A:Title: Molecular diversity of the calcium channel alpha2delta subun
 A:Reference number: Z20794
 A:Accession: T30256
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1091 <KLU>
 A:Cross-references: EMBL:AJ010949; PIDN:CAA09423.1
 A:Experimental source: brain
 C:Superfamily: calcium channel alpha-2 chain
 Query Match 20.3%; Score 1085; DB 2; Length 1091;
 Best Local Similarity 28.7%; Pred No. 4.4e-57;
 Matches 309; Conservative 222; Mismatches 416; Indels 128; (
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 Db 14 ASALLA-TALLVAAALGDVVRSEQQIPLSV-VKLWASAFGGBIKSIKAAKYSGLQLL
 QY 63 KYQDLTYTEPNARQIVELIARDIEKLSNRSKALVSLALEAEKVAQAQHWREDEP
 Db 72 EYKQDAVEEDGLQVCKLAKIMEEMPHKKSEAVRRLVEAAEAHLKHEFDADI-
 QY 123 VYNAK--DDLDPKNDSEPGSQRIKPVFIEDANFGR-QISVQHAHVHPTDIYEG
 Db 129 EYFNAVLINERDKGNFLELGEKFI---LAPNDFNNLPVNISLSDVQVPTNNMYN
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/FNITQFENKTNLKNQLILGVMGVDSLEDIKRLTPRFTLCPNGYFPAIDNGYVLL 523
/FS-----KQNETRSKG-ILLVGVGTDPVPKELLKTIKYLKGIHGYAFATNNGYILT 535
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[S--EDYT-QTGDFFGEVEGAVMKNLLTWGSKFRITLYDYQAMCR---ANKSSDSAH 918
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[EQCYFFDNDKSGSVGLDQNCRSRIHGEKLMNTNLIFFIMVESKGTCPDCT 1016
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Caenorhabditis elegans
habditis elegans
95 #sequence_revision 20-Feb-1995 #text_change 30-Jun-2001
17

EMBL Data Library, May 1993
Sequence of the C. elegans coemid C50C3.
r: S44627
17
nary
DNA

A;Residues: 1-734 <FAV>
A;Cross-references: EMBL:IL14433; NID:g289649; PID:g289650
C;Genetics:
A;Introns: 24/2, 87/3, 175/1, 259/1, 290/3, 346/3, 460/3, 538/3
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Db 94 EARSVRNDSTVNDPQSKSPFIRFMSAKQNGDGTIYESNHLKRLKVNKTSFNIL
QY 156 -GRQISVQHAHVHTPTIYEGSTIVLNLNMTSALDEVFKNREDEFSLLMQVFI
Db 154 YTLPTSSVSSAVHIPTPLDYRNEEDLLRKIDW-SDIDAVYRTNREETKDLAFQLFI
QY 215 ARYYPASPMV-DNSRTPNKIDLYDVRPWPYIQGAASPKDMLILVDVSGSVGL
Db 213 MRYTPAASWFWNQ--DEHLDLDFCRNTEWYINSATNSKNVILMLDMSGSMLGQI
QY 274 TSVSEMLETLSDDDFVNVAFSNSNA---QDVSCFOHLVQANVRNKKVLKDAVNN
Db 271 QTTEAILLETLSHNDYFNIMTFSKNTFLDGCNGTNGLLQATMRNKKALRRKMDT
QY 331 TDYKGFSPAFQLLNYN-----VSRANCKIIMLFTDGGEEARAEIIPNKYNKDI
Db 331 AEYEKALPLAFSVLLDINNGGDNRRGACENVIMLITDGAPNAYKKIFDMYNADI
QY 386 RFSVGOHNYERGPIQWACHNKGYEIPSGAIRINTQEYL-----DVLGRPMVI
Db 391 TFLVGDRAIDFNEVREMACNNRGYMHVANWADVDEKIHYYIRMSRVVGRHYKI
QY 442 KQVQNTNVYLDALGL--VITGTLPVFNITQGFENKTN-----
Db 451 ---WITGVYERLYLPRPEIFAEVPVITNQSFAMNKNKASRRKIRLOKSEARSP
QY 479 ---LNQLILGVGVDSLEDIKRLTPRFTLCPNGYFPAIDNGYVLLHPNLOI
Db 508 SYPVIVNETFMGAANVNIPLTEVAQKSHPANIGSKSYFFMLDQNGFVMTHPOLRI
QY 533 --KSQBPVTLDFLD-----AELENDIKVEI
Db 568 KYHKQYNNMDLLELVGQNVNRSQKSAQVSDLVCESGANYAECVDDLRKAVF
QY 562 GESGEKTFRLVKSQDERY----IDK---GNRTYTWTPVNGTDYSIALVITYSF
Db 628 CDNSD-----VQQLDVLVATELLDRVYPTNTYAAACINHANFVLGLAVAKGL
QY 615 KLEETITQARSKKGMK 631
Db 682 K-----QKKYDFGRVK 692

RESULT 6

T18770

Probable calcium channel protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T18770; T25249
R;Sulston, J.
submitted to the EMBL Data Library, June 1995
A;Reference number: Z19019
A;Accession: T18770
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1148 <WIL>
A;Cross-references: EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN00020; CESP
A;Experimental source: clone B0491

QY	27	FP	S	A	T	I	K	S	V	D	K	M	O	E	L	V	T	L	A	K	T	A	S	G	V	N	O	I	V	D	I	E	K	Y	Q	D	L	V	T	E	P	N	N	A	R	A	L	V	E					
Db	98	Y	P	G	N	K	E	K	E	V	A	Q	Y	E	K	A	V	S	G	K	T	A	G	---	L	V	K	A	S	G	R	K	E	K	T	F	S	V	N	V	N	A	A	G	S	K	V	T						
QY	87	E	K	L	L	N	R	S	K	A	L	V	S	L	A	E	K	Y	Q	A	A	H	O	R	E	D	F	A	S	N	E	V	V	Y	N	A	K	D	L	O	P	E	K	N	D	S	E	P	F					
Db	154	B	E	L	L	-	K	R	N	K	Y	E	M	V	L	K	V	Q	P	L	V	R	H	E	I	D	---	A	H	I	F	E	P	---																				
QY	147	P	V	I	E	D	A	N	F	G	R	Q	I	S	Y	Q	H	A	A	V	H	P	T	D	I	E	G	S	T	V	L	N	E	L	N	W	T	S	A	L	D	E	V	F	K	N	E	E	D	P				
Db	190	G	I	S	M	L	D	A	E	---	A	S	F	I	T	N	D	L	-	L	G	S	A	L	T	K	S	F	---																									
QY	207	V	E	G	S	A	T	G	L	A	R	Y	P	A	S	P	W	D	N	S	R	T	-	P	N	K	I	D	---	L	Y	D	V	E	R	R	P	---																
Db	215	---	S	G	K	K	H	V	S	F	K	P	S	L	D	Q	O	R	S	C	P	T	C	D	S	L	I	N	G	D	F	T	I	V	Y	D	N	R	E	S	P	G	N	V	I	Q								
QY	246	---	Q	-	A	A	S	P	K	D	M	L	I	V	D	S	G	S	G	L	T	K	L	I	R	T	S	V	S	E	M	L	E	T	L	S	D	D	F	P	N	V	A	S	F	N								
Db	270	F	A	P	Q	L	P	V	P	N	I	V	F	I	D	V	S	G	S	M	G	R	K	I	Q	T	R	E	A	L	K	I	L	D	D	V	E	D	Y	L	N	F	I	E	L	E	S	T						
QY	302	S	C	F	Q	-	H	L	V	Q	A	N	R	K	K	V	L	K	O	A	N	N	I	T	A	K	I	T	D	Y	K	K	G	S	F	A	F	E	Q	L	L	N	Y	N	V	S	R	A	N	-				
Db	327	T	T	W	K	H	L	V	Q	A	T	P	A	N	L	K	E	A	K	T	P	V	K	N	I	H	D	O	S	M	T	N	I	N	D	G	L	L	K	G	I	E	M	L	-	-	N	K	A	R	E	D	H	T
QY	355	N	K	I	M	L	P	T	D	G	---	G	E	B	E	R	A	E	I	F	N	K	Y	N	K	-	-	D	K	V	R	F	R	F	S	V	G	H	N	V	E	R	G	P	I	Q	M	A						
Db	384	T	S	I	I	M	L	T	D	G	A	N	T	G	E	S	R	E	P	K	I	Q	B	E	R	N	A	I	G	K	F	P	L	N	L	G	F	-	N	N	L	N	F	L	E	T	L	A						
QY	409	Y	Y	E	I	P	S	I	G	A	I	R	I	N	T	O	E	V	L	D	V	L	G	R	P	M	V	L	A	D	K	A	Q	V	Q	W	T	N	V	L	D	A	L	E	L	G	-	-	V	I	T			
Db	443	L	A	R	R	I	E	D	S	D	A	N	L	Q	I																																							

RESULT 9
S30350
inter-alpha-trypsin inhibitor heavy chain 3 precursor - human
NAlternate names: HC3; inter-alpha-trypsin inhibitor chain H3; pre-a
C.Species: Homo sapiens (man)
C.Date: 03-May-1994 #sequence revision 20-Feb-1995 #set change 04-Feb-
C.Accession: S30350; S34123; S02141; D34245; A39079; S50133; B53642;
C.Creation: S30350; S34123; S02141; D34245; A39079; S50133; B53642;

[illegible]

Conservative 154; Mismatches 342; Indels 335; Gaps 51

?PSAVTIKSWVDKMQEDL-VTLAKTASGVNLQVLD-----IYEYQDLYTEPNNNA 75
||| : : : : :
[KNARTSKG-ADU]TKOBIGTTIANTSISXIGIFDMTKGTAVVSQDYQFLLIQTQVNSN 191
JETAARDIEKLINRSKALVSLALE-----AEKVQAQHWRDEFPASNEVVYYNA 127
||| : : : : :
--LQDINSWLTKRYALISKILSTVVDKI TTAVSNINNANDHESDFALQI--YNV 243
DPEKND-----SEPGSORIKPVF-----IEDANFGR-QISYQH--A 164
VPFLNENISAACKNKSGDLSSSEINTVVKDSLKLQDALERINLGQTLLDDYHFIG 303
[PTDIYEGSTIVLINELNWTLSALDEVFKNR-BEDPSLLHQV-FGSATGLARYPA 220
||| : : : : :
DENNILEDVNGWANGKW-----PERNNAIBEINSIVEPLGRINGSDSTAADYDA 356
PWYDSNRTPN-----KIDLYDVRRRPWYIQGA 248
||| : : : : :
GDVDDNNIDNIKSVIAEKKQLKGKLNLAIEIKSAVEBYKTVLDPYDLIKK-----GT 411
GD-MULLIVDS-GSVSGL-----TLKLIRTSVSMELETSD-----DD 287
SYDNAIGLAGTVEDNTVMNELLKNRDIKTNKLQDNINSIIKSLEKINAGTDTPDD 471
IASFNENAQDVSCF-----CHLVQANVR-NKKVLKDAVNITAK-----328
J-NISSVTQNISFIRDIDIKTAQAGSLDKNGKIQDSVANSUKRLSAMDRINAGSA 530
DYK-----KGFSAFEQLMNYVRANCNKIIMLTGCGEEBAOEIFNKYNK-----378
|YNLGIIEGVTSDNLTFVANNQVGSKNCKTIDELKTKUSD-ALKLYDSYKNKVNNGDA 588
QKRVV-FRPSVGQHNVERGP IQMACENKGY-YEIPSIG---AIRN-----422
::: : : : :
YXLKIGIVIKIEBVTYNG----VFKGKNYFTLEELKVGINIAVRVRISTEINIKNG 643
-----TOEYLDVLGRPMVLAGDKAKOV-----QWTVNYL 451
JEDFTIAGTYGVTENIKYINKVIIIEGGDASPEAISNIITEVNVETQSIXRMSSGOV 703
ALELGL-VITGTLVPFNITQGPNENTNLIKQLILGMVGVDVLESLEIKRLTPRTPLC 507
|YKSLGLSVTEENISIYIMDRVVKNTYYSKVELIEAVEALIKEIYEYERINLQOATV 763
YFAI-----DPNGYVLLHPNLQPKNPKSQEPVTLDFDLDAELENDIKVB-----554
YIKYTGTVSVNITSINDVY-----KSGNLTTRRELQAKI---DVVIQTQS 810
-----IRNMKDIBSGSEKTFR-----TLVKSODERYIDKGNRTYTTPVNGTDYSIALVL 604
::: : : : :
DWIGVRNLGEANIISDFBFMGITVWNFSFNIQVVDHLKDDKYTTIDAIAKAATVVFV 870
FYPIYKALBEETIQARSKKGMKQSETLKPDPNFEBSSGYTFIAPRDYCNDLKITSDNN 664
HY-----EELN-----KGATUL-----DYNLSLGITVMT 898
LNFNEFI DRKTPNPNSCNADLINRVLLDAGFTNELVQNTWSKQNKIKGVKARFWVT 724
TVINLNKESSYFNAS---DIQTKV-----NALISVVGYYEEINKGEATVDVYT 948
[TRYYPEKAGENWQENPEYEDSPYKRSLDNDNVVTFAPTAFNKSGPCGAYESGIMVSK 784
||| : : : : :
[TGV-----TKENIIIFINTYIKE---GQYPDLTSLKS 980
-----YIQ---GXLLKPAVVGIKIDVNSWIENFTKTSIRDPFCAGVCDCRNSD 834
::: : : : :
LEEKYEAVVKITSGK-----AVUG-----DTYKGIKQVTTENTAIYMINID 1026
? 838
1030

```

RESULT 11
JC5576
inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Ma
C:Accession: JC5576; PC4486
E:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.
J. Biochem. 122, 71-82, 1997
A:Title: Molecular cloning and sequencing of cDNAs encoding three hea
sin inhibitor heavy chain family.
A:Reference number: JC5574; MUID:97420688; PMID:9276673
A:Accession: JC5576
A:Molecule type: mRNA
A:Residues: 1-889 <NA>
A:Cross-references: DDBJ:D89287
A:Experimental source: liver
A:Accession: PC4486
A:Molecule type: protein
A:Residues: 34-53;449-475;509-526 <NA>
C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy ch
that the complexes play important role for pancreatic cancer.
C:Superfamily: inter-alpha-trypsin inhibitor complex component II
F:236-239,664-865/Disulfide bonds: #status predicted

Query Match      3.1%; Score 164.5; DB 2; Length 889;
Best Local Similarity 23.2%; Pred. No. 0.079;
Matches 66; Conservative 56; Mismatches 112; Indels 51;

Qy 202 SILNQVFGSATGLARYYPASPWNST-PNKID-----LYDVRRL-PWYI
Db 211 SALTKSFSGKKGHSFKPS---LQQRSCTCTDSLINGDFTIVDVNRSEPGVI
Qy 249 -----ASPKDMLILDVSGSVGLTKLIRTSVSEMLETLSDDDFVNV
Db 268 YFVHFPAQGLPVVPKNIIVFIDISGSMAGRKIQOTFVALLKILDDMKQDDYLF
Qy 297 NADQVSCFQHLVQANVRNKKVLKDVANNIIPAKGITDKYKGFSAFEQLLN----YI
Db 328 GV--TTWKDSLIVQATPANLBEARTFVRSISDQGMNTINDGLLRIGRLMLTDAREQH
Qy 353 NCKNKLMLPTDG---GEERAQETFNKYNDKKVRFVSFG-QQNYERGPQWMI
Db 386 STSILIM--TGDANTGESRPKIQENVKAIISGRPLNLGFGNNLNTYFLDTWY
Qy 408 GYVEIPISGIAIRINQEYLDVLGRPMVLAGDKAKQVQWNTNYLD 452
Db 445 GYARIVSDSANLOLQGFVEEVANPIL-----TWVEVE 478

```

```

RESULT 12
T28155
variant-specific surface protein 1 - malaria parasite (Plasmodium falci-
N;Alternate names: erythrocyte membrane binding protein 1 (EMPI)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-
C;Accession: T28155
R;Rowe, J.A.; Moulds, J.M.; Newbold, C.I.; Miller, L.H.
Nature 388, 292-295, 1997
A;Title: Plasmodium falciparum rosetting is mediated by PfEMP1 and re-
A;Reference number: Z20477; MUID:97373957; PMID:9230440
A;Accession: T28155
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2706 <ROW>
A;Cross-references: EMBL:Y13402; PIDN:CAA73831.1
A;Experimental source: strain IT 4/25/5
C;Genetics:
A;Introns: 2493/3
A;Note: R29R+var1

```

Query Match 3.0%; Score 161; DB 2; Length 2706;

arity 18.2%; Pred. No. 0.75;
 Conservative 137; Mismatches 345; Indels 338; Gaps 46;
 QY QWEDLVITAKTASGVNQLVDIYKQYQDLYTVBPNN-----RQL 78
 Db : : : : :
 QY WAEBCFRIRKI-----KLENVKCECD-----EPNNKYCSGDHCKRYLYKNDITP 358
 Db : : : : :
 QY IARDIEKLSNRSKALVSLALEAEKYQAAHQWRDFAVNEVYVYNKADDDLPKND 138
 Db : : : : :
 QY ICPCRNACSNYTK-----WIEIQRKQFQKQK--YMEI-----KIKTINISNENDK 408
 Db : : : : :
 QY -----PQSRIKPVFIEDANFGQISYQAAHVHPDIDYEGSTIVLNLNWTALDE 191
 Db : : : : :
 QY NLDKKGYSTIN--TFLESNLHGKQC-----DN 438
 Db : : : : :
 QY QNREEDPSLQWFGSAGTLARYTASP-----WVDSNRTPNKI 233
 Db : : : : :
 QY QNKTNFKNL--ETFGP-----SGYCEACPIYGVKCSNEKCTPTVENWNSNRIPDTT 493
 Db : : : : :
 QY YVRRPWYIQGAASPQMDLILVDVSGSVGLTLKLRISVSEMLETSLDDDFVNVAS 293
 Db : : : : :
 QY ILM-----ATNIDMLVNDIGNAI-----515
 Db : : : : :
 QY IADQVSCFQHLVQAVRNK-----VLKDAVNNITAKGIDYKKGSPAPBQLL 345
 Db : : : : :
 QY IELKNCITYGILKGIKKQKQWQOYLNIDQCKINNVMSGYFDNKIAFNVLFQWL 573
 Db : : : : :
 QY 'SRANCKIIMLFTDGBERAQEIFNKYNKKVVRFSVQGHYERGPQIMWACE 405
 Db : : : : :
 QY 'RDHRLK-----EKIDVICIKENINENICIKCKTN-----CE 610
 Db : : : : :
 QY 'YIEPSIGAIRI-----NTQEVLDVGRPMVLADKAKQVQWNTVYLDALGLVIT 461
 Db : : : : :
 QY WLEKEAEWDKINQYHYNQKNIHFIIPYITGFYEK--ITPNDPFKALE-----DV 665
 Db : : : : :
 QY 'VFNITQGENKTNKQNLQVGMGVDSLEIDKRLTPRFTLPCPGYFAIDPBGVY 521
 Db : : : : :
 QY VLDITLKECD--THCKIEKIRST--DVDLKEIISWLNQKIEVCKS--HHDEDKHEYC 721
 Db : : : : :
 QY NLPQNPKSQBPVTLDFDLDALENDIKVEIRNKMIDGSGEKT-----PRT 571
 Db : : : : :
 QY DILPKSVDDDEEDD--EEVDEKEESSQITKEN--ISQKGTYSASCVKGAIVKG 775
 Db : : : : :
 QY QDERYID-----KGNRTYTW-----TPVNGTD-----YSLALVLPYSP 609
 Db : : : : :
 QY KSNGSIDNCNAKRNKKNWQCDKNTFVQNGVCMPPRRKSGICIHNLTLBEQTKNK 835
 Db : : : : :
 QY --YIKAKLEET--ITOARSKGKMDSETLK-----PDNFEE--SGYTFIAPRDC--N 656
 Db : : : : :
 QY EAFIKCAAKETNLLWDKYNDKNEABELLKXGKIPEDFMRIMFYTFGDFRDFCLEN 895
 Db : : : : :
 QY ---KISDNTBFLNFNEFIDRK-----TPNNPSC--NADLINRVLIDAGFINEL 703
 Db : : : : :
 QY DVDVKVKNINKVFNSSKRGFKKIDPENWNGPQIWNGLCALIHADTKDSIKN 955
 Db : : : : :
 QY -----W-----SKONKINGVKARFV 723
 Db : : : : :
 QY KYEKVITILAKRDSNGMTLSEFAKKPKPLRFVWEYDDYCKERQKYLTEVASTCKS 1015
 Db : : : : :
 QY ITRV-----YKPEAGENWQENPETYEDSFYKSLDN-----DNTV-- 762
 Db : : : : :
 QY QLKCDRGNNKCDYKYMRYKXGGEWNLQDKYYKDKRNGKIDGPIGIIIVKDYVL 1075
 Db : : : : :
 QY -----FTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVIGIKIDVNSWI-- 810
 Db : : : : :
 QY EYLKXKFTASCVTSGRKAQNSATBEVKKNIELLEEYQ-----YDADQYCGC 1126
 Db : : : : :
 QY --ENFTKTSIRDPACAGVCDCK-----RNSDVMDCVIL 841
 Db : : : : :
 QY HDDKYSKISGRSNCCGLNSDAKKNKIKWRNSDENKDYAPL 1169
 Db : : : : :
 QY

A44396
 P-type cation translocating ATPase - malaria parasite (Plasmodium fal
 C:Species: Plasmodium falciparum
 C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Ju
 C:Accession: A44396
 R:Krishna, S.; Cowan, G.; Meade, J.C.; Wells, R.A.; Stringer, J.R.; R
 J. Cell Biol. 120, 385-398, 1993
 A:Title: A family of cation ATPase-like molecules from Plasmodium fal
 A:Reference number: A44396; MUID:93132070; PMID:8421054
 A:Accession: A44396
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-1984 <KRI>
 A:Note: sequence extracted from NCBI backbone (NCBIP:122678)

Query Match 3.0%; Score 159; DB 2; Length 1984;
 Best Local Similarity 17.1%; Pred. No. 0.6; Mismatches 366; (Matches 179; Conservative 144; Indels 359; Indels 366;)
 QY 58 VDIYKQYQDLYTVBPNNARQLVIEIAARDIEKLSNR-----SKALVSLA
 Db : : : : :
 QY 128 INVY-RYNTSYIISSS-----ELVPGDIYEIKNNWTIPCDTIIILSGSVTSEHM
 Db : : : : :
 QY 107 VQAAHQWRDFAVNEVYVYNKADDDLPKND-----SEPGSQRKPVFIEDANF
 Db : : : : :
 QY 181 V-PIHKERLPPEGNAIINKNNKYDSNDEKDDYLRYYNNHASINMIKRNHLIBETL
 Db : : : : :
 QY 161 YQAAHVHPDIDYEGSTIVLNLN--TSALDEVPKKNEEOPSLWQVFGSATGL
 Db : : : : :
 QY 240 EYKSWTH-----DLCSMNKLCYNNYDDVHKNKMD-----
 Db : : : : :
 QY 220 ASPWVDNSRTFNKIDLYDVRPRPWIYQGA--ASPQMDLILVDVSGSVGLTLKLR
 Db : : : : :
 QY 273 ---YNNNNNNKKKKINLN---PVKGYINSNDLLY-----
 Db : : : : :
 QY 279 MLETSLDDDFVNVASFNNAQDVSCFQHLVQAVRNKVKVLDVANNITAKGIDTY
 Db : : : : :
 QY 304 -----DDKIGVNIPE--DDVNNMKH--KFNQRNINYYNKKDTNNL-----EY
 Db : : : : :
 QY 339 PAFEPOLLNYYNVRANCKIIMLFTDGBERAQEIFNKYNKKVVRFSVQGHN
 Db : : : : :
 QY 346 YIYDCLLKKVFAISQKNIY-----SNEDINKY-----
 Db : : : : :
 QY 399 IQMWACENKGYIYIPISIGAIRINTQEVLDVGRPMVLG-----DI
 Db : : : : :
 QY 375 ---MLYGGTVVSLYNINKIKYNNKEENRILGL-VIKTGFITTKGKIVNNLIYH
 Db : : : : :
 QY 445 QWTVYLDALDELGLVITGTLFVFNITQGFENKTNKQNLILG-----
 Db : : : : :
 QY 430 NLINDSVYKFLII-LIYALFVSFILLYITLSNVEYTHIIKCLDIITDAIPPALI
 Db : : : : :
 QY 488 MGVDSVLEIDIKRLTPRFTLPCPGYVFA-----IDPNGVYLLHPNLQ-----PK
 Db : : : : :
 QY 489 VQISIASRLKKSISCLCPHKINIAGQINWVFDKGTG-TLTENNLOFIIIGITQ
 Db : : : : :
 QY 536 EPTVLDPLDALENDIKVEIRNKMIDGSGEKTFTLVKSQDERYIDKGNRTYTW
 Db : : : : :
 QY 548 NWLS-DFTHIK-----EMNTESYIHSKDDNMIHNK-----
 Db : : : : :
 QY 596 TDYSIALVLPYSPYIYKAKLEETITQARSKKGKKO-----SETLKPDNE
 Db : : : : :
 QY 578 -----SIISYYIKDNMKNLHTSSK-KKSITKERSNLFVQTIKSCLLKDHVI
 Db : : : : :
 QY 646 YTFIAPRDCNDLKSINN--TEFLN-----FNEP--IDRKTPNNSCNADLNR
 Db : : : : :
 QY 628 KEYTNNYTCNDLHNDSTCSYLNSETKDAYCEYNNIDH-----LCD---INR
 Db : : : : :
 QY 697 AGFTNELVQNTWSKQKIKGVKARFVVTGQITRVYKPEAGENWQENPETYEDSFY
 Db : : : : :
 QY 679 INSKNELMGKYSKNELMGKTIKNELM-----GKYS
 Db : : : : :
 QY 757 DNDNVYTFAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVG-----IKTIDV
 Db : : : : :
 QY

ein b2270 - *Escherichia coli* (strain K-12)
 ichia coli
 97 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
 98
 Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 Mau, B.; Shao, Y.
 -1462, 1997
 lete genome sequence of *Escherichia coli* K-12.
 r: A64720; MUID:97426617; PMID:9278503
 98
 nary; nucleic acid sequence not shown; translation not shown
 DNA
 <BLAT>
 s: GB:AE000317; GB:U00096; NID:G1788605; PID:G1788606;
 urce: strain K-12, substrain MG1655

2.98; Score 157.5; DB 2; Length 575;
larity 21.64; Pred.No. 0.11;
Conservative 93; Mismatches 206; Indels 105; Gaps 25;

NARQLVEIARDIEKLLSNRSKALVSLVAEAKYQAAHQWREDFASNEVVYNAKDD 130
N : : : : : | | | | : : : : :
NKESQQQPSTPTEQQVLAQAQAIK---EAEQSAAA---AKALAQQEVQOYSKDQA 75
:
EKND-----SEPSQRKPVPFIEDANFGRLISYQHAA---VHIPTDI 172
: : : : : | : : : : :
RLQEAPTFARAAKAKATHIANPGTARYQQF---DNNPVKQVAQNPLATFSLDVDVTGS 132
:
STIVLNE-----LNWTSALDEVFKNKEBEDPSLLMQVFGSATGLARYY 218
| : : : : : | : : : : :
VRREFLNGQLLPPDAVRVEBIVNVFPDSWDI--KKQSIIPASKPIPFAMRVYELA--- 187
:
PWYDNSTRPNKIDLYDVRRPWPVIQGAASPDKMLILVDVSGS-VSGTLKLIRTSVS 277
: : : : : | : : : : :
PW-NEORTLKUVILAADRKSSELPAS---NLVFLDTGSGMISDRERLPLOQSLSK 241
:
ETLSDDDFVNVAASFNSNAQOVSCFOHLVQAVNRNKKVLKDAVNNTAKGITDYKKGF 337
:
KELREQDNIATIVYAGDSRTA----LPSISGSHKAENAIADSLDAGSTNGCAGL 296
:
FEOLLNVNVSRA NCKTIMLFTDG-----GEERAQBI FNKNYKDKKVVRFRFSVGQ 391
: : : : : | : : : : :
YOOATK-GFIKGGINR-ILLATGDGFNVGIDDPKSIESMWVKQRESGVITLTSTFGVN 354
:
ERGPIQWMACENKGYVEIFSPISGAIRINTQBYILDVLCRPVMVL--AGKAKAQVQ---- 445
:
NEAMVRIADVGNNGYSYIDTLS-----EAQVNLSENRMQLITVAKDVKAQIEFNPA 410
:
VYLDALELGLVITGTLPVFNITQGFENKTNLNQJLILGVMGVD-VSLEDI---KRLT 501
EY---RQIG-----YE-----KQLRVHEHFNNDNDVADGICAGKHIT 447

[illegible]

07:56:51 2004

February 20, 2004, 16:59:22
3 secB

se
JC

us-10-090-827-13.rpr

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

ein search, using sw model

February 20, 2004, 16:48:25 ; Search time 11.1043 Seconds
(without alignments)
4311.242 Million cell updates/sec

S-10-090-827-13

346

MAAGCLLALTLTLFQSLILG.....TNLIFIMVSKGTCTPCDTRL 1018

LOSUM62

apop 10.0 , Gapext 0.5

27863 seqs, 47026705 residues

its satisfying chosen parameters: 127863

igth: 0

igth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

MissProt_41.*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
red by analysis of the total score distribution.

SUMMARIES

Entry	Length	DB	ID	Description
10.0	1091	1	CIC2 HUMAN	P54289 homo sapien
6.2	1091	1	CIC2 RAT	P54290 rattus norv
6.0	1106	1	CIC2 RABIT	P13806 cynoethologus
3.4	1249	1	UN36-CAEEL	P34374 caenorhabdi
3.6	886	1	ITH3 MOUSE	Q61704 mus musculus
3.4	885	1	ITH3 HUMAN	Q06033 homo sapien
3.4	887	1	ITH3 RAT	Q63416 rattus norv
3.1	886	1	ITH3 MESAU	P97280 mesocricetu
3.0	1829	1	DPOL-THST	O33845 thermococcu
3.0	1956	1	ATX1-PLAPA	Q04956 plasmodium
2.9	575	1	YFBK-SCOLI	P76481 escherichia
2.9	946	1	ITH2 HUMAN	P19823 homo sapien
2.8	1290	1	BXC1-CLOBO	P18640 clostridium
2.8	420	1	Y103-SYNY3	Q55874 synecocyst
2.8	921	1	ITH4-PIG	P73263 sus scrofa
2.8	654	1	MCPC-BACSU	P54576 bacillus su
2.8	930	1	ITH4 HUMAN	Q14624 h inter-alp
2.8	964	1	DPOL-CBEPV	P30319 choriostoneu
2.7	1087	1	YXNX-CLOTM	P38535 clostridium
2.7	946	1	ITH2 MESAU	P97279 mesocricetu
2.7	1169	1	SMC-METJA	Q59037 methanococc
2.6	1251	1	RBF2-PLAEB	Q00799 plasmodium
2.6	935	1	ITH2-PIG	O02668 sus scrofa
2.6	2710	1	TOXA-CLODI	P16154 clostridium
2.6	3305	1	APLP-MANSE	Q25490 manduca aex
2.6	764	1	PAG-BACAN	P13423 bacillus an
2.6	1513	1	STU1-YEAST	P38198 saccharomyc
2.6	1180	1	CANA-BACTI	P16480 bacillus th
2.6	3063	1	CAIC HUMAN	Q99715 homo sapien
2.6	946	1	ITH2 MOUSE	Q61703 mus musculu
2.5	2077	1	TEGU-HSV6U	P52340 human herpe
2.5	862	1	MUTS-BOREU	O51737 borrelia bu
2.5	1323	1	ADRI-YEAST	P07248 saccharomyc

34	132.5	2.5	547	1	SYM-BUCAI	P57210 buc
35	132.5	2.5	929	1	CAIC-NOTVI	Q91145 not
36	132.5	2.5	1679	1	YIO9-YEARST	P40457 sac
37	132	2.5	697	1	YE9C-SCHPO	O13773 sc
38	131	2.5	1634	1	YD94-METJA	Q58295 met
39	130.5	2.4	987	1	YD94-METJA	Q58789 met
40	130.5	2.4	1018	1	YC14-METJA	Q58611 met
41	130.5	2.4	1036	1	Y946-ABCJU	O29316 arc
42	129.5	2.4	1658	1	YM67-YEARST	Q03661 sac
43	129	2.4	1244	1	Y307-MYCPN	P75342 myc
44	128.5	2.4	1254	1	UBCP-YEARST	P39538 sac
45	128	2.4	1113	1	Y140-MYCPN	P75033 myc

ALIGNMENTS

RESULT 1
CIC2_HUMAN
ID CIC2_HUMAN STANDARD; PRT; 1091 AA.
AC P54289;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.
DE subunits precursor.
GN CACNA2D1 OR CACNL2A OR CCHL2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=92110010; PubMed=1309651;
RA Williams M.E., Feldman D.H., McCue A.F., Brenner R.,
RA Velicelebi G., Ellis S.B., Harpold M.M.;
RT "Structure and functional expression of alpha 1, alpha 2, and beta subunits of a novel human neuronal calcium channel subtype";
RL Neuron 8:71-84(1992)
CC FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT R
CC EXCITATION-CONTRACTION COUPLING.
CC -! SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBU
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC -! SUBCELLULAR LOCATION: Integral membrane protein.
CC -! TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE ;
CC AORTA TISSUES.
CC -! PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSE
CC A PRECURSOR FORM (BY SIMILARITY).
CC -! SIMILARITY: TO OTHER SPECIES' ALPHA-2 SUBUNIT.
CC -! SIMILARITY: Contains 1 VWFA domain.

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CC entities requires a license agreement (see <http://www.isb-sib.ch/>
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CC EMBL; M76559; AAA51903.1; -;
CC PIR; JH0565; JH0565.
CC Genew; HGNC:1399; CACNA2D1.
CC MIN; 114204; -;
CC GO; GO:0005891; C: voltage-gated calcium channel complex; TAS.
CC GO; GO:0015270; F: dihydropyridine-sensitive calcium channel a. .
CC GO; GO:0006832; P: small molecule transport; TAS.
CC InterPro; IPR004010; Cache.
CC InterPro; IPR002035; VWF_A.
CC Pfam; PF02743; Cache; 1.
CC Pfam; PF00092; vwa; 1.
CC SMART; SM00327; VWA; 1.
CC PROSITE; PS50234; VWFA; 1.

1; Transmembrane; Ion transport; Voltage-gated channel;
 nel; Glycoprotein; Phosphorylation; Signal.
 1 24
 25 944 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT (BY
 (BY SIMILARITY)
 945 1091 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY
 SIMILARITY).
 446 469 POTENTIAL.
 906 930 POTENTIAL.
 967 1086 POTENTIAL.
 253 430 VMFA.
 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
 585 585 N-LINKED (GLCNAC. . .) (POTENTIAL).
 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
 663 663 N-LINKED (GLCNAC. . .) (POTENTIAL).
 769 769 N-LINKED (GLCNAC. . .) (POTENTIAL).
 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
 876 876 N-LINKED (GLCNAC. . .) (POTENTIAL).
 883 883 N-LINKED (GLCNAC. . .) (POTENTIAL).
 973 973 N-LINKED (GLCNAC. . .) (POTENTIAL).
 986 986 N-LINKED (GLCNAC. . .) (POTENTIAL).
 501 501 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
 333 833 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
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100.0%; Score 5346; DB 1; Length 1091;
 larity 100.0%; Pred. No. 3.6e-312;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 3CLLALTLTLFQSLILGPSSEEPSPSAVTIKSWVDKMOEDLVTLAKTASGVNQLVDI 60
 3CLLALTLTLFQSLILGPSSEEPSPSAVTIKSWVDKMOEDLVTLAKTASGVNQLVDI 60
 IQDLTYVEPNARQLVEIARDIEKLLSNRSKALVSLALAEKVAQAAHWRREDFASN 120
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 YNAKDDLDPEKNDSEPGSORIIPVFIEDANFGQISYQAAVHIPTDIYEGSTIVL 180
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 IQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDFVNVASFNSNAQD 300
 IQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDFVNVASFNSNAQD 300
 QHLVQANVKKVLKDVANNITAKGTDYKGFSAFPEQLLNLYNSRANCNKIIML 360
 QHLVQANVKKVLKDVANNITAKGTDYKGFSAFPEQLLNLYNSRANCNKIIML 360
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 QGERAQEIKFNKYNKDKVVFPSVGOHNVERGPIQMMACENKGYIYEIPSIGAR 420
 QEYLDVLRPMVLGAKAKQVQTNVYLDALGLVITGTLPVFNITGQPKNTNLK 480
 QEYLDVLRPMVLGAKAKQVQTNVYLDALGLVITGTLPVFNITGQPKNTNLK 480
 ILGMVGVDVSLDIKRLTPFTLCPNGYYPADIPNGVYLLHPLQPNPKSQBPVTL 540
 ILGMVGVDVSLDIKRLTPFTLCPNGYYPADIPNGVYLLHPLQPNPKSQBPVTL 540
 QAELENDIKVEIRNKMTDGSSEKFTLTKVSDERYIDKGNRTYTWTPNGTDYSL 600
 QAELENDIKVEIRNKMTDGSSEKFTLTKVSDERYIDKGNRTYTWTPNGTDYSL 600

QY 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKQDSETLKPDNFESGYTFIAPRDYC
 Db 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKQDSETLKPDNFESGYTFIAPRDYC
 QY 661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQYNSKQKNIK
 Db 661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQYNSKQKNIK
 QY 721 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSIDNDNYVFTAPYFNKSGPGA
 Db 721 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSIDNDNYVFTAPYFNKSGPGA
 QY 781 MYSKAVEIYIQGLLKPAVVGKIDVNSWIEFTKTSIRDPCAGPVCDCKRNSDV
 Db 781 MYSKAVEIYIQGLLKPAVVGKIDVNSWIEFTKTSIRDPCAGPVCDCKRNSDV
 QY 841 LDDGGFLLMANHDDVTNQIGRFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
 Db 841 LDDGGFLLMANHDDVTNQIGRFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
 QY 901 GAGHSAYVPSVADILQIGWATAAAMSTLQOFLLSLTTPRLLAEVEMEDDDFTA
 Db 901 GAGHSAYVPSVADILQIGWATAAAMSTLQOFLLSLTTPRLLAEVEMEDDDFTA
 QY 961 SCITEQTQYFFDNDKSFSGVLDGNCNSRIFHGEKLMNTNLIFIMVESKGTCPCD
 Db 961 SCITEQTQYFFDNDKSFSGVLDGNCNSRIFHGEKLMNTNLIFIMVESKGTCPCD
 RESULT 2
 C1C2 RAT STANDARD; PRT; 1091 AA.
 AC P54290;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta
 DE subunits precursor.
 GN CACNA2D1 OR CACNL2A OR CCHL2A.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ra
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92228762; PubMed=1314383;
 RA Kim H.L., Kim H., Lee P., King R.G., Chin H.;
 RT "Rat brain expresses an alternatively spliced form of the
 RT dihydropyridine-sensitive L-type calcium channel alpha 2 subunit
 RT Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).
 CC -! FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT R
 CC -! SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBU
 CC HETEROIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
 CC -! SUBCELLULAR LOCATION: Integral membrane protein.
 CC -! ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=1;
 CC Comment=2 isoforms are produced;
 CC Name=1;
 CC IsoId=P54290-1; Sequence=Displayed;
 CC -! PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSE
 CC A PRECURSOR FORM (BY SIMILARITY).
 CC -! SIMILARITY: TO OTHER SPECIES' ALPHA-2 SUBUNIT.
 CC -! SIMILARITY: Contains 1 WFA domain.
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51 2004

Fe

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38.1; --

Cache.

VWF A.

; 1.

1.

FA; 1.

membrane; Ion transport; Voltage-gated channel;

coprotein; Phosphorylation; Signal;

POTENTIAL.

L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT

(BY SIMILARITY).

L-TYPE CALCIUM CHANNEL DELTA SUBUNIT

(BY SIMILARITY).

POTENTIAL.

POTENTIAL.

POTENTIAL.

VWFA.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

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N-LINKED (GLCNAC. . .) (POTENTIAL).

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N-LINKED (GLCNAC. . .) (POTENTIAL).

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N-LINKED (GLCNAC. . .) (POTENTIAL).

51-975; 992-1000 AND 1033-1050.
 535; PubMed=2168391;
 Warner C., Catterall W.A.;
 purified calcium channels. Alpha 2 and delta are encoded
 gene.;
 . 265:14738-14741 (1990).
 CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
 N-CONTRACTION COUPLING.
 THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
 ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
 IERS THAT ARE DISULFIDE-LINKED.
 IER LOCATION: Integral membrane protein.
 IER PRODUCTS:
 alternative splicing; Named isoforms=1;
 =2 isoforms are produced;
 13806-1; Sequence=Displayed;
 13806-1; Skeletal muscle.
 13806-1; Skeletal muscle.
 A-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
 OR FORM.
 f: TO OTHER SPECIES' ALPHA-2 SUBUNIT.
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 ail to license@isb-sib.ch).

 AAA81562.1; -;
 ZHRBA2.
 004010; Cache.
 002035; VWF_A.
 ; Cache; 1.
 ; vwa; 1.
 7; vwa; 1.
 234; VWFA; 1.
 ; Transmembrane; Ion transport; Voltage-gated channel;
 ; Glycoprotein; Phosphorylation; signal;
 plicing.
 27 960
 27 960
 51 1106
 18 471
 21 945
 32 1101
 35 432
 34 94
 38 138
 36 186
 26 326
 50 350
 77 477
 36 606
 15 615
 78 678
 34 784
 27 827
 31 891
 98 898
 88 988
 01 1001
 03 503
 48 848
 06 AA; 125042 MW, B00DE7F3C877B618 CRC64;
 96.0%; Score 5132.5; DB 1; Length 1106;
 arity 94.7%; Pred. No. 2.2e-299;
 conservative 14; Mismatches 12; Indels 29; Gaps 4;
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1 MAAGRPLAWTLTLQAWLWLLIGPSEPPPSAVTIKSWVDKMQEDLVTLAKTASGV
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 61 DIYEKQDLYTTPENNAQQLVEIAARDIEKLLSNRSKALVSLALEAKVQAQHWNR
 119 SNEVYVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHPTDIYE
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 179 VLNELNWTSLDVFVKKNREEDPSLLWQVFGSATGLARYYPASPVWDSNTPNKID
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 239 RREPWTYOGAASPKDMLILVDVSGVSGLTGLIRTSSVSEMLETLSDDDFVNVASE
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 531 -----NPKSQEPVTLDFDAELENDDIKVEIRNKMIDGESGEKTRTLVKS
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 580 YIDKGNRTYTWTPVNGTDY--SLALVLPYTSFYIYKAKLEETITQARSKKGKMDSE
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 834 RDCAGPVCCKNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHL
 879 VYAFNKSVDYQSVCEPQAPKQAGHRSVAVPSVADILQIGWATAAASILQOFL
 894 VYAFNKSVDYQSVCEPQAPKQAGHRSVAVPSVADILQIGWATAAASILQOFL
 939 FPRLLAEVEMDDDDFTASLSKQSCITEQTQYFFDNDKSKFSGLVDCGNCRIHFGEI
 954 FPRLLAEVEMDDDDFTASLSKQSCITEQTQYFFDNDKSKFSGLVDCGNCRIHFGEI
 999 TNLIFIMVSKGTCPCDTRL 1018
 1014 TNLIFIMVSKGTCPCDTRL 1033

RESULT 4

STANDARD; PRT; 1249 AA.

; P34373;
rel. 28, Created)
rel. 42, Last sequence update)
rel. 42, Last annotation update)
rel. 42, Last annotation update)

unc-36 precursor (Uncoordinated
calcium channel

72 OR C50C3.9/C50C3.10/C50C3.11.
C. elegans.
Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Pselodermidae; Caenorhabdittis.
39;

N.A.
1 N2;
718; PubMed=7906398;
nough R., Anderson K., Baynes C., Berks M., Coulson A.,
Burton J., Connell M., Copsey T., Cooper J., Fraser A.,
Dear S., Du Z., Durbin R., Favello A., Hier M.,
Kardner A., Green P., Hawkins T., Hillier L., Hier M.,
Jones M., Kershaw J., Kirsten J., Laister N.,
Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Pericy C., Rifkin L., Roopra A., Saunders D., Shownteen R.,
McDon N., Smith A., Smith M., Sonhammer E., Staden K.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Watson A., Weinstock L., Wilkinson-Sproat J.,
contiguous nucleotide sequence from chromosome III of *C.*
2-38(1994).

i i
XOV-2002) to the EMBL/GenBank/DDBJ databases.

ND TISSUE SPECIFICITY.
295; Sanchez B.M., Kenyon C.J.;
cting sensitivity to serotonin in *Caenorhabditis elegans*.";
33-1219-1230(1996).
NN: May act as an auxiliary subunit of the UNC-2 voltage-
calcium channel which appears to trigger calcium-activated
pathways that control the serotonin response. Inhibiting
in sensitivity of the vulval muscle results in egg laying
. May act in both neurons and muscle cells to enhance motor
Y.

SPECIFICITY: Descendants of the cells AB and AB.p (that give
nearly all nonpharyngeal neurons), descendants of P1 (that
se to body muscle) and cell lineages that give rise to the
and juvenile motor neurons.
SPECIFICITY: Contains 1 VWFA domain.

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email to license@isb-sib.ch).

33; AAA27971.3; --
17; 544617
-50C3.9; CE322168.
IPR004010; Cache.
IPR002035; VWF_A.
2743; Cache; 1.
0092; vwa; 1.
00327; VWFA; 1.
PS50234; VWFA; 1.
Ionic channel; Ion transport; Voltage-gated channel;
channel; Signal; Glycoprotein.
19
POTENTIAL.

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ail to license@isb-sib.ch).

CAA73475.1; -
ITGO.
006172; DNA_pol_B.
006134; DNA_pol_B_dom.
006133; DNA_pol_B_exo.
003586; Hedgehog_hintC.
003587; Hedgehog_hintN.
006141; Intein.
006142; Intein.
004042; Intein_endonuc.
004578; Pol2.
; DNA_pol_B; 4.
; DNA_pol_B_exo; 1.
; HintC; 3.
; HintN; 3.
; POLBc; 1.
001443; intein_Cterm; 3.
001445; intein_Nterm; 3.
000592; Pol2; 2.
16; DNA_POLYMERASE_B; FALSE_NEG.
18; Intein_C TER; 3.
19; Intein_ENDONUCLEASE; 2.
17; Intein_N TER; 3.
NA-directed DNA polymerase; DNA replication;
hydrolyase; Endonuclease; Autocatalytic cleavage;
ng.
1 409 DNA POLYMERASE, 1ST PART (POTENTIAL).
0 769 INTEIN I.
0 855 DNA POLYMERASE, 2ND PART (POTENTIAL).
6 1392 INTEIN II.
3 1441 DNA POLYMERASE, 3RD PART (POTENTIAL).
2 1598 INTEIN III.
9 1829 DNA POLYMERASE, 4TH PART (POTENTIAL).
9 AA; 211875 MW; A113A8BC57EB9C83 CRC64;
3.0%; Score 161; DB 1; Length 1829;
rity 20.1%; Pred.No. 0.16;
nservative 101; Mismatches 301; Indels 282; Gaps 39;
PSSEPPPS-----AVTISWV-----DKMOEDLVILA 48
RDKEHPKPIHRMGDSFAVEIKRIHFDLPVVRRTINLPYTLVAVYVGLKT 288
VNQLVDIYKYQDL-----YTFVNNARQLVEIAARDIEKLLSNRSKALVSLALE 103
ABEATAAWETESMKKLAQYSME--DARATYEL-----GREFFPEAE 334
AAHQWREDFAS--NEWVY-----NAKDDLDPEKNDSEPGSRKIPVFI----- 150
GQSVWDVSRSTGNLVYLLRVAVERNELAPNPDSEYRRURRTYLGIVYKE 394
GRQISYQHAHVHPTD---IYEGSTIV-----LNELNMTSALDEVFKKRNREDPSL 203
WENTAYLDFRCH-PADTKVIVKGGIVNISDVKEGDIYLGIDG----- 441
GSATGLARYYPASPDVNSR---TPN-KIDLYDVRPPWYIQGAASPKDMLILDV 259
-RVKKWKYHYEGKLINGKLCTPNKHPVPVVTENDRQTRI-----RDSLAKSF 491
SGLTLKLIRTSVSEMLETLSDDDDFVNVASFNSN----- 297
KG---KIITTKL-----FEKIAEFKNKPSSEBILKGBLSGIIAEGTL 537
SCF-----OHLVQANV-RNKKVLKDAV-----NNITAKG----- 329

Db 538 LRKDIIEYFSDSRGKRISHQYRVEITIGENEKELLERILYIFDKLFGIRPSVKKKG
Qy 330 --ITDYKKGFSFAPEQLIANNVSRANKIIMLFTDGGERAQEI FNKYNKDKKVR
Db 598 LKITTAKAVYLQIEELK-NIESLYAPAVLRGF-----FERDATVN
Qy 388 SV-----GQHNRYERGPIQWMACENKGY---YYEIPSGAIRINTQEVLDVLRPMVL
Db 643 TIVVTQGTNNKWKIDIVAKLLDSIGIPYSRYEYKIENGKELTKHILEITGRD---
Qy 441 AKQVQWTVNYLDALEGLVITGLPVFNITQGF-----NKTNLKNQLILGV
Db 696 -----GLILFQTLVGFISSERKNEALEKALEVREMNRKKNNSFYNL
Qy 492 VSLEDIKRLTPFTLCPNGYVFAIDPNGVLLHPNLPQKNPKSQEPVTLDFLDAEL
Db 740 VSSEYKGEVYDITLGNPYFA--NG-ILTHNSLYPSIIVTHN-VSPDTLRE-
Qy 552 KVEIRNMIDGESGKTFRTLVKSODERYDKGNRTYTWTPVNGTIDYSLALVLPY.
Db 790 -----GCKNYDVAPIVG--YKFCCKDFPG-
Qy 612 IKAKLEETITQARSKKGKMKDSETLKPDNFEESGY-----TFIAPRDYCNDL
Db 812 IPSILGELITMROEIKKKMK--ATIDPIEKOMLDYRQRAVKLLANSILPNW---L
Qy 663 NNTFEFLNFNEFIDRKTNNPNSCNADLINRVLIDAGFTNELVQNYWSKOKNIKGVK
Db 867 NGEVVKVIGEDIDRYWESQKQKRVTVNDTEVLEVDNIFAFSLNKKSEIKKVK
Qy 723 VTDGGITRVYKGEAGE 738
Db 925 -----IRHKYKGEAYE 935
RESULT 10
ATX1_PLAFA STANDARD; PRT; 1956 AA.
AC Q04956;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable cation-transporting ATPase 1 (EC 3.6.3.-).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T9/96;
RX MEDLINE=93132070; PubMed=8421054;
RA Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,
RA Robson K.J.;
RT "A family of cation ATPase-like molecules from Plasmodium
falciparum";
RL J. Cell Biol. 120:385-398(1993).
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the cation transport ATPases family (P-
ATPases). Subfamily V.
CC
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modified and this statement is not removed. Usage by and for co
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or send an email to license@isb-sib.ch).
CC
CC EMBL; X65738; CAA46646.1; -
DR InterPro; IPR001757; ATPase_E1-E2.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 7.
DR PROSITE; PS00154; ATPASE_E1_E2; 1.

[illegible]

```

234; VMFA; 1.
protein; Complete proteome.
16 394 VMFA.
5 AA; 63634 MW; 7BB6A1A77A2BE111 CRC64;
arity 2.9%; Score 157.5; DB 1; Length 575;
conservative 93; Mismatches 206; Indels 105; Gaps 25;
ARQLVEIAARDIEKLNSRKALVSLALEAEKVOAAHQWREDFASNEVWVYNAKDD 130
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
KESQQQPSPTTEQVLLAAQAAIK---EAEQSAAA---AKALAAQVEVQVSDKQA 75
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
KND-----SEPGSRIKPVFIEDANFGRIQISYQHAA---VHIPTDI 172
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
LOEAPTFAAAKAKATHANPGTARYQQF---DDNPVKVQAQNPLATFSLDVTGTS 132
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
TIVLINE-----LNWTSALDEVFKKNEEDPSLLWQVFGSATGLARYY 218
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
RRFLNQGLPPDPDAVRVEEIVNYPSPWDI---KDKQSIKPKPIPFAMRYELA--- 187
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
WVNSRTPNKIDLVDRRRPWYIQGAASPKIMLILVDVSGS-VSGLTLKLIRTSVS 277
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
W-NEQRTLLKVDILAKDKSEELPAS---NLVFLITDSGMSISDERLPLIQSLK 241
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
TISDDDFVNVASFNNAQDVSCFHLVQAVNRNKKVLKADVNNITAKGITYKKGF 337
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
ELREQDNIAVTYAGDSRIA-----LPSISGSHKAEINAAIDSLDAGSTNGGAGL 296
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
EQILNVNVRANCNKIMLFTDG-----GEERAQEIFNKVYKDKVVRFRFVSQ 391
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
QKATK-GFIKGGINR-ILLATDGFNVGIDDPKSIEMSVKQRESGVTLSTFGVGN 354
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
RGIQWMAENKGYEIPSGAIRINTQBYLDVLRPMVL---AGDKAKQVQ--- 445
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
EAMVRIADVGNYSYIDTLS-----EAQKVLNEMEQMLITVAKDVKAQIEFNP 410
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
LDLALGLGLVITGLPVNTGTGFENKTNLKNQILLOVMGVD-VSLEDI---KRLT 501
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
---RQIG-----YE-----KRLRVEHFNNVDVADGIDGAGKHIT 447
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
LCPNGYFAIDPNGYVLLHNPLOPKPKSOE 536
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
TLNGQKASIDKLRYA---PDNKLAKSDKTYE 480
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
STANDARD; PRT; 946 AA.
; Q15484;
rel. 17, Created
rel. 17, last sequence update
rel. 42, last annotation update
Trypsin inhibitor heavy chain H2 precursor (ITI heavy
inter-alpha-inhibitor heavy chain 2) (Inter-alpha-trypsin
plex component II) (Serum-derived hyaluronan-associated
).
2.
(Human).
azooa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Catarrhini; Hominidae; Homo.
6;
N.A., AND PARTIAL SEQUENCE.
137; PubMed=2450046;
threitmueller T., Hochstrasser K., Wachter E.;
DNA and derived amino acid sequence of the precursor
three protein components of the inter-alpha-trypsin
plex."
;63-67(1988).
14-865 FROM N.A.
176; PubMed=2446322;

```

```

RA Salier J.-P., Diarra-Mehrpour M., Seaboue R., Bourguignon J.,
RA Benarous R., Ohkubo I., Kurachi S., Kurachi K., Martin J.P.,
RT "Isolation and characterization of cDNAs encoding the heavy chain
RT human inter-alpha-trypsin inhibitor (I alpha TI): unambiguous
RT evidence for multipolypeptide chain structure of I alpha TI."
RL Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).
[3]
RN SEQUENCE OF 384-766 FROM N.A.
RX MEDLINE=89076497; PubMed=2462430;
RA Salier J.-P., Diarra-Mehrpour M., Seaboue R., Bourguignon J.,
RA Martin J.P.;
RT "Human inter-alpha-trypsin inhibitor. Isolation and characterizat
RT of heavy (H) chain cDNA clones coding for a 383 amino-acid sequen
RT of the H chain."
RL Biol. Chem. Hoppe-Seyler 369:15-18(1988).
[4]
RN PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89024442; PubMed=3663330;
RA Schreitmueller T., Hochstrasser K., Resinger P.W.M., Wachter E.,
RA Gebhard W.;
RT "cDNA cloning of human inter-alpha-trypsin inhibitor discloses th
RT different proteins."
RL Biol. Chem. Hoppe-Seyler 368:963-970(1987).
[5]
RN SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.
RX MEDLINE=89380192; PubMed=2476436;
RA Engchild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;
RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin
RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma.
RT Polypeptide chain stoichiometry and assembly by glycan."
RL J. Biol. Chem. 264:15975-15981(1989).
[6]
RN SEQUENCE OF 55-64.
RC TISSUE=Plasma;
RX MEDLINE=93039735; PubMed=1384548;
RA Maiki N., Balduyck M., Maes P., Capon C., Mizon C., Han K.K.,
RA Tartar A., Fournet B., Mizon J.;
RT "The heavy chains of human plasma inter-alpha-trypsin inhibitor:
RT isolation, their identification by electrophoresis and partial
RT sequencing. Differential reactivity with concanavalin A."
RL Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).
[7]
RN SEQUENCE OF 55-64 AND 681-702, CROSS-LINK STRUCTURE, AND
RC CARBOHYDRATE-LINKAGE SITES THR-691.
RX MEDLINE=93232026; PubMed=7682553;
RA Engchild J.J., Salvesen G., Thøgersen I.B., Valnickova Z.,
RA Pizzo S.V., Hefta S.A.;
RT "Presence of the protein-glycosaminoglycan-protein covalent cross-
RT in the inter-alpha-inhibitor-related proteinase inhibitor heavy c
RT 2/bikunin."
RL J. Biol. Chem. 268:8711-8716(1993).
[8]
RN SEQUENCE OF 67-101, AND HYALURONAN BINDING.
RC TISSUE=Serum;
RX MEDLINE=94075371; PubMed=7504674;
RA Huang L., Yoneda M., Kimata K.;
RT "A serum-derived hyaluronan-associated protein (SHAP) is the heavy
RT chain of the inter alpha-trypsin inhibitor."
RL J. Biol. Chem. 268:26725-26730(1993).
[9]
RN SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE
RC TISSUE=Plasma;
RX MEDLINE=94229087; PubMed=7513643;
RA Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,
RA Michalski C., Fournet B., Mizon J.;
RT "Chondroitin sulphate covalently cross-links the three polypeptide
RT chains of inter-alpha-trypsin inhibitor."
RL Eur. J. Biochem. 221:881-888(1994).
[10]
RN CARBOHYDRATE-LINKAGE SITES, AND MASS SPECTROMETRY.
RX MEDLINE=98343966; PubMed=9677337;
RA Flahaut C., Capon C., Balduyck M., Ricart G., Sautiere P., Mizon J

```


N.A.
487; PubMed=2204031;
Lund M.W., Kurazona H., Binz T., Niemann H., Gill D.M.,
Poff M.R.;
sequence of Clostridium botulinum C1 neurotoxin.";
Res. 18:4924-4924 (1990).
N.A.
Stockholm / C-ST;
998; PubMed=2222445;
Jii N., Tsuzuki K., Murakami T., Indoh T.,
Takeshi K., Syuto B., Oguma K.;
nucleotide sequence of the gene coding for botulinum
in the C-ST phage genome.";
hys. Res. Commun. 171:1304-1311 (1990).
-25-
Stockholm / C-ST;
072; PubMed=2450068;
Okosawa N., Syuto B., Ohishi I., Fujii I., Kimura K.,
t of a monoclonal antibody recognizing an antigenic site
stridium botulinum type B, C1, D, and E toxins and
.";
. 56:898-902 (1988).
N OF SUBSTRATE.
966; PubMed=7901002;
man E.R., Yamaoka S., Binz T., Niemann H., Jahn R.;
rotoxin C1 blocks neurotransmitter release by means of
l/syntaxin.";
21-4828 (1993).
BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
CASE THAT CLEAVES SYNTAXIN.
ACTIVITY: Limited hydrolysis of proteins of the
toxis apparatus, synaptobrevins, SNAP25 or syntaxin. No
action on small molecule substrates.
Binds 1 zinc ion per subunit (by similarity).
DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A
IN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,
N- AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
AND TOXIN BINDING, RESPECTIVELY.
AR LOCATION: Secreted.
30US: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF
NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.
30US: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C
CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE
HAGE.
/: BELONGS TO PEPTIDASE FAMILY M27.
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CAA47060.1; -;
CAA51313.1; -;
CAA37780.1; -;
BAA14235.1; -;
CAA44263.1; -;
3BTA.
12; -;
00395; Bontoxilysin.
06025; Zn_MTPeptidase.
Peptidase_M27, 1.

DR PRINTS; PRO0760; BONTOKILYSIN.
DR ProDom: PD001963; Bontoxilysin; 1.
DR PROSITE; PS00142; ZINC PROTEASE; 1.
KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
FT INIT_MET 0 0
FT CHAIN 1 448 BOTULINUM NEUROTOXIN C1, LIGHT-CHAIN
FT METAL 449 1290 BOTULINUM NEUROTOXIN C1, HEAVY-CHAIN
FT METAL 228 228 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 229 229 BY SIMILARITY.
FT METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 436 452 INTERCHAIN (PROBABLE).
FT CONFLICT 84 84 P -> T (IN REF. 2).
SQ SEQUENCE 1290 AA; 148734 MW; 71PBE379F97129E8 CRC64;
Query Match 2.88; Score 152; DB 1; Length 1290;
Best Local Similarity 20.38; Pred. No. 0.32;
Matches 205; Conservative 125; Mismatches 346; Indels 334; G
QY 106 KQAAHOWREDFASNEVVYNAKDDLDPEKNDSEPGSQRIK---PVFIEDANFR-
DB 138 KTRQGNWVKTSINPSVIITG---PRENIIDPETSTFKLTNTNTFAAQEGFAL
QY 158 -----QISYQHAHVHIPTDIYEGS-----TIVLNELNWTSLDVEFK---
DB 193 ISPRFMLTYSNAT---NDVGEGRFSKSEFCMDPILILMHELN---HAMHNLGIAl
QY 199 EDPSLLWQVFGSATGLARYYP---ASPMVDNSRTPNKIDLYDVRPRPWIOGAA
DB 247 TISVTSNIFSYQNVKLEYAEIYAGGPID--LIPKSARKYFEKALDIYSIA
QY 254 MLILVDVG---SVSGTLKLIR-----TSVSEMLETSLDDDFVNVASFNSNAQD
DB 305 SITANPSSFNKYGIVKQKIRKRVVSSGEV--TVNRKFFVEL--YNELTQI
QY 305 QHLVQANVRKKV-LKAVNNITAK---GITYKKGFSAPEQL---LNNVNSR
DB 361 NYAKIYNQVRKYLNSVYTPVTANILDDNVYDIQNGFNIPKSNLNVLFMGQLSR
QY 352 --ANCKNIMLFT-----DGGEERAQEIFNK-----YKND-----KKV
DB 421 RKNVPENMLYLFKFKCHKAIDG---RSLYKNTLDCRELLVKNVTLDPFGDISDV.
QY 387 FSVQGHNYERGPIQWMAKENGYEIPSGAIRI--NTQEY--LDVL-----
DB 476 FLRKDINEETEVI-----YYPDNVSDQVILSKNTSEHQDLILYPSIDSES.
QY 431 GRPMVLAKGAKQOVQWVN--VYLDALGLGIVTGLTPVFNITGQFENKTN-----
DB 527 GENQVFNDRNTQNVYILNSYYLESQKL-----SDNVEDEFTFTRSI EALDNSAKVY
QY 479 -LKNQILGVMG-----VDVSLEDIKRLTPRFTLCPNGYYPFAIDPNGYVLLHPN.
DB 583 TLANKVNAVQGGGLFLMWANDVVEDEFTNLRKOTLDKISDVSAILP---YIGPA
QY 531 NPKSQBPVTLDP-----LDLELNDI-----KVEIRNMIDGSESEKTI
DB 639 NSVRRGNFTAEAVTGVITLLEAFEPFTPALGAFVIYSKVQVORNEII---KT
QY 573 VKSQDERYIDKGNRTVTM-----TPVNGTDYSLALVLPITYSYFYIKAKLEE.
DB 693 LEQRIKRWKD---STENRMGTWLSRIITQFNINISYQYDLSL-NYQAGAKKAKID--
QY 623 ARSKGKMKDSETLKP--DNFESGYTFIAPRDYCNLDKISDNNTFELNFEFFI--
DB 743 LEVKKYSGSDKENIKSQVENLKNs-----LDVKIS---EAMNINKFIRI
QY 676 -----DRKTPNPNPCNADLINRVLLDA-----
DB 788 TYLFKNMLPKVIDELNEFDRTN-----KAKLIN--LIDSHNIIILVGEVDLKLAKV
QY 698 -----GFTN-----ELVQNYM-----SKQNKIKGVKRVFTDGGITRVYPK
DB 840 QNTIPNIFSYTNNSLLKDIINEYFNININDSKILSLQNRKNTLVDTSG-----YNAI

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AA000024.1; -;
AAB46821.1; -;
-; NOT ANNOTATED_CDS.
JC4625.
006587; VIT.
002035; VWF_A.
; vwa; 1.
9; VIT; 1.
7; VWA; 1.
234; VWF; 1.
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1 27
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12 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
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ALIGNMENTS

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; Sequence 13, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 subu
; TITLE OF INVENTION: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-13

Query Match 100.0%; Score 5346; DB 14; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gap

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10-090-827-13
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SUMMARIES

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0 1036 14 US-10-090-827-14 Sequence 14, Appl
0 1063 14 US-10-090-827-15 Sequence 15, Appl
0 1091 9 US-09-875-423-4 Sequence 4, Appli
0 1091 14 US-10-162-012-17 Sequence 17, Appl
0 1091 14 US-10-090-827-16 Sequence 16, Appl
0 1091 15 US-10-162-102-17 Sequence 17, Appl
3 1086 15 US-10-375-253-49 Sequence 49, Appl
9 1084 15 US-10-375-253-53 Sequence 53, Appl
9 1018 14 US-10-090-827-6 Sequence 6, Appli
9 1036 14 US-10-090-827-7 Sequence 7, Appli
9 1063 14 US-10-090-827-8 Sequence 8, Appli
9 1069 14 US-10-090-827-9 Sequence 9, Appli
9 1091 14 US-10-090-827-5 Sequence 5, Appli
6 1103 15 US-10-375-253-47 Sequence 47, Appl

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plication US/10090827

US20030073132A1

ATION:

ner-Lambert

ATION: Method for the screening of alpha 2 delta-1 subunit

ATION: binding ligands

3: 179

ATION NUMBER: US/10/090,827

3 DATE: 2002-03-06

TION NUMBER: US/09/397,549

DATE: 1999-09-16

ID NOS: 21

antin Ver. 2.1

TYPE: PRT
ORGANISM: Homo sapiens
US-10-090-827-14
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0;
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20030073132A1

N:

-Lambert

N: Method for the screening of alpha 2 delta-1 subunit

N: binding ligands

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ON NUMBER: US/10/090,827

TE: 2002-03-06

NUMBER: US/09/397,549

: 1999-09-16

NOS: 21

n Ver. 2.1

sapiens

100.0%; Score 5346; DB 14; Length 1063;

city 100.0%; Pred. No. 0;

aservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-09-875-423-4

; Sequence 4, Application US/09875423

; Patent No. US20020081657A1

; GENERAL INFORMATION:

; APPLICANT: Curtis, Roly A. J.

; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL

; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

; FILE REFERENCE: 10448-059001

; CURRENT APPLICATION NUMBER: US/09/875,423

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/209,257

; PRIOR FILING DATE: 2000-06-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 1091

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-875-423-4

Query Match 100.0%; Score 5346; DB 9; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1016; Conservative 0; Mismatches 0; Indels 0; G

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us-10-090-827-13.rapb

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PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/US01/18247
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/227,068
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 09/928,530
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: PCT/US01/25475
PRIOR FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: US 60/226,770
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 09/934,421
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/US01/26096
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/279,281
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 10/109,029
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: PCT/US02/09728
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/290,288
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US (not assigned)
PRIOR FILING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 1091
TYPE: PRT
ORGANISM: Homo sapiens
US-10-162-012-17

Query Match 100.0%; Score 5346; DB 14; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; C

QY 1 MAAGCLLALTLTFLQSLIGPSSEPPFSAVTIKSWDKQEDLVTLAKTAGVNM
Db 1 MAAGCLLALTLTFLQSLIGPSSEPPFSAVTIKSWDKQEDLVTLAKTAGVNM
QY 61 YEKYQDLYTVEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHORE
Db 61 YEKYQDLYTVEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHORE
QY 121 EVVYINAKDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQAAVHIPTDIYE
Db 121 EVVYINAKDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQAAVHIPTDIYE
QY 181 NELNWTALDEVFKKREEDPSLLMQVFGSATGLARYYPASPVWDSNRTPNKID
Db 181 NELNWTALDEVFKKREEDPSLLMQVFGSATGLARYYPASPVWDSNRTPNKID
QY 241 RPYWYOGAASPKDMLLVDSVSGSLTLKLRITSVSEMLETLSDDDFVNVA
Db 241 RPYWYOGAASPKDMLLVDSVSGSLTLKLRITSVSEMLETLSDDDFVNVA
QY 301 VSCFQHLVQANVKNKVLKDAVNNITAKGITYKKGFSFAFEQLLNVNVRAN
Db 301 VSCFQHLVQANVKNKVLKDAVNNITAKGITYKKGFSFAFEQLLNVNVRAN
QY 361 FTDGGERAQEIENKYNKDKKVRVFSVQHNVERGPIOMMACENKGYIYEI
Db 361 FTDGGERAQEIENKYNKDKKVRVFSVQHNVERGPIOMMACENKGYIYEI
QY 421 INTQEYLDVLRPNVLAGDKAKQVQWNTNVYLDLLELGLVITGLTPVFNITQGF
Db 421 INTQEYLDVLRPNVLAGDKAKQVQWNTNVYLDLLELGLVITGLTPVFNITQGF
QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHFNLPKQNP
Db 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHFNLPKQNP

Application US/10162012
US20030051660A1
ATTN: RORY A.J. Immaculada
ilos-Santiago, Immaculada
u. Wei
ATTN: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
E: 10448-190001
CATION NUMBER: US/10/162,012
IG DATE: 2002-06-04
ACTION NUMBER: US 60/209,845
DATE: 2000-06-06
ACTION NUMBER: US 09/875,321
DATE: 2001-06-06
ACTION NUMBER: PCT/US01/18340
DATE: 2001-06-06
ACTION NUMBER: US 60/209,257
DATE: 2000-06-05
ACTION NUMBER: US 09/875,423
DATE: 2001-06-05
ACTION NUMBER: PCT/US01/18398
DATE: 2001-06-05
ACTION NUMBER: US 60/209,238
DATE: 2000-06-05
ACTION NUMBER: US 09/875,363

ATE: 2000-06-05
 ION NUMBER: US 09/875,423
 ATE: 2001-06-05
 ION NUMBER: PCT/US01/18398
 ATE: 2001-06-05
 ION NUMBER: US 60/209,238
 ATE: 2000-06-05
 ION NUMBER: US 09/875,363
 ATE: 2001-06-05
 ION NUMBER: PCT/US01/18247
 ATE: 2001-06-05
 ION NUMBER: US 60/227,068
 ATE: 2000-08-22
 Application data removed - See File Wrapper or PALM.
 ID NOS: 48
 SEQ for Windows Version 4.0

io sapiens

100.0%; Score 5346; DB 15; Length 1091;
 100.0%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AGLLALTTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60
 AGLLALTTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60
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 QYQDLTYVEPNARQVETIARDIEKLLNSRKALVSLALEAEKVQAAHQRDFASN 120
 YYNAKDDLDPEKNDSEPGSRQKPFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
 YYNAKDDLDPEKNDSEPGSRQKPFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
 LNWTSALDEVKKNREEDPSLLMQVFGSAGTLARYYPASPWDNSRTPNKIDLYDVR 240
 LNWTSALDEVKKNREEDPSLLMQVFGSAGTLARYYPASPWDNSRTPNKIDLYDVR 240
 WYIQGAASPKDMLTLVDVSGVSLTLKLRISVSEMLETLSDDDFVNVASFNSNAQD 300
 WYIQGAASPKDMLTLVDVSGVSLTLKLRISVSEMLETLSDDDFVNVASFNSNAQD 300
 CFQHLVQANVRNKKVLDVANNITAKGIDYKKGFSFAFQLLNYNVSRANCKIIML 360
 CFQHLVQANVRNKKVLDVANNITAKGIDYKKGFSFAFQLLNYNVSRANCKIIML 360
 DGGERAQETIPKNYKDKKVRFPFSGVGHYERGPQWMACENKGYVYIETPSIGATR 420
 DGGERAQETIPKNYKDKKVRFPFSGVGHYERGPQWMACENKGYVYIETPSIGATR 420
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 TQYELDLGRPMVLADKAKQVQNTVYLDALGLVITGLTFVFNITGQFENKTNLK 480
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 NLPTYSFYIYKAKLEETITQARKKGGKMDSETLKPDNFESSGYTFFIAPROYCNDLKI 660
 NNTFELLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKIKGVKAR 720
 NNTFELLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKIKGVKAR 720

QY 721 FVYTDGIGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNDNVFTAPYFNKSGPCF
 DB 721 FVYTDGIGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNDNVFTAPYFNKSGPCF
 QY 781 MYSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDY
 DB 781 MYSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDY
 QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPDLMRHLVNLISVYAFNKSVDYQVSCBPC
 DB 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPDLMRHLVNLISVYAFNKSVDYQVSCBPC
 QY 901 GAGHRSAYVPSVADIIQIGWATAAAWSILQFLLSLTFFPRLLEAVEMEDDDFTF
 DB 901 GAGHRSAYVPSVADIIQIGWATAAAWSILQFLLSLTFFPRLLEAVEMEDDDFTF
 QY 961 SCITEQTYFFDNDKSKFSGLDCGNCRIFFHGEKLMNTNLIFFIMVESKGTCPCI
 DB 961 SCITEQTYFFDNDKSKFSGLDCGNCRIFFHGEKLMNTNLIFFIMVESKGTCPCI

RESULT 8

US-10-375-253-49
 ; Sequence 49, Application US/10375253
 ; Publication No. US20040018510A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS
 ; FILE REFERENCE: SD9813DA
 ; CURRENT APPLICATION NUMBER: US/10/375,253
 ; CURRENT FILING DATE: 2003-02-27
 ; PRIOR APPLICATION NUMBER: 08/450,273
 ; PRIOR FILING DATE: 1995-05-25
 ; PRIOR APPLICATION NUMBER: 08/404,354
 ; PRIOR FILING DATE: 1995-02-15
 ; PRIOR APPLICATION NUMBER: 07/914,231
 ; PRIOR FILING DATE: 1992-07-13
 ; PRIOR APPLICATION NUMBER: 08/314,083
 ; PRIOR FILING DATE: 1994-09-28
 ; PRIOR APPLICATION NUMBER: 07/914,231
 ; PRIOR FILING DATE: 1992-07-13
 ; PRIOR APPLICATION NUMBER: 07/603,751
 ; PRIOR FILING DATE: 1990-11-09
 ; PRIOR APPLICATION NUMBER: 08/290,012
 ; PRIOR FILING DATE: 1994-08-11
 ; PRIOR APPLICATION NUMBER: 08/149,097
 ; PRIOR FILING DATE: 1993-11-05
 ; PRIOR APPLICATION NUMBER: 08/105,536
 ; PRIOR FILING DATE: 1993-08-11
 ; PRIOR APPLICATION NUMBER: 08/149,097
 ; PRIOR FILING DATE: 1993-11-05
 ; Remaining Prior Application data removed - See File Wrapper or PA
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 49
 ; LENGTH: 1086
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-10-375-253-49

Query Match 99.3%; Score 5306.5; DB 15; Length 1086
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1013; Conservative 0; Mismatches 0; Indels 5;

QY 1 MAAGCLLALTTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGS
 DB 1 MAAGCLLALTTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGS
 QY 61 YEKYQDLTYVEPNARQVETIARDIEKLLNSRKALVSLALEAEKVQAAHQR
 DB 61 YEKYQDLTYVEPNARQVETIARDIEKLLNSRKALVSLALEAEKVQAAHQR

us-10-090-827-13.rapb

:26:17 2004

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; PRIOR APPLICATION NUMBER: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354
; PRIOR FILING DATE: 1995-02-15
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 08/314,083
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 07/603,751
; PRIOR FILING DATE: 1990-11-09
; PRIOR APPLICATION NUMBER: 08/290,012
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: 08/105,536
; PRIOR FILING DATE: 1993-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 1084
; TYPE: PRT
; ORGANISM: Human
; US-10-375-253-53

Query Match      98.9%; Score 5289.5; DB 15; Length 1084;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1010; Conservative 0; Mismatches 1; Indels 7; G

QY 1 MAAGCCLLALTLTFLQSLLIGPSSSEPPSAVTIKSWVDKMQEDLVTLAKTASGVNQ
D 1 MAAGCCLLALTLTFLQSLLIGPSSSEPPSAVTIKSWVDKMQEDLVTLAKTASGVNQ
QY 61 YEKYQDLTYVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKQAAHQRREI
D 61 YEKYQDLTYVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKQAAHQRREI
QY 121 EVVYNKADLDPEKNDSEPGSQRIKPVFIEDANFGROI SYQHAAVHIPTDIYEG
D 121 EVVYNKADLDPEKNDSEPGSQRIKPVFIEDANFGROI SYQHAAVHIPTDIYEG
QY 181 NEFNWTSALDEVFVKKREEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDL
D 181 NEFNWTSALDEVFVKKREEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDL
QY 241 RPYIIOGAASPKDMLILVDVSGSVSGLTILKIRTSVSEMLETSLDDDFVNVASFN
D 241 RPYIIOGAASPKDMLILVDVSGSVSGLTILKIRTSVSEMLETSLDDDFVNVASFN
QY 301 VSCFQHLVQANVRNKVLDKAVNNITAKGITDYKKGFSFAFEQLLNVNVRANC
D 301 VSCFQHLVQANVRNKVLDKAVNNITAKGITDYKKGFSFAFEQLLNVNVRANC
QY 361 FTDGGEERAEQIFNKYNKDKKVRVFRFSGQHNHYERGP IOWMACENKGYVEIPI
D 361 FTDGGEERAEQIFNKYNKDKKVRVFRFSGQHNHYERGP IOWMACENKGYVEIPI
QY 421 INTQEYLDVLRGPMVLADGKAKQVQNTNVLDALELGLVITGTLPVFNITQOFE
D 421 INTQEYLDVLRGPMVLADGKAKQVQNTNVLDALELGLVITGTLPVFNITQOFE
QY 481 NQILLGVNGVDVSLIEDIKRLTPRFTLCPNGYYPFADDPNGYVLLHLPNLPKPKS
D 481 NQILLGVNGVDVSLIEDIKRLTPRFTLCPNGYYPFADDPNGYVLLHLPNLPKPKS
QY 541 DFLDAELENIDIKVEIRNKMDGESGEKTFRTLVKSQDERYIDKGNRTYTWTPV
D 541 DFLDAELENIDIKVEIRNKMDGESGEKTFRTLVKSQDERYIDKGNRTYTWTPV

```

pplication US/10375253

US20040018510A1

ATION: E SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES

ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

ENTION: METHODS

RE: SD9813DA

ICATION NUMBER: US/10/375,253

IG DATE: 2003-02-27

26:17 2004

YSFYIKAKLETTTQARY-----SETLKPDNEESGYTFIAPRDYCNLDKI 660
YSFYIKAKLETTTQARY-----SETLKPDNEESGYTFIAPRDYCNLDKI 653
3FLNNEFTDRKTPNNPSCNADLINRVLLDAGFTNELVQYWSKQKNIKGVAR 720
3FLNNEFTDRKTPNNPSCNADLINRVLLDAGFTNELVQYWSKQKNIKGVAR 713
3GTRVVPKEAGENWQENPETEYDSFKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
3GTRVVPKEAGENWQENPETEYDSFKRSLDNDNYVFTAPYFNKSGPGAYESGI 773
VEIYIQGKLLKPAVVGIIKIDVNSWIENTFTKTSIRDPKAGPVCDCRNSDVMDCVI 840
VEIYIQGKLLKPAVVGIIKIDVNSWIENTFTKTSIRDPKAGPVCDCRNSDVMDCVI 833
VEIYIQGKLLKPAVVGIIKIDVNSWIENTFTKTSIRDPKAGPVCDCRNSDVMDCVI 900
FLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVTAFNKSVDYQSVCEPGAAPKQ 900
FLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVTAFNKSVDYQSVCEPGAAPKQ 893
3SAYVPSVADILQIGWATAAASIILOQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960
3SAYVPSVADILQIGWATAAASIILOQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 953
EQTOYFFDNDKSFSGVLDGNCNCSRI FHGEKLMNTNLI FIMVESKGTCPDTRL 1018
EQTOYFFDNDKSFSGVLDGNCNCSRI FHGEKLMNTNLI FIMVESKGTCPDTRL 1011
EQTOYFFDNDKSFSGVLDGNCNCSRI FHGEKLMNTNLI FIMVESKGTCPDTRL 1011
ication US/10090827
US20030073132A1
TION:
er-Lambert
TION: Method for the screening of alpha 2 delta-1 subunit
TION: binding ligands
: 179
ATION NUMBER: US/10/090,827
DATE: 2002-03-06
ION NUMBER: US/09/397,549
ATE: 1999-09-16
ID NOS: 21
ntIn Ver. 2.1
; scrofa
98.9%; Score 5288; DB 14; Length 1018;
ilarity 98.8%; Pred. No. 0;
Conservative 5; Mismatches 7; Indels 0; Gaps 0;
AGCLLALTLFQSLIGPSSSEPPPSAVTIKSWDKQEDLVTLAKTASGVNQLVDI 60
AGCLLALTLFQSLIGPSSSEPPPSAVTIKSWDKQEDLVTLAKTASGVNQLVDI 60
KYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120
KYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120
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ELNWTSLALDEVEKKNREEDPSLLMQVFGSATGLARYYPASPWVDNSRTNPKIDLYVRR 240
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ELNWTSLALDEVEKKNREEDPSLLMQVFGSATGLARYYPASPWVDNSRTNPKIDLYVRR 300
PWYIQGAASPKDMLILVDVSGVSGLTILKLI RTSVSEMLETSLDSDDFNVASFNNSAQD 300
PWYIQGAASPKDMLILVDVSGVSGLTILKLI RTSVSEMLETSLDSDDFNVASFNNSAQD 300

301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKGFSAFQELNNVNSRANCKI
301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKGFSAFQELNNVNSRANCKI
361 FTDGGEERAQBEI FNKYNKDKKVRFRFSVGOHNYERGPIONMACENKGYIYEI PSIG
361 FTDGGEERAQBEI FNKYNKDKKVRFRFSVGOHNYERGPIONMACENKGYIYEI PSIG
421 INTOEYLDVLRPMVLADGKAKQVQMTNVLDALELGLVITGLTPVFNITQGFENKT
421 INTOEYLDVLRPMVLADGKAKQVQMTNVLDALELGLVITGLTPVFNITQGFENKT
481 NQILIGVMGVDSLEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHNPLOPKNPKSQE
481 NQILIGVMGVDSLEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHNPLOPKNPKSQE
541 DFLDALENDIKVEIRNKMIDGESGEKTRFTLVKSODERYIDKGNRTYTWTPVNGTI
541 DFLDALENDIKVEIRNKMIDGESGEKTRFTLVKSODERYIDKGNRTYTWTPVNGTI
601 ALVLPYVSFYIYI KAKLEETITQARSKKGMKDSSETLKPDNFEESGYTFIAPRDYCN
601 ALVLPYVSFYIYI KAKLEETITQARSKKGMKDSSETLKPDNFEESGYTFIAPRDYCN
661 SDNNTTELLANFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKG
661 SDNNTTELLANFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKG
721 FVWTDGGITRVYVPKEAGENWQENPETEYDSFKRSLDNDNYVFTAPYFNKSGPGAI
721 FVWTDGGITRVYVPKEAGENWQENPETEYDSFKRSLDNDNYVFTAPYFNKSGPGAI
781 MVSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENTFTKTSIRDPKAGPVCDCRNSDVI
781 MVSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENTFTKTSIRDPKAGPVCDCRNSDVI
841 LDGCGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVTAFNKSVDYQSVCEPGA
841 LDGCGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVTAFNKSVDYQSVCEPGA
901 GAGHRSAYVPSVADILQIGWATAAASIILOQFLLSLTFPRLLAEVEMEDDDFTFA
901 GAGHRSAYVPSVADILQIGWATAAASIILOQFLLSLTFPRLLAEVEMEDDDFTFA
961 SCITEQTOYFFDNDKSFSGVLDGNCNCSRI FHGEKLMNTNLI FIMVESKGTCPCI
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RESULT 11
US-10-090-827-7
; Sequence 7, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 s
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-090-827-7
Query Match 98.9%; Score 5288; DB 14; Length 1036;
Best Local Similarity 98.8%; Pred. No. 0;

;	Sequence 8.	Application	US/10090827
;	Publication	No.	US20030073132A1
;	GENERAL INFORMATION:		
;	APPLICANT:	Warner-Lambert	
;	BEST Local Similarity	Method for the screening of alpha 2 delta-1 su	
;	TITLE OF INVENTION:	binding ligands	
;	FILE REFERENCE:	179	
;	CURRENT APPLICATION NUMBER:	US/10/090,827	
;	CURRENT FILING DATE:	2002-03-06	
;	PRIOR APPLICATION NUMBER:	US/09/397,549	
;	PRIOR FILING DATE:	1999-09-16	
;	NUMBER OF SEQ ID NOS:	21	
;	SOFTWARE:	PatentIn Ver. 2.1	
;	SEQ ID NO 8		
;	LENGTH:	1063	
;	TYPE:	PRT	
;	ORGANISM:	Sus scrofa	
;	US-10-090-827-8		
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	Best Local Similarity	98.8%;	Pred. No. 0;
	Matches 1006;	Conservative	5; Mismatches 7; Indels 0;
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Db	1	MAAGCLLALTLFOSLILIGSSSEPPESVATIKSWVDKMQQEDLVTLAKTASGV	
Qy	61	YEKYQDLYTVEPNNAQQLVEAARDIEKLLSNRSKALVSLAEAEKVQAAHQWRI	
Db	61	YEKYQDLYTVEPNNAQQLVEAARDIEKLLSNRSKALVRLAEAEKVQAAHQWRI	
Qy	121	EVVYYNKADDLPEKNDSEPGSQRIKPVFIEDANFGROI SQYQHAHAVHPTDIYE	
Db	121	EVVYYNKADDLPEKNDSEPGSQRIKPVFIEDANFGROI SQYQHAHAVHPTDIYE	
Qy	181	NELNWTSSALDEVFKKRRDEPSLLMQVFGSATGLARYYPASPWDNSRTPNKID	
Db	181	NELNWTSSALDEVFKKRRDEPSLLMQVFGSATGLARYYPASPWDNSRTPNKID	
Qy	241	RPWYIQGAASPDKMLILVDVSGVSGLTCLKIRTSVSEMLFTLSDDDFVNVASF	
Db	241	RPWYIQGAASPDKMLILVDVSGVSGLTCLKIRTSVSEMLFTLSDDDFVNVASF	
Qy	301	VSCFQLVQANVRNKKVLXDAVNNITAKGITDYKKGFSFAPEQLLNVNVRANC	
Db	301	VSCFQLVQANVRNKKVLXDAVNNITAKGITDYKKGFSFAPEQLLNVNVRANC	
Qy	361	FTDGGERAQEIFNKYNDKKYRVFRFSVQGHNYERGP IQMWACENKGYGYEIP	
Db	361	FTDGGERAQEIFAKYNDKKYRVFTFSVQGHNYDRGP IQMWACENKGYGYEIP	
Qy	421	INTQEYLDVLRPMVLADKAKQVQNTVYLDALHLGLVITGTLPVFNITGQFE	
Db	421	INTQEYLDVLRPMVLADKAKQVQNTVYLDALHLGLVITGTLPVFNITGQNE	
Qy	481	NQLILGVMGVDVLSLEIDIKRLTPRFTLCPNGYFADIPNGYVLLHNPLOPKNPKS	
Db	481	NQLILGVMGVDVLSLEIDIKRLTPRFTLCPNGYFADIPNGYVLLHNPLOPKNPKS	
Qy	541	DFLDAELENDIKVEIRNKMIDGESSEKTRFTLVKSQDERYIDKGNRTYTWTPVN	
Db	541	DFLDAELENDIKVEIRNKMIDGESSEKTRFTLVKSQDERYIDKGNRTYTWTPVN	
Qy	601	ALVLPYTSFYFYIKAKLEETITQARSKGKKQKQSETLKPONFRESGVTFTIAPRDY	
Db	601	ALVLPYTSFYFYIKAKLEETITQARSKGKKQKQSETLKPONFRESGVTFTIAPRDY	
Qy	661	SDNNTEFLNFNSEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQVWSKQKNI	
Db	661	SDNNTEFLNFNSEFIDRKTNNPNSCNTDLINRVLLDAGFTNELVQVWSKQKNI	
Qy	721	FWVTDGGITRYVYPKEAGENQENPETYVESFYKRSIDNNYVFTAPYFNKSGPE	

VTDGIIIVYVYKKEAGENWQENPETYEDSFYKRSLDNDNDYVFTAPYFNKSGPGAYESGI 780
 SKAVEIYIOGKLLKPAVVGIGKIDVNSWENFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840
 SKAVEIYIOGKLLKPAVVGIGKIDVNSWENFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840
 DGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPAGAPKQ 900
 DGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPAGAPKQ 900
 GHRSAIVPSVADILQIGMWATAAAWSILQQFLSLTPRLEAVEMEDDDFTASLSKQ 960
 GHRSAIVPSIADILHIGMWATAAAWSILQQFLSLTPRLEAVEMEDDDFTASLSKQ 960
 TTEOTQYFFDNDKSFSGVLDGNCGRIFHVEKLMNTNLIIFIMVESKGTCPDTRL 1018
 TTEOTQYFFDNDKSFSGVLDGNCGRIFHVEKLMNTNLIIFIMVESKGTCPDTRL 1018
 Application US/10090827
 . US20030073132A1
 rner-Lambert
 ACTION: Method for the screening of alpha 2 delta-1 subunit
 ACTION: binding ligands
 E: 179
 ACTION NUMBER: US/10/090,827
 IG DATE: 2002-03-06
 ACTION NUMBER: US/09/397,549
 DATE: 1999-09-16
 ID NOS: 21
 entin Ver. 2.1
 is scrofa
 98.9%; Score 5288; DB 14; Length 1069;
 ilarity 98.8%; Pred. No. 0;
 Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 AGCLLALTLTQSLIGSSPEPPSAVTIKSWDKMQEDLVTLAKTASGWNQVLDI 60
 AGCLLALTLTQSLIGSSPEPPSAVTIKSWDKMQEDLVTLAKTASGWNQVLDI 60
 KYQDLYTVEPNARQVLAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDPASN 120
 KYQDLYTVEPNARQVLAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDPASN 120
 VYNNKADLDPEKNSPEGSQRIKPVFTEDANFGQISYQHAHVHIPTDIYEGSTIVL 180
 VYNNKADLDPEKNSPEGSQRIKPVFTEDANFGQISYQHAHVHIPTDIYEGSTIVL 180
 3LNTSALDVFVKNEEDPSILQVFGSATGLARYYPASPWVDNSRTNPKIDLYDVR 240
 3LNTSALDVFVKNEEDPSILQVFGSATGLARYYPASPWVDNSRTNPKIDLYDVR 240
 PWYIQGAASPKDMLILVDVSGVSGLTFLKIRTSVSEMLETLDSDDPVNVASFNNAQD 300
 PWYIQGAASPKDMLILVDVSGVSGLTFLKIRTSVSEMLETLDSDDPVNVASFNNAQD 300
 SCFOHLVQANVRNKKVLKDAVNNITAGKITDYKGFSAFEQLLNNVNSANCNKIIML 360
 SCFOHLVQANVRNKKVLKDAVNNITAGKITDYKGFSAFEQLLNNVNSANCNKIIML 360
 TDGGEERAQELFNKYNKDKVRVPRFVSGOHNHYERGPIQWACENKGYEIEPSIGAIR 420
 TDGGEERAQELFNKYNKDKVRVPRFVSGOHNHYERGPIQWACENKGYEIEPSIGAIR 420
 NTQBYLDVLRPMVLADGKAKQVQWNTVYLDALGLVITGTLPVFNITQGFENKTNLK 480

Db 421 INTQBYLDVLRPMVLADGKAKQVQWNTVYLDALGLVITGTLPVFNITQGFENKTNLK 480
 QY 481 NOLILGWGVDVSLIEDIKRLTPRFTLCBNGYVFAIDPBGVLLHNPLOPKNPKS 480
 Db 481 NOLILGWGVDVSLIEDIKRLTPRFTLCBNGYVFAIDPBGVLLHNPLOPKNPKS 480
 QY 541 DFLDAELENDIKVELIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTWTPVN 541
 Db 541 DFLDAELENDIKVELIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTWTPVN 541
 QY 601 ALVLPYSPYIYKAKLETTITQARSKGKMKDSEITLKPDPFESGTYFTAPRDY 601
 Db 601 ALVLPYSPYIYKAKLETTITQARSKGKMKDSEITLKPDPFESGTYFTAPRDY 601
 QY 661 SONNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNVLVQYWSKQKNI 661
 Db 661 SONNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNVLVQYWSKQKNI 661
 QY 721 FVVTDGIIIVYVYKKEAGENWQENPETYEDSFYKRSLDNDNDYVFTAPYFNKSGPC 721
 Db 721 FVVTDGIIIVYVYKKEAGENWQENPETYEDSFYKRSLDNDNDYVFTAPYFNKSGPC 721
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 Db 781 MYSKAVEIYIOGKLLKPAVVGIGKIDVNSWENFTKTSIRDPKAGPVCDCKRNSI 781
 QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEI 841
 Db 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEI 841
 QY 901 GAGHRSAIVPSVADILQIGMWATAAAWSILQQFLSLTPRLEAVEMEDDDFT 901
 Db 901 GAGHRSAIVPSIADILHIGMWATAAAWSILQQFLSLTPRLEAVEMEDDDFT 901
 QY 961 SCITEQYFFDNDKSFSGVLDGNCGRIFHVEKLMNTNLIIFIMVESKGTCP 961
 Db 961 SCITEQYFFDNDKSFSGVLDGNCGRIFHVEKLMNTNLIIFIMVESKGTCP 961
 RESULT 14
 US-10-090-827-5
 ; Sequence 5, Application US/10090827
 ; Publication No. US20030073132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert
 ; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 ;
 ; TITLE OF INVENTION: binding ligands
 ; FILE REFERENCE: 179
 ; CURRENT APPLICATION NUMBER: US/10/090,827
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US/09/397,549
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 1091
 ; TYPE: PRT
 ; ORGANISM: Sus scrofa
 US-10-090-827-5
 Query Match 98.9%; Score 5288; DB 14; Length 1091;
 Best local Similarity 98.8%; Pred. No. 0;
 Matches 1006; Conservative 5; Mismatches 7; Indels 0;
 QY 1 MAAGCLLALTLTQSLIGSSPEPPSAVTIKSWDKMQEDLVTLAKTASG 1
 Db 1 MAAGCLLALTLTQSLIGSSPEPPSAVTIKSWDKMQEDLVTLAKTASG 1
 QY 61 YEKYQDLYTVEPNARQVLAARDIEKLLSNRSKALVSLALEAEKVQAAHQW 61
 Db 61 YEKYQDLYTVEPNARQVLAARDIEKLLSNRSKALVSLALEAEKVQAAHQW 61

KDLDPEKNDSEPGSQRKPVFIEDANFGRIQISYQHAHVHPTDIYEGSTIVL 180
PRIOR FILING DATE: 1995-05-25
PRIOR APPLICATION NUMBER: 08/404,354
PRIOR FILING DATE: 1995-02-15
PRIOR APPLICATION NUMBER: 07/914,231
PRIOR FILING DATE: 1992-07-13
PRIOR APPLICATION NUMBER: 08/314,083
PRIOR FILING DATE: 1994-09-28
PRIOR APPLICATION NUMBER: 07/914,231
PRIOR FILING DATE: 1992-07-13
PRIOR APPLICATION NUMBER: 07/603,751
PRIOR FILING DATE: 1990-11-09
PRIOR APPLICATION NUMBER: 08/290,012
PRIOR FILING DATE: 1994-08-11
PRIOR APPLICATION NUMBER: 08/149,097
PRIOR FILING DATE: 1993-11-05
PRIOR APPLICATION NUMBER: 08/105,536
PRIOR FILING DATE: 1993-08-11
PRIOR APPLICATION NUMBER: 08/149,097
PRIOR FILING DATE: 1993-11-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 1103
TYPE: PRT
ORGANISM: Human
US-10-375-253-47

1 MAAGCLLALTLTFLQSLILGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQ
1 MAAGCLLALTLTFLQSLILGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQ
61 YEKYQDLTYVEPNNAQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWRED
61 YEKYQDLTYVEPNNAQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWRED
121 EVVYNAKDDLDPKNDSEPGSQRIKEVFEJEDANFGRIQISYQHAHVHPTDIYEGS
121 EVVYNAKDDLDPKNDSEPGSQRIKEVFEJEDANFGRIQISYQHAHVHPTDIYEGS
181 NELNWTSAIDVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLI
181 NELNWTSAIDVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLI
241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRISVSSEMLETLSDDDFVNVASFNI
241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRISVSSEMLETLSDDDFVNVASFNI
301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNINVSANCN
301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNINVSANCN
361 FTDGGERAQEIENKYNKDKKVRVFRFSVQHNHYERGPQIMMACENKGYIYEIIPS
361 FTDGGERAQEIENKYNKDKKVRVFRFSVQHNHYERGPQIMMACENKGYIYEIIPS
421 INTQEVLDVLRGPMVLADGKAKOVQNTVYLDALGLVITGTLPVFNITQGFEN
421 INTQEVLDVLRGPMVLADGKAKOVQNTVYLDALGLVITGTLPVFNITQGFEN
481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHNPQLQPKPIGY
481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHNPQLQPKPIGY
531 -----NFKSOEPTVTLDFDAELENDDIKVEIRNKMIDGESGEKTFRTLVKS
541 LRKRPNQONPKSQBPVTLDFDAELENDDIKVEIRNKMIDGESGEKTFRTLVKS
582 DKGNTYTWTPVNGTDSIALVLPYISFYIYKAKLEETITQARSKKGMKDSET

Application US/10375253
US20040018510A1
INVENTOR: SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
ATTORNEY: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
E: SD9813DA
CATION NUMBER: US/10/375,253
G DATE: 2003-02-27
TION NUMBER: 08/450,273

Query Match 98.6%; Score 5270; DB 15; Length 1103;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1010; Conservative 1; Indels 26; G:
QY 1 MAAGCLLALTLTFLQSLILGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQ
Db 1 MAAGCLLALTLTFLQSLILGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQ
QY 61 YEKYQDLTYVEPNNAQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWRED
Db 61 YEKYQDLTYVEPNNAQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWRED
QY 121 EVVYNAKDDLDPKNDSEPGSQRIKEVFEJEDANFGRIQISYQHAHVHPTDIYEGS
Db 121 EVVYNAKDDLDPKNDSEPGSQRIKEVFEJEDANFGRIQISYQHAHVHPTDIYEGS
QY 181 NELNWTSAIDVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLI
Db 181 NELNWTSAIDVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLI
QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRISVSSEMLETLSDDDFVNVASFNI
Db 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRISVSSEMLETLSDDDFVNVASFNI
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNINVSANCN
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNINVSANCN
QY 361 FTDGGERAQEIENKYNKDKKVRVFRFSVQHNHYERGPQIMMACENKGYIYEIIPS
Db 361 FTDGGERAQEIENKYNKDKKVRVFRFSVQHNHYERGPQIMMACENKGYIYEIIPS
QY 421 INTQEVLDVLRGPMVLADGKAKOVQNTVYLDALGLVITGTLPVFNITQGFEN
Db 421 INTQEVLDVLRGPMVLADGKAKOVQNTVYLDALGLVITGTLPVFNITQGFEN
QY 481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHNPQLQPKPIGY
Db 481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHNPQLQPKPIGY
QY 531 -----NFKSOEPTVTLDFDAELENDDIKVEIRNKMIDGESGEKTFRTLVKS
Db 541 LRKRPNQONPKSQBPVTLDFDAELENDDIKVEIRNKMIDGESGEKTFRTLVKS
QY 582 DKGNTYTWTPVNGTDSIALVLPYISFYIYKAKLEETITQARSKKGMKDSET

us-10-090-827-13.rapb

6:26:17 2004

|||||
TYTWPVNGIDYSLALVLPYTSFYIYKAKLEETITQARY-----SETLKPDNF 653
TFIAPROYCNDLKI SDNNTTELLNFNEFIDRKTNNPSCNADLINRVLLDAGFTN 701
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YWSKKNIKGVKARFVVTDDGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNY 761
YWSKKNIKGVKARFVVTDDGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNY 773
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YFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRD 833
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YDQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTEPR 953
VEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGNCNCSRI FHGEKLMNTNL 1001
VEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGNCNCSRI FHGEKLMNTNL 1013
WESKGTCECDTRL 1018
WESKGTCECDTRL 1030

March 17, 2004, 20:26:51
: secs

GenCore version 5.1.6
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in search, using sw model

February 20, 2004, 16:51:31 ; Search time 37,2255 Seconds
(without alignments)
7181.696 Million cell updates/sec

3-10-090-827-14

143
MAAGCCLLTLTLFQSLIG.....RLLIQAQTSQGNPCDMVK 1036

LOSUM62

apop 10.0 , Gapext 0.5

30525 seqs, 258052604 residues

its satisfying chosen parameters: 830525

ngth: 0

ngth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SPTREMBL 23:*

: sp_archaea:*

: sp_bacteria:*

: sp_fungi:*

: sp_human:*

: sp_invertebrate:*

: sp_mammal:*

: sp_mhc:*

: sp_organelle:*

: sp_phase:*

: sp_plant:*

: sp_rodent:*

: sp_virus:*

: sp_vertebrate:*

: sp_unclassified:*

: sp_rvirus:*

: sp_bacteria:*

: sp_archaeap:*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query Match	Length	DB	ID	Description
99.4	1110	4	Q9UIU0	Q9uiU0 homo sapien
98.8	1091	6	O77773	O77773 aus scrofa
97.2	1091	11	Q9ERS3	Q9ers3 rattus norv
96.1	1084	11	O8CFG7	O8cfg7 rattus norv
96.0	1103	11	O08532	O08532 mus musculu
95.4	1079	11	O8VHS9	O8vhs9 rattus norv
67.4	745	4	Q9UDQ3	Q9udq3 homo sapien
54.2	1150	4	Q9NY47	Q9ny47 homo sapien
53.7	1157	11	O8CFG6	O8cfg6 rattus norv
53.7	1143	4	Q9NY48	Q9ny48 homo sapien
53.6	1156	11	Q9EQG2	Q9eqg2 mus musculu
53.6	1148	11	O8CGR8	O8cgr8 mus musculu
53.4	1145	4	Q9Y268	Q9y268 mus sapien
53.2	1098	11	O8CHE9	O8che9 mus musculu
53.2	1084	11	Q920H6	Q920h6 mus musculu
53.0	1076	4	Q9UEW0	Q9uew0 homo sapien

17	2717	49.9	975	4	Q9NSA6	Q9nsa6 hom
18	1090	20.0	1085	11	O8CFG5	O8cfg5 ral
19	1085	19.9	1091	11	Q9Z1L5	Q9z1l5 mu
20	1084	19.9	1091	4	O8IZS8	O8izs8 hom
21	1063	19.5	1120	4	O8IZS9	O8izs9 hom
22	1015	18.6	997	4	Q9NY16	Q9ny16 hom
23	1007	18.5	1218	5	O9V6T7	O9v6t7 dro
24	982.5	18.1	1170	5	O8IP22	O8ip22 dro
25	929.5	17.1	2190	5	Q9VJM0	Q9vjm0 dro
26	886	16.3	1255	5	Q9NK83	Q9nk83 dro
27	877	16.1	1120	5	Q9VJN7	Q9vjn7 dro
28	875	16.1	170	4	Q9UDL7	Q9udl7 hom
29	738.5	13.6	519	4	Q9NY18	Q9ny18 hom
30	658	12.1	317	11	Q920H5	Q920h5 mu
31	572	10.5	1148	5	O17517	O17517 cae
32	539.5	9.9	942	5	Q9SR75	Q9sr75 dro
33	526.5	9.7	394	13	Q8AVY7	O8avy7 xe
34	514.5	9.5	104	4	Q9UD81	Q9ud81 hor
35	506	9.3	100	6	Q9GLH1	Q9glh1 bos
36	498.5	9.2	121	4	Q9UD82	Q9ud82 hor
37	482	8.9	98	4	Q9UDU5	Q9udu5 hor
38	465	8.5	97	4	Q9UD80	Q9ud80 hor
39	459	8.4	100	11	O8C6Y3	O8c6y3 ml
40	402	7.4	77	4	O95026	O95026 hor
41	365.5	6.7	223	11	O9R142	O9r142 ml
42	337.5	6.2	1185	4	O9HCJ9	O9hcj9 hor
43	231	4.2	978	6	Q95KE0	Q95ke0 mac
44	227	4.2	43	6	O8HYX0	O8hyx0 bof
45	223	4.1	1449	5	Q9V917	Q9v917 drt

ALIGNMENTS

RESULT 1

Q9UIU0	PRELIMINARY;	PRT: 1110 AA.
ID	Q9UIU0	
AC	Q9UIU0;	
DT	01-MAY-2000 (Tremblrel. 13, Created)	
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)	
DT	01-MAY-2000 (Tremblrel. 20, Last annotation update)	
DE	Dihydropyridine receptor alpha 2 subunit.	
GN	CACNA2D1.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]_	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20005942; PubMed=10534405;	
RA	Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;	
RT	"Genomic structure and functional expression of a human alpha(2	
RT	calcium channel subunit gene (CACNA2).";	
RL	Genomics 61:201-209(1999).	
DR	EMBL; AF083854; AAF03259.1;	JOINED.
DR	EMBL; AF083817; AAF03259.1;	JOINED.
DR	EMBL; AF083818; AAF03259.1;	JOINED.
DR	EMBL; AF083819; AAF03259.1;	JOINED.
DR	EMBL; AF083820; AAF03259.1;	JOINED.
DR	EMBL; AF083821; AAF03259.1;	JOINED.
DR	EMBL; AF083822; AAF03259.1;	JOINED.
DR	EMBL; AF083823; AAF03259.1;	JOINED.
DR	EMBL; AF083824; AAF03259.1;	JOINED.
DR	EMBL; AF083825; AAF03259.1;	JOINED.
DR	EMBL; AF083826; AAF03259.1;	JOINED.
DR	EMBL; AF083827; AAF03259.1;	JOINED.
DR	EMBL; AF083828; AAF03259.1;	JOINED.
DR	EMBL; AF083829; AAF03259.1;	JOINED.
DR	EMBL; AF083830; AAF03259.1;	JOINED.
DR	EMBL; AF083831; AAF03259.1;	JOINED.
DR	EMBL; AF083832; AAF03259.1;	JOINED.
DR	EMBL; AF083833; AAF03259.1;	JOINED.
DR	EMBL; AF083834; AAF03259.1;	JOINED.

[illegible][illegible]

501	Db	DKGNRTYTWTPVNGTDYSIALVLETPYSFYIKAKLJLII
642	QY	BESGYTIIAPRDYCNDLKI SDNNTEFLNFNEFIDRKT PNNPCSNADLINRVLLDAG
661	Db	BESGYTIIAPRDYCNDLKI SDNNTEFLNFNEFIDRKT PNNPCSNADLINRVLLDAG
702	QY	ELVQNYNSKQKNIKGVKARFVVTDGGITRVYPKAGENQWENPETYEDSFYKRSLDN
721	Db	ELVQNYNSKQKNIKGVKARFVVTDGGITRVYPKAGENQWENPETYEDSFYKRSLDN
762	QY	VFTAPYFNKSGPAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENTKTSI
781	Db	VFTAPYFNKSGPAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENTKTSI
822	QY	CAGPVCDCXKNSDVMDCVILDDGGFLLMANHDDYTNOIGRPFGEIDPSLMRLHVLNI
841	Db	CAGPVCDCXKNSDVMDCVILDDGGFLLMANHDDYTNOIGRPFGEIDPSLMRLHVLNI
882	QY	FNKSXDYQSVCEPGAAPKQAGHSAYVPSVADILQIGMWATAAWSILQQFLLSL
901	Db	FNKSXDYQSVCEPGAAPKQAGHSAYVPSVADILQIGMWATAAWSILQQFLLSL
942	QY	LLBAVENEDDDFTASLSKQSCITTEQTYRPFDDNSKSFSGVLDGNCNSRI FPHGKLM
961	Db	LLBAVENEDDDFTASLSKQSCITTEQTYRPFDDNSKSFSGVLDGNCNSRI FPHGKLM
1002	QY	IFIMVBSKGTCPCDTRLIIQAEQTS DGNPCDMVK 1036
1021	QY	IFIMVBSKGTCPCDTRLIIQAEQTS DGNPCDMVK 1055

RESULT 2	OT7773	PRELIMINARY;	PRT; 1091 AA.
ID	OT7773		
AC	077773;		
DT	01-NOV-1998 (TReMBUrel. 08, Created)		
DT	01-NOV-1998 (TReMBUrel. 08, Last sequence update)		
DT	01-OCT-2002 (TReMBUrel. 22, Last annotation update)		
DE	Voltage-dependent calcium channel alpha-2 delta subunit		
DE	precursor.		
DE	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OC	NCBI_TaxID=9823;		
FN	[1]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Brain cortex;		
RC	MEDLINE=98411353; PubMed=9738015;		
EX	Brown J.P., Gee N.S.;		
RA	"Cloning and deletion mutagenesis of the alpha2 delta calcium cl		
RT	subunit from porcine cerebral cortex. Expression of a soluble f		
RT	the protein that retains [3H]gabapentin binding activity.";		
RL	J. Biol. Chem. 273:25458-25465(1998).		
DR	EMBL; AF077665; AAC36289.1; -.		
DR	InterPro; IPR004010; Cache.		
DR	InterPro; IPR002035; VWF_A.		
DR	Pfam; PF02743; Cache; 1.		
DR	Pfam; PF00092; vwa; 1.		
DR	SMART; SMO0327; VWA; i.		
DR	PROSITE; PS50234; VWFA; 1.		
KW	Signal.		
FT	SIGNAL	1 24	POTENTIAL.
FT	CHAIN	25 1091	VOLTAGE-DEPENDENT CALCIUM CHANNEL
FT			DELTA SUBUNIT.
SO	SEQUENCE	1091 AA; 123150 MW; 293DDC7EBE9EE60E CRC64;	

Query Match 98.8%; Score 5380; DB 6; Length 1000
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1023; Conservative 6; Mismatches 7; Indels 0;
1 MAAGCLLALTLTLFQSLILGPSSEFFPPSAVIKSNVDKMQEDLVLTAKTASG

ID	Q9ERS3	PRELIMINARY;	PRT;	1091	AA.
RC	Q9ERS3:				
01-MAR-2001	(TrEMBLrel. 16, Created)				
01-MAR-2001	(TrEMBLrel. 16, Last sequence update)				
01-JUN-2002	(TrEMBLrel. 21, Last annotation update)				
DE	Voltage-gated calcium channel alpha2/delta-1 subunit.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ratt				
OX	NCBI_TaxID=10116;				
OX	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Sprague-Dawley; TISSUE=Superior cervical ganglion;				
RP	Lin Y., Lipscombe D.;				
RA	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.				
RL	EMBL; AF286488; RAG28164.1; --				
DR	InterPro; IPR004010; Cache.				
DR	InterPro; IPR002035; VWF_A.				
DR	Pfam; PF02743; Cache; 1.				
DR	Pfam; PF00092; vwa; 1.				
DR	SMART; SM00327; VWA; 1.				
DR	PROSITE; PS02234; VWFA; 1.				
DR	VARIANT 209 212	GSAT -> AADR.			
FT	VARIANT 338 338	S -> T.			
FT	VARIANT 599 600	SL -> RY.			
FT	VARIANT 869 869	S -> R.			
FT	SEQUENCE 1091 AA; 123467 MW; C155088971628E19 CRC64;				
SQ					
	Query Match	97.2%;	Score 5291;	DB 11;	Length 1091;
	Best Local Similarity	96.4%;	Pred. No. 0;		
	Matches 999;	Conservative 22;	Mismatches 15;	Indels 0;	
QY	1	MAAGCLLALTTLFQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVN			
DB	1	MAAGCLLALTTLFQSLIGPSSEPPPSVPTIKSWDKMQEDLVTLAKTASGVY			
QY	61	YEKYQDLTYVFNNAQVLVEIARAARDIEKLNSRKALVSLAEKVKQAHHQWREI			
DB	61	YEKYQDLTYVFNNAQVLVEIARAARDIEKLNSRKALVRLAMEAEKVAQAHHQWRE			
QY	121	EVVYVNAKDDLPKNDSPGSGRIKPVIEDANFGRQISYQAAVHIPTDIYEG			
DB	121	EVVYVNAKDDLPERNESGSGRIKPVIEDANFGRQISYQAAVHIPTDIYEG			
QY	181	NELNWTLSALDEVFKRNEBDDPSLLMQVFSATGLARYYPASPWDNSRTPNKIDI			
DB	181	NELNWTLSALDEVFKRNRDEPTLLQVFGSATGLARYYPASPWDNSRTPNKIDI			
QY	241	RPWTYQGAASPQDMLILVDVSGVSGVGLTKLIRTSVSEMLETLSDDDFVNVSFT			
DB	241	RPWTYQGAASPQDMLILVDVSGVSGVGLTKLIRTSVSEMLETLSDDDFVNVSFT			
QY	301	VSCFQHLVQAVNRNKKVLDVANNITAKGTDYKKGFSFAFQQLNLYNVSRAHCI			
DB	301	VSCFQHLVQAVNRNKKVLDVANNITAKGTDYKKGFSFAFQQLNLYNVSRAHCI			
QY	361	FTDGGEERAQBEIFNKYNKKVRVFRSVGHNVERGPIQWMAENKGYGYEIP			
DB	361	FTDGGEERAQBEIFAKYNKKVRVFTFSVQHNVDGPIQWMAENKGYGYEIP			
QY	421	INTQBYLDVLGHPMWLAGDKAQVQWNTVNYLDALGLVITGTLPVFNITGQFE			
DB	421	INTQBYLDVLGHPMWLAGDKAQVQWNTVNYLDALGLVITGTLPVFNITGQFE			
QY	481	NQLILGVMGVDSLEDIKELTPRFTLCPNGYFFALDPNGYVLLHPNLQPKNPKS			
DB	481	NQLILGVMGVDSLEDIKELTPRFTLCPNGYFFALDPNGYVLLHPNLQPKNPKS			
QY	541	DFLDLAELENDIKVEIRNKMIDEGSGEKFTLVKSQDERYIDKGNRITYTWTPTV			
DB	541	DFLDLAELENDIKVEIRNKMIDEGSGEKFTLVKSQDERYIDKGNRITYTWTPTV			
QY	601	ALVLPYTSFYIYKALEETITQARSKKGMQKQSETLKPONFRESGYTFFIAPRDI			

LALTLTLFQSLLLGPSQEPFSAVITKSWWDQWQEDLVTLAKTASGVNQLVDI 60
 LYTVEPNNARQLVEIAARDIEKLLSNRSKALVSLALEAKSVQAAHQWREDFASN 120
 LYTVEPNNARQLVEIAARDIEKLLSNRSKALVELALEAKSVQAAHQWREDFASN 120
 LYTVEPNNARQLVEIAARDIEKLLSNRSKALVELALEAKSVQAAHQWREDFASN 180
 NAKDLDLPEKNDSEFGSORIKPVFIEDANFGRQISYQHAAVHIPTDIYEGSTIVL 180
 NAKDLDLPEKNDSEFGSORIKPVFIEDANFGRQISYQHAAVHIPTDIYEGSTIVL 180
 TSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWDSRPNKIDLYDVER 240
 TSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWDSRPNKIDLYDVER 240
 TSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWDSRPNKIDLYDVER 240
 QGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFNVVASFNSNAQD 300
 QGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFNVVASFNSNAQD 300
 QGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFNVVASFNSNAQD 300
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 JHLVQANVRNKVLDKDAVNNTAKGITYKKGFSFAFEQLLNVNVRANCKIIML 360
 JHLVQANVRNKVLDKDAVNNTAKGITYKKGFSFAFEQLLNVNVRANCKIIML 360
 J3ERAQEIFPNKYNKDKKVRVFRFSYQGHNYERGPIMQMACENKGYIIEISGAIR 420
 J3ERAQEIFPNKYNKDKKVRVFRFSYQGHNYERGPIMQMACENKGYIIEISGAIR 420
 J3ERAQEIFPAKNKDKKVRVFRFSYQGHNYDRGPIMQMACENKGYIIEISGAIR 420
 EYLDVLGRPMVLADKAKQVQNTVYLDALGLVITGTLVPFNITGQFNKTNLK 480
 EYLDVLGRPMVLADKAKQVQNTVYLDALGLVITGTLVPFNITGQFNKTNLK 480
 EYLDVLGRPMVLADKAKQVQNTVYLDALGLVITGTLVPFNITGQFNKTNLK 480
 LGWGVQDVLSLEDKRLTPRTPLCPNGYYFPAIDPNGVYLLHPLNPKNPKSQEPVTL 540
 LGWGVQDVLSLEDKRLTPRTPLCPNGYYFPAIDPNGVYLLHPLNPKNPKSQEPVTL 540
 LGWGVQDVLSLEDKRLTPRTPLCPNGYYFPAIDPNGVYLLHPLNPKNPKSQEPVTL 540
 JAELENDIKVBI RNKMIDGESGKTRFLVKSQDERVIDKGNRTYTPWNGTDYSL 600
 JAELENDIKVBI RNKMIDGESGKTRFLVKSQDERVIDKGNRTYTPWNGTDYSL 600
 JAELENDIKVBI RNKMIDGESGKTRFLVKSQDERVIDKGNRTYTPWNGTDYSL 600
 JPTYSFYIYIKALBETITQARSKKGKMDSETLXPDNPFESGYTPIAPRDYCNLDKI 660
 JPTYSFYIYIKALBETITQARSKKGKMDSETLXPDNPFESGYTPIAPRDYCNLDKI 660
 JPTYSFYIYIKALBETITQARSKKGKMDSETLXPDNPFESGYTPIAPRDYCNLDKI 660
 NTEFLNLFNEFIDRKTNNPNSCNADLINRVLDDAGFTNELVQNTWSKQXKIKGVYKAR 720
 NTEFLNLFNEFIDRKTNNPNSCNADLINRVLDDAGFTNELVQNTWSKQXKIKGVYKAR 720
 NTEFLNLFNEFIDRKTNNPNSCNADLINRVLDDAGFTNELVQNTWSKQXKIKGVYKAR 720
 TDGGITRVVPKEAGENQENPETIYEDSFYKRSLDNDNVYTFAPYFNKSGPAYESGI 780
 TDGGITRVVPKEAGENQENPETIYEDSFYKRSLDNDNVYTFAPYFNKSGPAYESGI 780
 TDGGITRVVPKEAGENQENPETIYEDSFYKRSLDNDNVYTFAPYFNKSGPAYESGI 780
 KAVEIYITQGLKLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCCKKNSDVMDCVI 840
 KAVEIYITQGLKLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCCKKNSDVMDCVI 840
 KAVEIYITQGLKLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCCKKNSDVMDCVI 840
 JGGFLLMANHDDYTYNQIGRFFGEDIPLSLMRHLVNI SVYAFNKSVDYQSVCEPAAKQ 900
 JGGFLLMANHDDYTYNQIGRFFGEDIPLSLMRHLVNI SVYAFNKSVDYQSVCEPAAKQ 900
 JGGFLLMANHDDYTYNQIGRFFGEDIPLSLMRHLVNI SVYAFNKSVDYQSVCEPAAKQ 900
 J3RSAYVPSVADILQIGWATAAASWIIQQFLLSTTPPRLLEAVEMEDDDPTASLSKQ 960
 J3RSAYVPSVADILQIGWATAAASWIIQQFLLSTTPPRLLEAVEMEDDDPTASLSKQ 960
 J3RSAYVPSVADILQIGWATAAASWIIQQFLLSTTPPRLLEAVEMEDDDPTASLSKQ 960
 JTBQCYFFDNDSKSFSGVLDGCGNSRI FPHGKLMNTNLI F1WVESKGTCPCDTRLII 1020
 JTBQCYFFDNDSKSFSGVLDGCGNSRI FPHGKLMNTNLI F1WVESKGTCPCDTRLII 1020
 JTBQCYFFDNDSKSFSGVLDGCGNSRI FPHGKLMNTNLI F1WVESKGTCPCDTRLII 1020
 JEQTSQGNPCDMYK 1036
 JEQTSQGNPCDMYK 1036
 JEQTSQGNPCDMYK 1036

241	QY	RPHYIOGAASP	KDMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFNVNVAFSN
241	Db	RPHYIOGAASP	KDMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFNVNVAFSN
301	QY	VSCFOHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFEQOLLNNTSVRANCNK	
301	Db	VSCFOHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFEQOLLNNTSVRANCNK	
361	QY	PTDGGERRAQEIKENKNDKKVRVPRFSVGQHYNERGPIOMWACENKGYIYEIPSI	
361	Db	PTDGGERRAQEIPAKNKDKKVRVTFFSVGQHYNDRGPIOMWACENKGYIYEIPSI	
421	QY	INTQEYLDVLGRPMWLADGAKAKOVQWNTYVLDALGLGVIITGTLPVFNVTGQSENK	
421	Db	INTQEYLDVLGRPMWLADGAKAKOVQWNTYVLDALGLGVIITGTLPVFNVTGQSENK	
481	QY	NQLILGVNGVDVSLIEDIKRUTPFTLCPNGYIFAIDPNGYVLLHPNLQPKPKSQE	
481	Db	NQLILGVNGVDVSLIEDIKRUTPFTLCPNGYIFAIDPNGYVLLHPNLQPKPKSQE	
541	QY	DFDLDAELENIDKVEIRNKKWDGSGEKTFTLVKSQDERYIDKGNRTYTWTPVNG	
541	Db	DFDLDAELENIDKVEIRNKKWDGSGEKTFTLVKSQDERPIDKGNRTYTWTPVNG	
601	QY	ALVLPYSPYYIKAKLETTIOARSKKGMKQSETLKPDNFEESSGYTFIAPDYCI	
601	Db	ALVLPYSPYYIKAKIETITQARY-----SETLKPDNFEESSGYTFIAPREYC	
661	QY	SDNNTFELNPFNEFIDRKTNNPNSCNADLNRLVLLDAGFTNELVONWYSKQNNIK	
654	Db	SDNNTFELNPFNEFIDRKTNNPNSCNTDLINRLDLAGFTNELVONWYSKQNNIK	
721	QY	FVVTDGGITRVYPKEAGENQENPTEYEDSPYKKSLLDNNDNYVFTAPYFNKSGPGA	
714	Db	FVVTDGGITRVYPKEAGENQENPTEYEDSPYKKSLLDNNDNYVFTAPYFNKSGPGF	
781	QY	MYSKAVRIYIOGKLLKPAVVGIKIDVNSWIENFTWTSIRDPACAGPVCDCRNSDY	
774	Db	MYSKAVRIYIOGKLLKPAVVGIKIDVNSWIENFTWTSIRDEPACAGPVCDCRNSDY	
841	QY	LDDGGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNI5VYAFNKSXDYDYSVCEPK	
834	Db	LDDGGFLLMANHDDYTNQIGRPFGEIDPSMRHLVNI5LYAFNKSXDYDYSVCDPK	
901	QY	GAGHRSAYVPSVADILQIGWATAAASWLSIQOFLSLTFPRLLLEAVEMEDDDFT	
894	Db	GAGHRSAYVPSITDILQIGWATAAASWLSILQOLLSLTFPRLLLEAVEMEDDDFT	
961	QY	SCITBQTOYFPDNDKSPSGVLDCGNC5RIFHGEKLMNTNLFIIMVBSKGTGCP	
954	Db	SCITEBQTOYFFKNDTKSP5GLLDCGNC5RIFHVEKLMNTLVFIIMVBSKGTGCP	
1021	QY	QABQTSIDGPNPCDMWK 1036	
1014	Db	QABQTSIDGPPCDMWK 1029	

RESULT	5	PRT:	1103 AA.
008532	PRELIMINARY;		
ID	008532;	008535;	008536;
AC	008533;	008534;	008535;
DT	01-JUN-1998	(TREMELrel. 06, Created)	
DT	01-JUN-1998	(TREMELrel. 06, Last sequence update)	
DT	01-JUN-1998	(TREMELrel. 06, Last annotation update)	
DT	01-MAR-2003	(TREMELrel. 23, Last annotation update)	
DE	Dihydropyridine-sensitive L-type, calcium channel	alpha-2/delta	
DE	subunits precursor.		
DE	CACNA2D1 OR CACNA2.		
GN	CACNA2D1 OR CACNA2.		
OS	Mus musculus (Mouse).		
OS	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleosteo	
OC	Mammalia; Eutheria;	Rodentia; Sciurognathi; Muridae; Murinae;	
OC	NCBI_TaxID=10090;		
OX	11		
PN	[1]		

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TYSFYI KAKIETITQASKKGKMDSETLKPDPNFESSGYTFLIAPRYCNDLKP 660
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
EFLNFNEFIDRKTNNPSCNADLINRVLLDAGFTELQVNTWSQKNIKGVKAR 720
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
EFLNFNEFIDRKTNNPSCNTDOLINRILLDAGFTELQVNTWSQKNIKGVKAR 720
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OGGITRVVPKEAGENMQENPETYEDSFYKRSLDNDNVTFAPYFNKSGPGAYESGI 780
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OGGITRVVPKEAGENMQENPETYEDSFYKRSLDNDNVTFAPYFNKSGPGAYESGI 780
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
AVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCRKNSDVMDCVI 840
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
AVELXIQGLKLPAPVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCRKNSDVMDCVI 840
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
GFLLMANHDYTNQIGRFFGEIDPSLMRHLVNI SYAFNKS YDVSQVCEPGAAPKQ 900
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
GFLLMANHDYTNQIGRFFGEIDPSMRHLVNI SYAFNKS YDVSQVCEPGAAPKQ 900
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RSRVSVPVADIIQIGWATAAWSILQOFLSLTTPRLLEAVEMEDDFTASLSKQ 960
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RSRVSVPVSIITDIIQIGWATAAWSILQOFLSLTTPRLLEAVEMEDDFTASLSKQ 960
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
EQOYQYFPDNDKSFSGVLDCGNCRSRIFHGKLMNTNLIFIMVESKGTCTCDTRLII 1020
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
EQOYQYFPKNDTKSFSGVLDCGNCRSRIFHGKLMNTNLIFIMVESKGTCTCDTRLII 1020
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QTSQGNPCDMVK 1036
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QYTSQGDGDDPCDMVK 1036
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

PRELIMINARY; PRT; 1084 AA.

(TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
nel alpha-2 delta-1 subunit isoform e.
gicus (Rat).
metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
0116;

JOM N.A.
gue-Dawley; TISSUE=Heart atrium;
est P.M.;
vegic voltage-dependent calcium channel alpha-2 delta-1
form e (CACNA2D1e) mRNA";
form e (CACNA2D1e) mRNA";
FE8-2002) to the EMBL/GenBank/DBJ databases.
276; AA014652.1; -.
1084 AA; 122711 MW; 6269E92D8F1657FF CRC64;
96.1%; Score 53.0; DB 11; Length 1084;
ilarity 95.6%; Pred. No. 0;
Conservative 23; Mismatches 16; Indels 7; Gaps 1;

AAGCLLALTTLFQSLILIGPSSEPPFSAVTIKSWDKMQEDLVTAKTAGVNLVDI 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
AAGCLLALTTLFQSLILIGPSSEPPFSAVTIKSWDKMQEDLVTAKTAGVNLADI 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
EKYQDLYTVENPNARQVEIARIDIEKLLNRSKALVSLAEKVAQAAHQWREDFASN 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
EKYQDLYTVENPNARQVEIARIDIEKLLNRSKALVSLAEKVAQAAHQWREDFASN 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
VYVYNKADLDPEKNDSPGSGRIKPFVIEDANFGQISYQHAAVHPITDIYEGSTIVL 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
VYVYNKADLDPEKNDSPGSGRIKPFVIEDANFGQISYQHAAVHPITDIYEGSTIVL 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
ELNWTLSALDEVFKONREDDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLYVRR 240
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
ELNWTLSALDEVFKONREDDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLYVRR 240
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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61	YKYYQDLYTVEPNNAQQLVEIAARDIEKLKSNRSKALVSLALEAEKVAQAHOHRED	QY	61	YKYYQDLYTVEPNNAQQLVEIAARDIEKLKSNRSKALVSLALEAEKVAQAHOHRED	QY
61	YKYYQDLYTVEPNNAQQLVEIAARDIEKLKSNRSKALVSLALEAEKVAQAHOHRED	Db	61	YKYYQDLYTVEPNNAQQLVEIAARDIEKLKSNRSKALVSLALEAEKVAQAHOHRED	Db
121	EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFCRQISYQHAHVHPDIIYEGS	QY	121	EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFCRQISYQHAHVHPDIIYEGS	QY
121	EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFCRQISYQHAHVHPDIIYEGS	Db	121	EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFCRQISYQHAHVHPDIIYEGS	Db
181	NELNWTALDEVPFKNRBEDPSLLQVFGSATGLARYYPASPMVDNSTRPNKIDLY	QY	181	NELNWTALDEVPFKNRBEDPSLLQVFGSATGLARYYPASPMVDNSTRPNKIDLY	QY
181	NELNWTALDEVPFKNRBEDPSLLQVFGSATGLARYYPASPMVDNSTRPNKIDLY	Db	181	NELNWTALDEVPFKNRBEDPSLLQVFGSATGLARYYPASPMVDNSTRPNKIDLY	Db
241	RPWYIQGAASPDKMLILVDVSGSUGLTLKLRISVSEMLETLSDDDFVNVSFNS	QY	241	RPWYIQGAASPDKMLILVDVSGSUGLTLKLRISVSEMLETLSDDDFVNVSFNS	QY
241	RPWYIQGAASPDKMLILVDVSGSUGLTLKLRISVSEMLETLSDDDFVNVSFNS	Db	241	RPWYIQGAASPDKMLILVDVSGSUGLTLKLRISVSEMLETLSDDDFVNVSFNS	Db
301	VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAPEQLLNINVSANCNK	QY	301	VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAPEQLLNINVSANCNK	QY
301	VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAPEQLLNINVSANCNK	Db	301	VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAPEQLLNINVSANCNK	Db
361	FTDGGEEAQAQEIFNKYNKOKKVRFRFSVQGNHYERGPIOMMACENKGYIYEIPSI	QY	361	FTDGGEEAQAQEIFNKYNKOKKVRFRFSVQGNHYERGPIOMMACENKGYIYEIPSI	QY
361	FTDGGEEAQAQEIFNKYNKOKKVRFRFSVQGNHYERGPIOMMACENKGYIYEIPSI	Db	361	FTDGGEEAQAQEIFNKYNKOKKVRFRFSVQGNHYERGPIOMMACENKGYIYEIPSI	Db
421	INTQBYLDVLRPMVLADGKAKQVQNTNVLDALEGLVITGTLPVFNITQGFENH	QY	421	INTQBYLDVLRPMVLADGKAKQVQNTNVLDALEGLVITGTLPVFNITQGFENH	QY
421	INTQBYLDVLRPMVLADGKAKQVQNTNVLDALEGLVITGTLPVFNITQGFENH	Db	421	INTQBYLDVLRPMVLADGKAKQVQNTNVLDALEGLVITGTLPVFNITQGFENH	Db
481	NOLILGVNMGVDSLEDIKRLTPRFTLCPNGYFYFAIDPNGYVLLHNPLOK----	QY	481	NOLILGVNMGVDSLEDIKRLTPRFTLCPNGYFYFAIDPNGYVLLHNPLOK----	QY
481	NOLILGVNMGVDSLEDIKRLTPRFTLCPNGYFYFAIDPNGYVLLHNPLOK----	Db	481	NOLILGVNMGVDSLEDIKRLTPRFTLCPNGYFYFAIDPNGYVLLHNPLOK----	Db
531	-----NPKSQBPVTLDFLDALENDIKVEIRNKMIDGESGKERTFLVKSQ	QY	531	-----NPKSQBPVTLDFLDALENDIKVEIRNKMIDGESGKERTFLVKSQ	QY
541	LKRKRPVQNPQSQBPVTLDFLDALENEIKVEIRNKMIDGESGKERTFLVKSQ	Db	541	LKRKRPVQNPQSQBPVTLDFLDALENEIKVEIRNKMIDGESGKERTFLVKSQ	Db
582	DIGNRTYTWTPVNGTDYSALVLPYFVYIKAKLEETITQARSKKGMKDSSETL	QY	582	DIGNRTYTWTPVNGTDYSALVLPYFVYIKAKLEETITQARSKKGMKDSSETL	QY
601	DKGNRTYTWTPVNGTDYSALVLPYFVYIKAKLEETITQARSKKGMKDSSETL	Db	601	DKGNRTYTWTPVNGTDYSALVLPYFVYIKAKLEETITQARSKKGMKDSSETL	Db
642	ESGTYTPIAPRDYCNLKI SDNNTFELNFEFIDRKTNNPNSCNADLINRVLID	QY	642	ESGTYTPIAPRDYCNLKI SDNNTFELNFEFIDRKTNNPNSCNADLINRVLID	QY
654	ESGTYTPIAPRDYCNLKI SDNNTFELNFEFIDRKTNNPNSCNADLINRVLID	Db	654	ESGTYTPIAPRDYCNLKI SDNNTFELNFEFIDRKTNNPNSCNADLINRVLID	Db
702	ELVQNTWSKQKNIKGVKARFVVDGKITRYPKEAGENQENPETEYDSFYKRSI	QY	702	ELVQNTWSKQKNIKGVKARFVVDGKITRYPKEAGENQENPETEYDSFYKRSI	QY
714	ELVQNTWSKQKNIKGVKARFVVDGKITRYPKEAGENQENPETEYDSFYKRSI	Db	714	ELVQNTWSKQKNIKGVKARFVVDGKITRYPKEAGENQENPETEYDSFYKRSI	Db
762	VFTAPYFNKSGPGAYESGIMVSKAVETIYQKLLKPAVVGKIDVNSWIENFTKI	QY	762	VFTAPYFNKSGPGAYESGIMVSKAVETIYQKLLKPAVVGKIDVNSWIENFTKI	QY
774	VFTAPYFNKSGPGAYESGIMVSKAVETIYQKLLKPAVVGKIDVNSWIENFTKI	Db	774	VFTAPYFNKSGPGAYESGIMVSKAVETIYQKLLKPAVVGKIDVNSWIENFTKI	Db
822	CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVA	QY	822	CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVA	QY
834	CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVA	Db	834	CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVA	Db
882	FNKSYDYQSVCEPGAAPKQAGHRSATVPSVADILQIGMWATAAAMSILOQFLIK	QY	882	FNKSYDYQSVCEPGAAPKQAGHRSATVPSVADILQIGMWATAAAMSILOQFLIK	QY
894	FNKSYDYQSVCEPGAAPKQAGHRSATVPSVADILQIGMWATAAAMSILOQFLIK	Db	894	FNKSYDYQSVCEPGAAPKQAGHRSATVPSVADILQIGMWATAAAMSILOQFLIK	Db
942	LLEAVEHEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDCGNCRSRIFHGEKI	QY	942	LLEAVEHEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDCGNCRSRIFHGEKI	QY
954	LLEAVEHEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDCGNCRSRIFHGEKI	Db	954	LLEAVEHEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDCGNCRSRIFHGEKI	Db
1002	IFIMVESKGTCPCTRLLIQAEQTSDFGNPCDMVK 1036	QY	1002	IFIMVESKGTCPCTRLLIQAEQTSDFGNPCDMVK 1036	QY
1014	VFMVESKGTCPCTRLLMQAEQTSDFGNPCDMVK 1048	Db	1014	VFMVESKGTCPCTRLLMQAEQTSDFGNPCDMVK 1048	Db
RESULT 6					
Q8VHS9 PRELIMINARY; PRT; 1079 AA.					
ID	Q8VHS9				

N.A.

14; PubMed=8955374;
Hofmann F.J.
'331-337(1996).
CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
I-CONTRACTION COUPLING.
THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
ALPHA-2, BETA AND GAMMA.
ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-
AR LOCATION: INTEGRAL MEMBRANE PROTEIN.
VE PRODUCTS: 5 ISOFORMS; 2A (SHOWN HERE), 2B, 2C, 2D AND
REDUCED BY ALTERNATE SPLICING.
IS SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AND
IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D IS
IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN
SCL. ALL FIVE ISOFORMS ARE EXPRESSED IN THE
CULAR SYSTEM.
A-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
OR FORM.
Y: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
AAB50139.1; -
AAB50140.1; -
AAB50138.1; -
AAB50141.1; -
AAB50142.1; -
5; Cacta2d1.
.004010; Cache.
.002035; WVF.A.
; Cache; 1.
; vwa; 1.
; vwa; 1.
1234; WVF.A; 1.
; Transmembrane; Ion transport; Voltage-gated channel;
rel; Glycoprotein; Phosphorylation; Signal;
splicing.
1 24
25 957
958 1103
446 469
918 942
079 1098
501 501
845 845
92 92
136 136
184 184
324 324
348 348
475 475
604 604
613 613
675 675
781 781
824 824
888 888
895 895
985 985
998 998
531 549
531 554
644 644
1103 AA; 124629 MW; 103773B4735120D4 CRC64;
96.0%; Score 5223; DB 11; Length 1103;
ilarity 94.1%; Pred.No.0;
Conservative 22; Mismatches 14; Indels 26; Gaps 2;
AGCLLALTLTFLQSLGSGSEEPFSPVAVTIKSWDKMQEDLVTLAKTASGVNLVDI 60
AGCLLALTLTFLQSLGSGSEEPFSPVAVTIKSWDKMQEDLVTLAKTASGVNLVDI 60

(TREMELrel. 20, Created)
 (TREMELrel. 20, Last sequence update)
 (TREMELrel. 21, Last annotation update)
 um channel alpha2/delta subunit.
 gicus (Rat).
 etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 cheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 0116;
 M N.A.
 r; TISSUE=Heart;
 1730; PubMed=11604404;
 agashima M., Tauteuura M., Kobayashi T., Seki S.,
 orio Y., Tohse N.;
 a functional splice variant of L-type calcium channel
 t from rat heart.*;
 m. 276:47163-47170(2001).
 62; AAL47093.1; -.
 R004010; Cache.
 R002035; VWF_A.
 13; Cache; 1.
 12; vwa; 1.
 127; VWA; 1.
 10234; VWF; 1.
 1079 AA; 122172 MW; DC4A3641195B546C CRC64;
 95.4%; Score 5195; DB 11; Length 1079;
 ilarity 95.2%; Pred. No. 5.7e-317; Indels 12; Gaps 2;
 Conservative 22; Mismatches 16; Indels 12; Gaps 2;
 AGCLLALTLFOSLLIGPSEPPFPSPVAVIKSWVDKMQEDLVLTAKTAGVGNQVLVDI 60
 |||||
 AGCLLALTLFOSLLIGPSEPPFPSPVAVIKSWVDKMQEDLVLTAKTAGVGNQVLVDI 60
 |||||
 KYQDLTYVEPNNAQLVEIAARDIEKLLNSKALVSLALEAKVQAAHQRDEPASN 120
 |||||
 KYQDLTYVEPNNAQLVEIAARDIEKLLNSKALVSLALEAKVQAAHQRDEPASN 120
 |||||
 VYTNAKDDLPEKNDSPGSRQIKPVFIEDANFGRIQSYOHAAVHIPTDIYEGSTIVL 180
 |||||
 VYTNAKDDLPEKNDSPGSRQIKPVFIEDANFGRIQSYOHAAVHIPTDIYEGSTIVL 180
 |||||
 LNWTSADEVFKKREDEPDLMLQVFGSATGLARYYPASPMVDNSRTPNKIDLYDVR 240
 |||||
 LNWTSADEVFKKREDEPDLMLQVFGSATGLARYYPASPMVDNSRTPNKIDLYDVR 240
 |||||
 WYIQGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETLSDDDFVNVSFNSNAQD 300
 |||||
 WYIQGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETLSDDDFVNVSFNSNAQD 300
 |||||
 CFQHLVQANVRNKKVLDVANNITAKGTTDYKGFSPAFEQLLNYSRANCNKIIML 360
 |||||
 CFQHLVQANVRNKKVLDVANNITAKGTTDYKGFSPAFEQLLNYSRANCNKIIML 360
 |||||
 DGGEERAQEIIFKNYKDKKVRVFRPSVQGHYERGIQWMACENKGYIYEPISGAIR 420
 |||||
 DGGEERAQEIIFKNYKDKKVRVFRPSVQGHYERGIQWMACENKGYIYEPISGAIR 420
 |||||
 JTOEYLDVLRPMVLADKAKQVQWTVNVDLDALEGLVITGTLPVENITGQENKTNLK 480
 |||||
 JTOEYLDVLRPMVLADKAKQVQWTVNVDLDALEGLVITGTLPVENITGQENKTNLK 480
 |||||
 JTLIGVWGVDVSDIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLQPKNSQBPVTL 540
 |||||
 JTLIGVWGVDVSDIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLQPKNSQBPVTL 540
 |||||
 FLDAELNDIKVEIRNWKIDGESSEKTFRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600
 |||||
 FLDAELNDIKVEIRNWKIDGESSEKTFRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 595
 |||||
 LVLPTYSFYIYKAKLEETITQARY-----SETLKPDNFEEGYTFTIAPREYC
 |||||

Db 596 ALVLPYSFYIYKAKLEETITQARY-----SETLKPDNFEEGYTFTIAPREYC
 QY 661 SNNTFELNFEFTDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIK
 Db 649 SNNTFELNFEFTDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIK
 QY 721 FVVTDCGITRVYPKAENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGA
 Db 709 FVVTDCGITRVYPKAENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGA
 QY 781 MVSKAVERIYQGLKLPAAVVGIIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDV
 Db 769 MVSKAVERIYQGLKLPAAVVGIIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDV
 QY 841 LDGGFLLMANHDDYTNQIGRPFGEIDPSLRHLVNLISVYAFNKSVDYQSVCPGC
 Db 829 LDGGFLLMANHDDYTNQIGRPFGEIDPSLRHLVNLISVYAFNKSVDYQSVCPGC
 QY 901 GAGHSAYVPSVADIIQIGWATAAAMSIIQQFLLSLTFFPRLLAEVEMEDDDFTI
 Db 889 GAGHSAYVPSVADIIQIGWATAAAMSIIQQFLLSLTFFPRLLAEVEMEDDDFTI
 QY 961 SCITEQTYFFDNDKSKFSFVLDGCGNSRIFHGKLMNTNLIFIMVSKGTCPCI
 Db 949 SCITEQTYFFDNDKSKFSFVLDGCGNSRIFHGKLMNTNLIFIMVSKGTCPCI
 QY 1021 QAEQTSQDPNPCDMVK 1036
 Db 1009 QAEQTSQDPNPCDMVK 1024

RESULT 7

Q9UDQ3 PRELIMINARY; PRT; 745 AA.
 ID Q9UDQ3;
 AC 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMELrel. 23, Last annotation update)
 DE WUGSC:H DJ0560014.1 protein (fragment).
 GN WUGSC:H DJ0560014.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99063792; PubMed=9847074;
 RA Sulston J.E., Waterston R.;
 RT "Toward a complete human genome sequence.";
 RL Genome Res. 8:1097-1108(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Mead K., Bauer C.;
 RT "The sequence of Homo sapiens PAC clone RP4-560014.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX Waterston R.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC006145; AAD20938.1; -.
 DR InterPro; IPR004010; Cache.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF02743; Cache; 1.
 DR Pfam; PF00092; vwa; 1.
 DR PROSITE; PS0234; VWF; 1.
 FT NON TER 1
 SQ SEQUENCE 745 AA; 84396 MW; BC07B53484B71EA4 CRC64;

Query Match 67.4%; Score 3667; DB 4; Length 745;
 Best Local Similarity 99.7%; Pred. No. 2.1e-221;
 Matches 686; Conservative 1; Mismatches 1; Indels 0;

QY 347 YNVSRANCNKIIMLFTDGEERAQEIIFKNYKDKKVRVFRPSVQGHYERGI

DR	EMBL; AJ251368; CAB86193.1; -
DR	InterPro; IPR004010; Cache.
DR	InterPro; IPR002035; VWF_A.
DR	Pfam; PF02743; Cache; 1.
DR	Pfam; PF00092; vwa; 1.
DR	SMART; SM00327; VWA; 1.
DR	PROSITE; PS0234; VWFA; 1.
SQ	SEQUENCE 1150 AA; 129876 MW; 37B75F687AFES73C CRC64;
	Query Match 54.2%; Score 2948; DB 4; Length 1150;
	Best Local Similarity 54.5%; Pred.No.Se-176;
	Matches 573; Conservative 168; Mismatches 281; Indels 30; G+
QY	7 LALTLTLPQSLLIGPSSBPFPASVITKSWDKWQBDLVTLAKTAGSNQLDIYEI
Db	44 LMULLPLPELLAAPGASATVPQQHTMQHWARRLEQEVGDGVNRIFGVGQOLREIYK
QY	67 LVYVEPNNAQLVETIAARDIEKLNSRSTALYSIALAEKVQAHAHQWRDFFASNVE
Db	104 LFEVQENEPQKLEKVGAGDIESLDRKVOALKRLADAAENFQKAHRWDNIKEED:
QY	127 AKDDL---DPKKNDSPGSQ--RIKPVFTEDANFGRQISYQHAHAVHPDTIYEGST
Db	164 AKADAELDDPESEDVERGSKASTLRDLFDIEDPFNKKNKYNYSAAVQIPTDIYKGST
QY	182 ELMTWSALDVFVKKNREDPSLLNQVFGSATGLARYYPASPWNDSNTPKNIDLYC
Db	224 ELNWTEALENVFMENRRQDPTLLMOWFGSATGVTRYYPATEW----RAPKKIDITY
QY	242 PWYTQGAASPQMILLVDVSGSVSGLTKLIRTSVSEMLTSLSDDDDFVNVSFNFSN
Db	280 PWYIQGASSPKDMVIIIVDVSGSVSGLTKLMKTTSVCMLDTLSDDDYNNVASFNEI
QY	302 SCFOHLVQANTRNKKVLKDAVNNITAKGITDYKKGFSAFEPQLLNYNVSRANKCK
Db	340 SCFTHLVQANYNRNKKVFKEAIVQGWAKGTTCYKAGFEVAPDOLQNSNITRANCNK
QY	362 TDGGERAQEIPFNKYN-KDKKVRVFRFSVGQHINBERGPIQMAWCKNGYYEIPS
Db	400 TUGGEDRVQDVEPKYNNWPNRVTVRVTFSGVGHNYDVTFLQMWACANKGYTFEIPS
QY	421 INTQEYLDVLGRPMWLADGKAKQVQNTWNYLDALSELGLVITGLTVFNVIITQGQFN
Db	460 INTQEYLDVLGRPMWLAGEKARQVQNTWNYVEDALGLGLVVTGLTPVENLTQ--DG
QY	481 NQLILGMWGVDYSLEDIKELTRPFLTCPNGYYFAIDPNGSYVILLHNPLOPKNPKSQ
Db	518 NQLILGMWGIQDALNDIKELTTPNYTLGANGYVFAIDLNGYVLLHNPCLKPQTTFNR
QY	541 DFLDAELENDIKVEIRNMKDGESEBKTRPTLVKSODERYIDKGNRTYTWTPVNG
Db	578 DFLDAELENDKEEIRRSMDGNKGHKQIRTLVKSLDERYIDVETRYTWTPIRE
QY	601 ALVLPYVSFYIIKALETTTOARSKKGKWQSETLKPDNFEBESGYTFIAPRDYC
Db	638 GLVLPYSTTYLQANLSDQILQVKIRISKLDKFELLPSSEFEGEHVFIAPREYC
QY	661 SDNNTEFLMFNFEDIRKTPNNPSCNADLINRVLLDAGFTNELVQNYWSKQ-N
Db	698 SDNNTEFLKHFIELMEKVTPDSDKCNFFLHNLTILDGTITQQLVERVMRDQDLN
QY	720 RFVVTGSGITRVYKPEAGENWQENPETYESFYKRSLDNDNNYVTPAYFYNK-SG
Db	758 VFAATDGGITRFVFPNKAADWTENPEPFNASFYRRSLDNHGIVFKPHQDALLR
QY	779 ---GIMYSKAVEIYOGKLLPAVVVGIKIDVNSMIENF-----TKTSIRD-P-C
Db	818 DTVGILVSTAVELSIGRTRLPAVVGVKLDLEAAEKFKVLASNRTHQDOQPQKC
QY	826 -VCDCKRSNDYDCVILLDDCGCFLLMANHDDYTNQIGRPFGSIDPSLSMRHLNYS
Db	877 CSMDCVANNEDLLCVIIDGGFLVLSNQNHQWDQVGRFFESEVDANLMALNLYNS

```

PRELIMINARY;      PRPT;  1150 AA.

(TREMBLrel. 15, Created)
(TREMBLrel. 15, Last sequence update)
(TREMBLrel. 23, Last annotation update)
mel, alpha 2/delta subunit 2.

; (Human).
; Metazoa; Chordata; Vertebrata; Euteleostomi;
; Ichtheria; Primates; Catarrhini; Hominidae; Homo.
)606;

OM N.A.
cid;

..
DEC-1999) to the EMBL/GenBank/DBJ databases.

OM N.A.
oid;
ai S., Marais E., Lacinova L.;
istribution and functional characterization of the calcium
hazdelta-2 subunit.";
APR-2000) to the EMBL/GenBank/DBJ databases.

```

519 KKNQILGVGMDIVALNDIKRLTPNTYLLGANGYVFAIDNLGVLLHPNLKPIQITIN
539 TLDFLDAELNDIKVEIRKMDIGSEGEKFTFLVKSDODERYIDKNGNTYTWTPVN
579 TLDFLDAELENDENKEETRRSMIDDKGHQKQIRTLVKSLDERYIDEVIRNYTWVPIR
599 SLALVLPYSPYTIKAEETITQARSKKGKMKDSETLKPNDFESGVTFTAPRDY
639 SLGLVLPYSPYTIYIQANLSQIILQVKLPISKLDPEFLLPSSFESEGHVFTAPREY
659 KISDNNTTEFLANFNEFIDRKTTPNNPCSNADLINRVLLDAGFTNELVQNVWSKQ-N
699 NASDNNTTEFLKNFTIELMEKVTPOSKQCNFLGLHNLIDTGITQQULVERVWRDQDLA
718 KARFVVTGGITRVVYPKAEAGENQENPETYEDSFYKRSILDNDNTYFTAPFNK-SC
759 LAVFAATDGGITRVFPNKAEDWTENPEFNASFYRSRLDNRGYIFPKPHQDSILF
777 ES---GIMVSKAVEIYIQGLLKPAVVGIKIDVNSWIENF-----TKTSIRDP---
819 ENDTVGLVSTAVELSLGRTRLREAVVGVKLDLEAWAEKFKVLASNRTRHODQPOK
826 ----VCDKRNQSDVMDCVILDDGGFLLMAHDDYTQIGRFFCEIDPDSLMLHLVN
878 SSHCEMDCEVNNEDLLCVLIDDGGFVLISQNHQMDQVGRFFSEVDANLMLALYNI
882 FNKSYDYQSVCEPGAAPKQGAHRSAYVPSVADILQIGMWATAAASLIQQFLLS
938 RKESYDYQACAPQPPGNLGAAPGVFTIADFLNLAWTSAANSLFQQLLYG
942 LLBAVEMEDDDFTASLSKOSCTEQTQFFNDKSFSGVLDCNCSRIPTHGKL
998 WFOADPAEAG-SPEPRESSCMVKQTYFYFSGVASNAIYDNCNCSRLFHAORL
1002 IFIMWSKGTCPDTFLLIQAEQ--TSDGPNPCDMVK 1036
1057 LFVVAEPLKSCQCEVGRLLQKETHCPADGPEQCELVQ 1093

RESULT 10
Q9NY48 PRELIMINARY; PRT; 1143 AA.
AC Q9NY48
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Calcium channel, alpha 2/delta subunit 2.
GN CACNA2D2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Klugbauer N.;
EL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Hobom M., Dai S., Marais E., Lacinova L.;
RT "Neuronal distribution and functional characterization of the c
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251367; CAB86192.1; --
DR InterPro; IPR004010; Cache.
DR pfam; PF02743; Cache; 1.
DR pfam; PF00092; vwa; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS02034; VWF; 1.
SQ SEQUENCE 1143 AA; 129085 MW; 492556C9919A0CES CRC64;

:56:54 2004

53.7%; Score 2920.5; DB 4; Length 1143;
ity 54.3%; Pred. No. 2.6e-174;
servative 166; Mismatches 278; Indels 37; Gaps 14;

LFQSLIIPSSSEPPSAVITKSWDKQEDLVTLAKTASGVNQLVDIYKYQD 66
LLPLAAPGASAYSFPQOHTMQHARLEOEVDGVMRIFGVQQLRIYKDNRN 103
ANARQLVEIARDIEKLSNRSKALVSLAEAKVQAHAHQWREDFASNEVVYN 126
NEPQKLVKAVAGDIESLDRKQALKRLADAENFQKAHRWQDNIKEEDIVYD 163
---DPKNDSEPGSQ--RIKPVFIEDANFGRLSQISYQHAHVHIPTDIYESTVILN 181
ELDDPSESDVERGSKASTLELDIEDPNFKNKVNSYAAVQIPTDIYKSTVILN 223
3ALDEVFKKQREEDPSLLMQVFGSATGLARYYPASPWNDSRTPNKIDLYDVER 241
3ALENFMENRRQDPTLLMQVFGSATGVTRYYPATPW----RAPKKIDLYDVER 279
3AASPDKMLILVDVSGVSGTLKLRISYSEMLETLSDDDFVNVSFNSNAQDV 301
GASSPKDMVILVDVSGVSGTLKLRISYSEMLETLSDDDFVNVSFNSNAQDV 339
LVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAPFQGLLNVNVSBRANCKIMLF 361
LVQANVRNKKVFKKAVQMGVAKGTYGKAGPEYAFDQLQNSNITRANCNMIMPF 399
ERAQEIENKYN-KDKKVVFRFSVQGHYERGPLOMACENKGVYFELPSIGAIR 420
DRVQDVFEKYNWNRTRVFTVFSVQGHYDVTPLQMACANKGVYFELPSIGAIR 459
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 480
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 517
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 540
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 577
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 600
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 637
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 660
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 690
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 719
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 750
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 778
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 810
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 825
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 859
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 884
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 929
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 944
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 989
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 1004
YLDVLGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQFENKTNLK 1048

DB 1049 VAEKPLCSQCEAGRLLOKETHSDGPEQCELVQ 1080

RESULT 11

Q9EQG2 PRELIMINARY; PRT; 1156 AA.

ID Q9EQG2

AC Q9EQG2; 01-MAR-2001 (T-REMBLrel. 16, Created)

DT 01-MAR-2001 (T-REMBLrel. 16, Last sequence update)

DT 01-MAR-2003 (T-REMBLrel. 23, Last annotation update)

DE Voltage-dependent calcium channel alpha-2-delta-2 subunit.

GN CACNA2D2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=TKDU;

RC MEDLINE=21015416; PubMed=11130987;

RA Barclay J., Rees M.;

RT "Genomic organization of the mouse and human alpha2delta2 voltage-dependent calcium channel subunit genes.";

RL Mamm. Genome 11:1142-1144 (2000).

DR EMBL; AF247139; AAG47846.1; --

DR MGD; MGI:1929813; CACNA2D2.

DR InterPro; IPR004010; Cache.

DR InterPro; IPR002035; VWF_A.

DR Pfam; PF02743; Cache; 1.

DR Pfam; PF00092; vwa; 1.

DR SMART; SM00327; VWA; 1.

DR SMART; PS50234; VWF_A; 1.

DR PROSITE; P1156 AA; 130611 MW; A732545A2B302A52 CRC64;

SQ

Query Match 53.6%; Score 2918.5; DB 11; Length 1156;
Best Local Similarity 53.8%; Pred. No. 3.6e-174; Indels 33; G
Matches 568; Conservative 173; Mismatches 282;

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105 RNLFEVQENEPQKLVKAVQMGVAKGTYGKAGPEYAFDQLQNSNITRANCNIKEE
125 YNAKDDL---DPEKNDSEPGSQ--RIKPVFIEDANFGRLSQISYQHAHVHIPTDIYEC
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341 PVSCFTHLVQANVRNKKVFKKAVQMGVAKGTYGKAGPEYAFDQLQNSNITRANC
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419 IRINTQBYLDVGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQF
461 IRINTQBYLDVGRPWLAGDKAKQVQWNTVYLDALGLVITGTLVPNITGQF
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3SKGTCPCDTRLLIQAEQTSQDGNPCDMVK 1036

105 RNLFVQENEPQKLVKVGADGIESLLDRKQVALKRLADAAENFOKAHRWQDNKIEEB
125 YNAKDDL---DPEKNDSEPGSQ--RIKPVFTEDANFGRQISQYHAAVHIPDITVEGS
165 YDAKADABLDPESEDMEGSKTSALRLDFIEDPNFKKNVKNYSYAVQIPDITDYKGS
180 LNELNWTLSALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPMVDNSRSTPNKIDLY
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300 DVSCFOHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFEGQLLYNVNVRANCNH
341 FVSCFTHLVQANVRNKKVFKEAQGVMAKGTTCYKAGFEYAFDQLQSNITRANCNI
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519 KKNQILLGVMGIDVALNDIKELTPNYTLGANGYYFAIDLNGYVILLHPNLKFOQTTFE
539 TLDFDLABELNDIKVEIRNKMIDGESGKTFERTLVKSQDERIYIDKGNRTYTWTPV
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718 KARFVTDGIGITAVYKEAGENQWENPETVEDSFYKRSIGDNDNYVTFAYFNK-S
752 LAVFAATDGGITRVFPKAAEDWTENPEPNASFYRSLDNHGYYIKFPHQDSLL
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3MBLrel. 23, Last annotation update)

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ria; Primates; Catarrhini; Homiidae; Homo.

;

A.

F.-M., Latif F., Ding J., Lin J., Mathis M.,

candidate human tumor suppressor gene located in the

all lung cancer homozygous deletion region homologous to

i calcium channel alpha 2/ delta subunit."

-1998) to the EMBL/GenBank/DBJ databases.

;A.

f F., Duh F.-M., Adreazzoli-Angeloni D., Kashuba V.,

Johnson B., Lerzan M.I.;

delta subunit of the L-type voltage gated calcium

s in the lung cancer critical region on 3p21.3.;"

-1998) to the EMBL/GenBank/DBJ databases.

N.A.

45; PubMed=9628581;

ikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,

the coding sequences of unidentified human genes. IX.

sequences of 100 new cDNA clones from brain which can

proteins in vitro.;"

39(1998).

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; BAA25484.1; -

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02035; VWF_A.

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 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
 RA Ohara O., Koga H.;
 RA "Prediction of the coding sequences of mouse homologues of KIAA
 RT 1. The complete nucleotide sequences of 100 mouse KIAA-homolog
 RT cDNAs identified by screening of terminal sequences of cDNA clor
 RT randomly sampled from size-fractionated libraries."
 RT Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

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11      VKSLDERYIDEVRNTWTPISTWYSLGLVLPYSTYTLYOANLRDQILOKLPL 594
12      OSETLKPDNEFEESGYTFIAPRDYCNDLKISDNMTPELLNFEDIRKCPNNPSCN 686
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GenCore version 5.1.6
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10-090-827-14
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SUMMARIES

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00.0	1091	12	US-10-162-102-17	Sequence 17, Appl
00.0	1091	15	US-10-162-102-17	Sequence 17, Appl
00.0	1091	15	US-10-090-827-16	Sequence 16, Appl
99.3	1086	12	US-10-375-253-49	Sequence 49, Appl
99.0	1084	12	US-10-375-253-53	Sequence 53, Appl
98.8	1036	15	US-10-090-827-7	Sequence 7, Appl
98.8	1063	15	US-10-090-827-8	Sequence 8, Appl
98.8	1069	15	US-10-090-827-9	Sequence 9, Appl
98.8	1091	15	US-10-090-827-5	Sequence 5, Appl
98.6	1103	12	US-10-375-253-47	Sequence 47, Appl
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98.2	1018	15	US-10-090-827-13	Sequence 13, Appl

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ALIGNMENTS

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; Sequence 14, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 sui
; FILE REFERENCE: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; TYPE: PRT
; LENGTH: 1036
; ORGANISM: Homo sapiens
US-10-090-827-14

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US-10-090-827-15

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QY      61  YEKYQDLYTVEPNNAQQLVEIAARDIEKLNSRKALVSLALEAEKVOAAHQWRD
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QY      121  EYVYVYNAKDDLDPKNDSEPGSQRIKPFIEDANFGROI SYQHAHVHIPTDIIYEGS
DB      121  EYVYVYNAKDDLDPKNDSEPGSQRIKPFIEDANFGROI SYQHAHVHIPTDIIYEGS

QY      181  NELNWTSAIDVEFKKNEEDPSLLQVFGSATGLARYYPASPWDNRSRTPNKIDLY
DB      181  NELNWTSAIDVEFKKNEEDPSLLQVFGSATGLARYYPASPWDNRSRTPNKIDLY

QY      241  RPWYIQGAASPKDMLILVDVSGVSGVLTKLITTSVSEMLETLSDDDFVNVA SFNS
DB      241  RPWYIQGAASPKDMLILVDVSGVSGVLTKLITTSVSEMLETLSDDDFVNVA SFNS

QY      301  VSCFQHLVQANVRNKKVLKDAVNNITAKGIDTYKGGFSFAFQLLNYNVSRANCNF
DB      301  VSCFQHLVQANVRNKKVLKDAVNNITAKGIDTYKGGFSFAFQLLNYNVSRANCNF

QY      361  FTDGGERAQEIFNKYNKKVVRFRFSVGOHNYVERGPIQWACENKGYVYIPEPSI
DB      361  FTDGGERAQEIFNKYNKKVVRFRFSVGOHNYVERGPIQWACENKGYVYIPEPSI

QY      421  INTQEYLDVLGRPMVLADGKAKQVQNTNVYLDLLEGLGVITGLPVFNITGQFENI
DB      421  INTQEYLDVLGRPMVLADGKAKQVQNTNVYLDLLEGLGVITGLPVFNITGQFENI

QY      481  NQLITLGVMGVDVLSLEIDIKLTTPRTILCPNGYYFAIDPNGVVLHPNLQPKNPKSQ
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QY      541  DFLDAELENDIKVEIRNKMIDGESGKTPRTLKVSQDERYIDKGNRTYTTWTPVNG
DB      541  DFLDAELENDIKVEIRNKMIDGESGKTPRTLKVSQDERYIDKGNRTYTTWTPVNG

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DB      601  ALVLPFTSYFYIKAKBETITQARSKKGRKMDSETLKPDPNFEEGGYTFIAPRDYC

QY      661  SDNNTEFLNFEEDIRKTPNPNPSCNADLINRVLLDAGFTNELVONTWSKQKNI
DB      661  SDNNTEFLNFEEDIRKTPNPNPSCNADLINRVLLDAGFTNELVONTWSKQKNI

QY      721  FVVTGGITRVYPKEAGENQENPETTYDSFYKRSLLDNDNYVFTAPYFNKSGPGG
DB      721  FVVTGGITRVYPKEAGENQENPETTYDSFYKRSLLDNDNYVFTAPYFNKSGPGG

QY      781  MYSKAVEIYIQGLLKPAVVGKIDVNSMIENFTKTSIRDP CAGVPCOCKRNSD
DB      781  MYSKAVEIYIQGLLKPAVVGKIDVNSMIENFTKTSIRDP CAGVPCOCKRNSD

QY      841  LDDGGFLMANHDDVTNQIGRFFGEIDPSIMRHLVNI SVYAFNKSVDYQSVCPEI
DB      841  LDDGGFLMANHDDVTNQIGRFFGEIDPSIMRHLVNI SVYAFNKSVDYQSVCPEI

QY      901  GAGHSAYPVSVDIILQIGWATAAAWSILQQOFLLSLTPRLLLEAVEMEDDDFT
DB      901  GAGHSAYPVSVDIILQIGWATAAAWSILQQOFLLSLTPRLLLEAVEMEDDDFT

```

Publication US/10090827
 US20030073132A1
 INVENTOR:
 Erner-Lambert
 INVENTION: Method for the screening of alpha 2 delta-1 subunit
 INVENTION: binding ligands
 E: 179
 CATION NUMBER: US/10/090,827
 G DATE: 2002-03-06
 INVENTION NUMBER: US/09/397,549
 DATE: 1999-09-16

:56:53 2004

541 DFLDAELNDIKVEIRNKMDGESGKTRTLVKSQDERYIDKGNRTYTWTVPNGTDY
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601 ALVLPTYSFYIYKAKLEETITQARSKGKMDSETLKPDNPFESGYTFAPRDYCNDL
601 ALVLPTYSFYIYKAKLEETITQARSKGKMDSETLKPDNPFESGYTFAPRDYCNDL
661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINVLLDAGFTNVLQVYWSKQKNIKGVK
661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINVLLDAGFTNVLQVYWSKQKNIKGVK
721 FVYTDGGITRVYVKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYEE
721 FVYTDGGITRVYVKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYEE
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841 LDDGGFLLMANHDDYTQIGRPFGEIDPISLHRHLVNI SVYAFNKSIDYQSVCEPGAA
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901 GAGHRSAYVPSVADILQIGWWATAAASILQOFLSLTFPRLRAVENEDDDFTASL
901 GAGHRSAYVPSVADILQIGWWATAAASILQOFLSLTFPRLRAVENEDDDFTASL
961 SCITBOTOYFFDNDKSPFSGVLDCGNCRIHFHGEKLMNTLIFIMVESKGTCPDCTR
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1021 QABQTSDDGPNPCDMVK 1036
1021 QABQTSDDGPNPCDMVK 1036

RESULT 4
US-10-162-102-17
Sequence 17, Application US/10162102
Publication No. US20030232336A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
APPLICANT: Silos-Santiago, Immaculada
APPLICANT: Gu, Wei
TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY
FILE REFERENCE: 10448-130001
CURRENT APPLICATION NUMBER: US/10/162,102
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 60/209,845
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: US 09/875,321
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: PCT/US01/18340
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/209,257
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: US 09/875,423
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/US01/18398
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/209,238
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: US 09/875,363
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/US01/18247
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/227,068
PRIOR FILING DATE: 2000-08-22
Remaining prior application data removed - See File Wrapper or PAL
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Fast-Seq for Windows Version 4.0
SEQ ID NO 17

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DGNPCDMVK 1036
DGNPCDMVK 1036
ation US/09875423
081657A1
N:
Rory A.J.
N: 21784, A NOVEL HUMAN CALCIUM CHANNEL
N: FAMILY MEMBER AND USES THEREOF
ON NUMBER: US/09/875,423
ATE: 2001-06-05
I NUMBER: US 60/209,257
I: 2000-06-05
NOS: 6
2 for Windows Version 4.0
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rity 100.0%; Pred. No. 0;
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100.0%;	Score 5443;	DB 12;	Length 1091;	
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conservative	0;	Mismatches 0;	Indels 0; Gaps 0;	
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LLAALTTLFQSLILIGPSEBPPFP	SAVTIKSWDKMQEDLVT	LAKTAGSVNQ	LDI 60	
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NAKDDLDPEKNDSPGSGORIKPVFI	EDANFORQISYQHA	VHIPTDIYEGSTIVL 180		
NAKDDLDPEKNDSPGSGORIKPVFI	EDANFORQISYQHA	VHIPTDIYEGSTIVL 180		
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NTEFLLFNFEFIDRKTNNP	NSCNADLINRVL	LDAGTNELVQNYWSKOKN	IKGVKAR 720	
TDGGITRVPYKPEAGENWOEN	PETTEDSYKESL	ONDNDVFTFAPYFNKSGPGAYESGI 780		
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RESULT 6
US-10-090-827-16
; Sequence 16, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 subunit
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-16
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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lication US/10375253
JS20040018510A1
ION: SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
ION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ION: METHODS

SD9813DA
TION NUMBER: US/10/375,253
DATE: 2003-02-27
ON NUMBER: 08/450,273
TE: 1995-05-25
ON NUMBER: 08/404,354
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ON NUMBER: 07/914,231
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TE: 1993-11-05
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ON NUMBER: 08/149,097
TE: 1993-11-05
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ID NOS: 65
SEQ for Windows Version 4.0

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QY 361 FTDGGEERAQEI FNKYNKDKKVRFRFSVGOHNYERGP IQMMAENKGYIYIEIPSI
Db 361 FTDGGEERAQEI FNKYNKDKKVRFRFSVGOHNYERGP IQMMAENKGYIYIEIPSI
QY 421 INTQEVLDVLRPMVLADGKAKQVQNTNYLDALELGLVITGTLPVFNITGQFENK
Db 421 INTQEVLDVLRPMVLADGKAKQVQNTNYLDALELGLVITGTLPVFNITGQFENK
QY 481 NQILGVMGVDVSLIEDIKRLTPRTICPNGYFAIDPBGVYLHPNLQPNPKSQE
Db 481 NQILGVMGVDVSLIEDIKRLTPRTICPNGYFAIDPBGVYLHPNLQPNPKSQE
QY 541 DFDAELNDIKVEIRNKMIDGESGKFTLVKSQDERYIDKGNRTYTWTPVNGT
Db 541 DFDAELNDIKVEIRNKMIDGESGKFTLVKSQDERYIDKGNRTYTWTPVNGT
QY 596 ALVLPYSFYIYKAKLEETITQARSKKGKMDSETLXPDNPEESGYTFIAPRDIYN
Db 596 ALVLPYSFYIYKAKLEETITQARSKKGKMDSETLXPDNPEESGYTFIAPRDIYN
QY 661 SDNNTFLLNFNEFIDRKTNNPCNADLINRVLLDAGFTNELVQNYWSKQKNIK
Db 661 SDNNTFLLNFNEFIDRKTNNPCNADLINRVLLDAGFTNELVQNYWSKQKNIK
QY 721 FVWTDGGITRVYPKEAGENMOENPETVEDSYKRSLONDNTVFTAPYFNKSGPGA
Db 721 FVWTDGGITRVYPKEAGENMOENPETVEDSYKRSLONDNTVFTAPYFNKSGPGA
QY 776 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDPKAGVPCDCKRNSDV
Db 776 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDPKAGVPCDCKRNSDV
QY 841 LDDGGFLLMANHDDVTNQIGRPFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCPEPG
Db 841 LDDGGFLLMANHDDVTNQIGRPFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCPEPG
QY 896 GAGHSAYVPSVADILIQGWATAAASILQOFLSLTPRLLLEAVEMEDDDFTFA
Db 896 GAGHSAYVPSVADILIQGWATAAASILQOFLSLTPRLLLEAVEMEDDDFTFA
QY 961 SCITEQTOYFFNDNSKFSFGLVDCGNCRI FHGKLMNTNLIFIMVESKGTCPCI
Db 961 SCITEQTOYFFNDNSKFSFGLVDCGNCRI FHGKLMNTNLIFIMVESKGTCPCI
QY 1021 QAEQTSOGPNPCDMVK 1036
Db 1016 QAEQTSOGPNPCDMVK 1031

RESULT 8
US-10-375-253-53
; Sequence 53, Application US/10375253
; Publication No. US20040018510A1

15:56:53 2004

us-10-090-827-14.rapb

P

N: LK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
N: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
N: METHODS

D9813DA

ON NUMBER: US/10/375,253

TE: 2003-02-27

NUMBER: 08/450,273

1: 1995-05-25

NUMBER: 08/404,354

2: 1995-02-15

NUMBER: 07/914,231

3: 1992-07-13

NUMBER: 08/314,083

4: 1994-09-28

NUMBER: 07/914,231

5: 1992-07-13

NUMBER: 07/603,751

6: 1990-11-09

NUMBER: 08/290,012

7: 1994-08-11

NUMBER: 08/149,097

8: 1993-11-05

NUMBER: 08/105,536

9: 1993-08-11

NUMBER: 08/149,097

E: 1993-11-05

Application data removed - See File Wrapper or PALM.

NOS: 65

Q for Windows Version 4.0

99.0%; Score 5386.5; DB 12; Length 1084;

Identity 99.2%; Pred. No. 0;

Insertive 0; Mismatches 1; Indels 7; Gaps 1;

11ALATLTLFQSLIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

11ALATLTLFQSLIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

11ALATLTLFQSLIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

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11ALATLTLFQSLIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

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; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1063
; TYPE: PRT
; ORGANISM: Sus scrofa
; ORGANISM: Sus scrofa
; US-10-090-827-8

Query Match          98.8%; Score 5380; DB 15; Length 1063;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0

QY      1  MAACLLALTLTIFQSLILGPSEPPFPSAVTIKSWDKMQEDLVTLAKTASGVNQI
DB      1  MAACLLALTLTIFQSLILGPSSQPPFPSAVTIKSWDKMQEDLVTLAKTASGVNQI

QY      61  YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWRED
DB      61  YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWRED

QY      121  EVVYNKADLLDPEKNDSEPGSQRIKPVFIEDANFGROI SYQHAHVHPTDIIYEGS
DB      121  EVVYNKADLLDPEKNDSEPGSQRIKPVFIEDANFGROI SYQHAHVHPTDIIYEGS

QY      181  NELNWTSAIDVEFKKNEEDPSLLIQQVFGSATGLARYYPASPVWDSNTPNKIDLY
DB      181  NELNWTSAIDVEFKKNEEDPSLLIQQVFGSATGLARYYPASPVWDSNTPNKIDLY

QY      241  RPWYIQGAASPKOMLILVDVSGSVSGILTKLIRTSYSEMLETLSDDDFVNVASFNS
DB      241  RPWYIQGAASPKOMLILVDVSGSVSGILTKLIRTSYSEMLETLSDDDFVNVASFNS

QY      301  VSCFQHLVQANVRNKKVILKDAVNNITAKGITDYKGFSAFAPQLLNNVNSRANCNH
DB      301  VSCFQHLVQANVRNKKVILKDAVNNITAKGITDYKGFSAFAPQLLNNVNSRANCNH

QY      361  FTDGGERAQEITFNKYKDKKVRVFRSVQGHNVVERGPQIOWMACENKGYIYFIPS.
DB      361  FTDGGERAQEITFAKYNKDKKVRVFTSVQGHNVDRGPQIOWMACENKGYIYFIPS.

QY      421  INTQEVLDVLGRPMVLADGKAKQVQWNTNVYLDALDELGLVITGTLPVFNITGQFENI
DB      421  INTQEVLDVLGRPMVLADGKAKQVQWNTNVYLDALDELGLVITGTLPVFNITGQFENI

QY      481  NQLILGWGVDVLSLEDIKRLTPRFTLCPNGYTFPAIDPNGVYLLHPNLQPNKPSQ
DB      481  NQLILGWGVDVLSLEDIKRLTPRFTLCPNGYTFPAIDPNGVYLLHPNLQPNKPSQ

QY      541  DFLDAELENDIKVETRNKMDGESGEKTRFLTVKSDQDERYIDKGNRTYTWTPVNG
DB      541  DFLDAELENDIKVEIRNKMIDGESGEKTRFLTVKSDQDERYIDKGNRTYTWTPVNG

QY      601  ALVLPTYSFYIYIKALEEITTOARSKGKMKDSETLKPDNPFESGYTTFIAPRDYC
DB      601  ALVLPTYSFYIYIKALEEITTOARSKGKMKDSETLKPDNPFESGYTTFIAPRDYC

QY      661  SDNNTEFLIAFNFEFIDRKTNNPNSCNADLINRVILDAQFTNELVQWWSKQKILK
DB      661  SDNNTEFLIAFNFEFIDRKTNNPNSCNADLINRVILDAQFTNELVQWWSKQKILK

QY      721  FVVTDDGTRIVYPKEAGENQWENPETYEDSFYKRSILDNDNTVFTAPYFNKSGPGF
DB      721  FVVTDDGTRIVYPKEAGENQWENPETYEDSFYKRSILDNDNTVFTAPYFNKSGPGF

QY      781  MYSKAVEIYIOGKLLKPAVVGKIDVNSMIENFTKTSIRDPGAGVDCCKENSQI
DB      781  MYSKAVEIYIOGKLLKPAVVGKIDVNSMIENFTKTSIRDPGAGVDCCKENSQI

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NOTION: binding rigours

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DB	481	NQLILGVMGVDSLE	DIKRLTPRFTLCPNGYYFAIDP	NGYVLLHNPLOPKNPKSQBE	
QY	541	DFDLAELENDIKVE	IRNKMIDGESSEKTFRTL	VKSODERYIDKGNRTYTWTPVNGTL	
DB	541	DFDLAELENDIKVE	IRNKMIDGESSEKTFRTL	VKSODERYIDKGNRTYTWTPVNGTL	
QY	601	ALVLPTYSFYI	KAKLEETITQARSKKGKWKDSE	LKPDNPFESGYTFIAPRDYCNM	
DB	601	ALVLPTYSFYI	KAKLEETITQARSKKGKWKDSE	LKPDNPFESGYTFIAPRDYCNM	
QY	661	SDNNTTEFLNFNE	FIDRKTNNPNSCNADILNR	VLLDAGFTNELVQNYWSKQNKIKG	
DB	661	SDNNTTEFLNFNE	FIDRKTNNPNSCNTDLINR	VLLDAGFTNELVQNYWSKQNKIKG	
QY	721	FVYTDGGITRVP	PKAGENQWENPETEYDSFY	KRSLDNDNYVFTAPYFNKSGPGGAYI	
DB	721	FVYTDGGITRVP	PKAGENQWENPETEYDSFY	KRSLDNDNYVFTAPYFNKSGPGGAYI	
QY	781	MVSKAVEIYIQGL	LKPAVVGIIKIDVNSMIEN	FTKTSIRDP	PCAGPVCDCKGNSDVM
DB	781	MVSKAVEIYIQGL	LKPAVVGIIKIDVNSMIEN	FTKTSIRDP	PCAGPVCDCKGNSDVM
QY	841	LDDGGFLLMAN	HDDYTNQIGRPFTEIDPS	LMRHLVNI	SVYAFNKSVDYQSVCEPFGA
DB	841	LDDGGFLLMAN	HDDYTNQIGRPFTEIDPS	LMRHLVNI	SVYAFNKSVDYQSVCEPFGA
QY	901	GAGHRSAYV	SVADILQIGWATAA	WSILQQFLLSLT	PPRLLEAVEMEDEDDFTAS
DB	901	GAGHRSAYV	SVADILQIGWATAA	WSILQQFLLSLT	PPRLLEAVEMEDEDDFTAS

[illegible]

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
FILE REFERENCE: SD9813DA
CURRENT APPLICATION NUMBER: US/10/375,253
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: 08/450,273
PRIOR FILING DATE: 1995-05-25
PRIOR APPLICATION NUMBER: 08/404,354
PRIOR FILING DATE: 1995-02-15
PRIOR APPLICATION NUMBER: 07/914,231
PRIOR FILING DATE: 1992-07-13
PRIOR APPLICATION NUMBER: 08/314,083
PRIOR FILING DATE: 1994-09-28
PRIOR APPLICATION NUMBER: 07/914,231
PRIOR FILING DATE: 1992-07-13
PRIOR APPLICATION NUMBER: 07/603,751
PRIOR FILING DATE: 1990-11-09
PRIOR APPLICATION NUMBER: 08/290,012
PRIOR FILING DATE: 1994-08-11
PRIOR APPLICATION NUMBER: 08/149,097
PRIOR FILING DATE: 1993-11-05
PRIOR APPLICATION NUMBER: 08/105,536
PRIOR FILING DATE: 1993-08-11
PRIOR APPLICATION NUMBER: 08/149,097
PRIOR FILING DATE: 1993-11-05
Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Fast-Seq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 1103
TYPE: PRT
ORGANISM: Human
US-10-375-253-47

Query Match 98.6%; Score 5367; DB 12; Length 1103;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1028; Conservative 0; Mismatches 1; Indels 26;

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QY 61 YEKYQDLTYVEPNNAQVLAARDIEKLLSNRSKALVSLALEAEKVAQAQHWREI
DB 61 YEKYQDLTYVEPNNAQVLAARDIEKLLSNRSKALVSLALEAEKVAQAQHWREI
QY 121 EVVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGRQISYQHAAVHIPTDIYEG
DB 121 EVVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGRQISYQHAAVHIPTDIYEG
QY 181 NELNWTSLALDEVFKKREEDPSLLWQVFGSATGLARYYPASPMVDNSRTPNKIDL
DB 181 NELNWTSLALDEVFKKREEDPSLLWQVFGSATGLARYYPASPMVDNSRTPNKIDL
QY 241 RPWVIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFN
DB 241 RPWVIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFN
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGSPAFPEOLLNINVSBRANC
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGSPAFPEOLLNINVSBRANC
QY 361 PTDCGEERAQIEIFNKYNKKVRFVRSVQGHNYERGFIOVMACENKGYIYEIP
DB 361 PTDCGEERAQIEIFNKYNKKVRFVRSVQGHNYERGFIOVMACENKGYIYEIP
QY 421 INTQBYLDVLRPMVLADGKAKQVQWNTNVYLDALGLVITGTLPVFNITGQFEI
DB 421 INTQBYLDVLRPMVLADGKAKQVQWNTNVYLDALGLVITGTLPVFNITGQFEI
QY 481 NQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYVFAIDPNGYVLLHPNLQPKIGV
DB 481 NQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYVFAIDPNGYVLLHPNLQPKIGV

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IQTSDGPNPCDMVK 1036

pplication US/10375253
US20040018510A1
ATTION:
E SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES

GenCore version 5.1.6
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in search, using sw model

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(without alignments)
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-10-090-827-14
43
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OSUM62

pop 10.0 , Gapext 0.5

7863 seqs, 47026705 residues

ts satisfying chosen parameters: 127863

gth: 0

gth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

WISSProt_41.*

; the number of results predicted by chance to have a
; r than or equal to the score of the result being printed,
; ed by analysis of the total score distribution.

SUMMARIES

very	Arch Length	DB	ID	Description
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96.2	1091	1	CIC2 RAT	P54290 rattus norv
96.0	1106	1	CIC2 RABIT	P13806 onctolagus
13.1	1249	1	UN36 CAEL	P34374 caenorhabdi
3.6	886	1	ITH3 MOUSE	Q61704 mus musc
3.3	885	1	ITH3 HUMAN	Q06033 homo sapien
3.3	887	1	ITH3 RAT	Q63416 rattus norv
3.0	886	1	ITH3 MESAU	P97280 mesocricetu
3.0	1829	1	DPOL_THERST	C13845 thermococcu
2.9	1956	1	ATX1_PLAFA	Q04956 plasmodium
2.9	575	1	YFBK ECOLI	P76481 escherichia
2.8	946	1	ITH2 HUMAN	P19823 homo sapien
2.8	1290	1	BXCI_CLOBO	P18640 clostridium
2.8	420	1	Y103_SYNY3	Q55874 synechocyst
2.8	921	1	ITH4_PIG	P79263 sus scrofa
2.8	654	1	MCPC_BACSU	P54576 bacillus su
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2.6	1169	1	SMC_METJA	Q59037 methanococc
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2.6	3305	1	APLP_MANSE	Q25490 manduca sex
2.6	764	1	PAG_BACAN	P13423 bacillus an
2.6	1513	1	STUL_YEAST	P38198 saccharomyc
2.5	1180	1	C4AA_BACTI	P16480 bacillus th
2.5	3063	1	CAIC_HUMAN	Q99715 homo sapien
2.5	946	1	ITH2_MOUSE	Q61703 mus musc
2.5	2077	1	TEGU_HSVGU	P52340 human herpe
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2.4	1323	1	ADRI_YEAST	P07248 saccharomyc

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38	131	2.4	1634	1	DPOL_METJA	Q58295 meth
39	131	2.4	1658	1	YM67_YEAST	Q03661 sacc
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41	130.5	2.4	1018	1	YC14_METJA	Q58611 meth
42	130.5	2.4	1036	1	Y946_ARCFU	O29316 arch
43	129	2.4	1244	1	Y307_MYCPN	P75342 myco
44	128.5	2.4	1254	1	UBPC_YEAST	P39538 sacc
45	128	2.4	1113	1	Y140_MYCPN	P75033 mycc

ALIGNMENTS

RESULT 1
ID -CIC2 HUMAN STANDARD; PRT; 1091 AA.
AC P54289;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.
DE CACNA2D1 OR CACNL2A OR CCHL2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92110010; PubMed=1309651;
RA Williams M.E., Feldman D.H., McCue A.P., Brenner R.,
RA Velicelebi G., Ellis S.B., Harpold M.M.;
RT "structure and functional expression of alpha 1, alpha 2, and be subunits of a novel human neuronal calcium channel subtype";
RL Neuron 8:71-84(1992)
CC - FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT R
CC - EXCITATION-CONTRACTION COUPLING.
CC - SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBU
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE
CC AORTA TISSUES
CC - PFM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSE
CC A PRECURSOR FORM (BY SIMILARITY).
CC - SIMILARITY: TO OTHER SPECIES' ALPHA-2 SUBUNIT.
CC - SIMILARITY: Contains 1 VMFA domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a col
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the European Bioinformatics Institute. There are no restric
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modified and this statement is not removed. Usage by and for
entities requires a license agreement (See <http://www.isb-sib.ch>
or send an email to license@isb-sib.ch).
CC
CC EMBL; M76559; AAA51903.1; --
CC PIR; JH0565; JH0565.
CC Genew; HGNC:1399; CACNA2D1.
CC MIM; 114204; --
CC GO; GO:0005891; C: voltage-gated calcium channel complex; TAS.
CC GO; GO:0015270; F: dihydropyridine-sensitive calcium channel a..
CC GO; GO:0006832; P: small molecule transport; TAS.
CC InterPro; IPR004010; Cache.
CC InterPro; IPR002035; VNF_A.
CC Pfam; PF02743; Cache; 1.
CC Pfam; PF00092; vwa; 1.
CC SMART; SM00327; VWA; 1.
CC PROSITE; PS50234; VMFA; 1.

Transmembrane; Ion transport; Voltage-gated channel;
1; Glycoprotein; Phosphorylation; Signal.
24
15 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT
15 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY
SIMILARITY).
46 469
06 930
57 1086
53 430
92 92
36 136
84 184
24 324
48 348
75 475
85 585
94 594
63 663
69 769
12 812
76 876
83 883
73 973
86 986
501 501
333 833
391 AA; 123183 MW; 284E13EE29A47837 CRC64;
100.0%; Score 5443; DB 1; Length 1091;
arity 100.0%; Pred. No. 6.3e-318; Indels 0; Gaps 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
3CLIALTLTQSLILIGSPSEPPSAVTKISWVDMQEDLVTLAKTASGVNQLVDI 60
GCLLALTLTQSLILIGSPSEPPSAVTKISWVDMQEDLVTLAKTASGVNQLVDI 60
YQDLYTVEPNARQVLEIARDIEKLSNRKALVSLALEAEKVQAAHWRDEPASN 120
YQDLYTVEPNARQVLEIARDIEKLSNRKALVSLALEAEKVQAAHWRDEPASN 120
YNNAKDDLDPKNDSEPSQRIKPVFIEDANFGQISYQAAVHPTDIYEGSTIVL 180
YNNAKDDLDPKNDSEPSQRIKPVFIEDANFGQISYQAAVHPTDIYEGSTIVL 180
NNTSALDEVFKKREEDPSLLMQVFGSATGLARYYPASPVWDSNRTPKNIDLYVRR 240
NNTSALDEVFKKREEDPSLLMQVFGSATGLARYYPASPVWDSNRTPKNIDLYVRR 240
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YTIQGAASPKDMLILVDVSGVSGLTCLKLIRTSVSEMLETLSDDDFVNVSFNSAQD 300
YFOHLVQANRKNKVLKDAVNNITAKGITDYKKGFGFAFQQLNLYNVRANCKIIML 360
YFOHLVQANRKNKVLKDAVNNITAKGITDYKKGFGFAFQQLNLYNVRANCKIIML 360
DGGERAQEILFNKYNKDKKVRFRFSVQGHNYERGPQWACNKGYYIPISGAIR 420
DGGERAQEILFNKYNKDKKVRFRFSVQGHNYERGPQWACNKGYYIPISGAIR 420
TQEYLDVLRPMVLGAKQVQWNTVNVLDALGLVITGLTPVFNITGQFENKTNLK 480
TQEYLDVLRPMVLGAKQVQWNTVNVLDALGLVITGLTPVFNITGQFENKTNLK 480
YILGVMGVDSLEDIKRLTPFTLCPNGYVFAIDPBGVLLHPNLQPNKPSQBPVTL 540
YILGVMGVDSLEDIKRLTPFTLCPNGYVFAIDPBGVLLHPNLQPNKPSQBPVTL 540
YDAELENIDKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTPVNGTDYSL 600
YDAELENIDKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTPVNGTDYSL 600

601 ALVLPYSPYIIKAKLEETITQARSKKGKMDSETLKPONFESGYTFIAPRYCNI
601 ALVLPYSPYIIKAKLEETITQARSKKGKMDSETLKPONFESGYTFIAPRYCNI
661 SDNNTFLNPNFIDRKTNNPNSCNADLNRLVLLDAGFTNELVQNTWSQKNIKG
661 SDNNTFLNPNFIDRKTNNPNSCNADLNRLVLLDAGFTNELVQNTWSQKNIKG
721 FVVTGGITRYPKAGENQENPETTYEDSFYKRSKNDNDNVFTAPYFNKSGPGAY
721 FVVTGGITRYPKAGENQENPETTYEDSFYKRSKNDNDNVFTAPYFNKSGPGAY
781 MVSXAVIYIYQGLLKPAVVGIKIDVNSWENFTKTSIRDFCAGPVCDCCKNSDVW
781 MVSXAVIYIYQGLLKPAVVGIKIDVNSWENFTKTSIRDFCAGPVCDCCKNSDVW
841 LDDGGFLLMANHDDYTQIGRFFGEIDPSPMRHLVNIISVYAFNKSVDYQSCVCEPG
841 LDDGGFLLMANHDDYTQIGRFFGEIDPSPMRHLVNIISVYAFNKSVDYQSCVCEPG
901 GAGHSAYVPSVADILQIGWATAAANSILOQFLSLTFPRLLLEAVEMEDDDFTAI
901 GAGHSAYVPSVADILQIGWATAAANSILOQFLSLTFPRLLLEAVEMEDDDFTAI
961 SCITETQYTFPNDKSPSGVLDCGNCRIFFHGEKLMNTLIFIMVESKGTCPD
961 SCITETQYTFPNDKSPSGVLDCGNCRIFFHGEKLMNTLIFIMVESKGTCPD
1021 QAEQTSDEGNPCDMVK 1036
1021 QAEQTSDEGNPCDMVK 1036
RESULT 2
CIC2 RAT STANDARD; PRT; 1091 AA.
ID_CIC2 RAT AC P54250; 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta
DE subunits precursor.
DE CACNA2D1 OR CACNA2A OR CCHL2A.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; R
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92228762; PubMed=1314383;
RA Kim H.L., Kim H., Lee P., King R.G., Chin H.;
RT "Rat brain expresses an alternatively spliced form of the
RT dihydropyridine-sensitive L-type calcium channel alpha 2 subunit;
RT Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).
CC -!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT
CC EXCITATION-CONTRACTION COUPLING.
CC -!- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUB
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=2 isoforms are produced;
CC Name=1;
CC IsoId=P54250-1; Sequence=Displayed;
CC -!- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESS
CC A PRECURSOR FORM (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER SPECIES' ALPHA-2 SUBUNIT.
CC -!- SIMILARITY: Contains 1 WFA domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a cc
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BLDRVVPQNTYTYAECINHANFVLGLAVAKDDYRV-----VKQKK 729
LKPNEFESGYTFIAPDYC--NDLKISDNNT-FLNNEFIDR-KTPNPNPCN 686
VNDWMDGKRWLHPHMYCFLNDTDTMSKEEAFIYAQQMSDGSKAPLLCEYR 789
RVLLDAGFTNELVQWYKQKNIK--VKARFVVDGGITRVYP-----733
KILLDMEATSNLDS-WDTQFMFMKNLHLIAFFATPSPGMIRYNTLTDQYDID 848
-----KEAGENWQE--NPETEDSFYKRS-----LDNDNYVF 763
[FPHGHLISIERAQSYNHFTDLNRKSTDDRYRRAVRMKTDMFVSNNSKI 908
FNKSGGAYESGIMVSKAVE-IVYQKLLKPAVVGKIDVNSWIENTKTSIRDPC 822
IQLTGYGLNENLWLGQAFKAIY--LDKAVLG-----SGFE-FAYDHVVDTM 957
CDCKRSDVMDCVLLDGGELLMAHDDYT-----NOIGRFFGEIDPSLMRH 873
-GCPASDRKWCVLDDHAYVFFSNQNDISVEDYLVGKGKHSQYFGGLNRIARA 1015
SVYAFNKS-----DYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAW 927
ALLVENFYKLTITDQAVCAEKVVTSGNRLRPEYPIPRFLMQTFNFWRLAS 1072
QFLSLTFPRLLEAVEMEDDFTASLSQS-----CITEQCYFFDNDKSPSGV-- 981
GFLIWLPIQFTEA-----YTASFHEGTDVYPCQSSFFYKNGKNGRPGTH 1125
N-----CSRIFHGEKLMNTLFIWV-ESKGTCP 1014
NRSERPCONAKCSVKMEASFVDGTLNVWITQDKASENC 1170

STANDARD; PRT; 886 AA.
(Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
trypsin inhibitor heavy chain H3 precursor (ITI heavy
ater-alpha-inhibitor heavy chain 3).
(Mouse).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
0090;
M N A.
/6N; TISSUE=Liver;
4326; PubMed=7534067;
ler J.-L., Raguez G., Salier J.-P.;
eavy-chain precursors for the inter-alpha-inhibitor
ase; new members of the multicopper oxidase protein group
ntial transcription in liver and brain."
306:505-512(1995).
I: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
IG THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
ATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
AL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
ITY).
: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
: INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
JUN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
AVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
TE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
ITY).

CC CC -!- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC CC -!- SIMILARITY: Contains 1 WFPA domain.
CC CC This SWISS-PROT entry is copyright. It is produced through a colla
CC between the Swiss Institute of Bioinformatics and the EMBL out;
CC the European Bioinformatics Institute. There are no restrictions
CC use by non-profit institutions as long as its content is in
CC modified and this statement is not removed. Usage by and for c
CC entities requires a license agreement (See <http://www.isb-sib.ch/>;
CC or send an email to license@isb-sib.ch).
CC CC EMBL: X70393; CAA49843.1; -;
DR PIR: S54355; S54355.
DR MGI: 96620; Itih3.
DR InterPro: IPR006587; VIT.
DR InterPro: IPR002035; WVF_A.
DR Pfam: PF00092; vwa; 1.
DR SMART: SM00609; VIT; 1.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS0234; WVF_A; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 18
FT PROPEP 19 30
FT CHAIN 31 646
FT FT
FT FT
FT PROPEP 647 886
FT DOMAIN 279 439
FT CARBOHYD 88 88
FT CARBOHYD 577 577
FT BINDING 646 646
FT FT
FT SEQUENCE 886 AA; 98977 MW; 15955308CF5030A CRC64;
Query Match 3.6%; Score 194.5; DB 1; Length 886;
Best Local Similarity 19.9%; Pred. No. 0.00054; Indels 261; (
Matches 185; Conservative 138; Mismatches 347;
QY 27 FPSATVTSKWDKQEDLVTLAKTAGSVNQLVDIYEKTDLYTVPEPNNAQVLEI
Db 98 YFGNKEKEVAQKQYKAVSQKTAG----LVKASGRKLEKFTVSVNVAAGSKVT
QY 87 EKLNSRKALVSLALEAEKQVAAHQWREDFASNEVVVYNAKDDLDPEKNDSEPG
Db 154 EELL-KXNGKYEMLKVPKQLVRHFEID-----AHIFEP-
QY 147 PVFIEDANFGRQISYOHAAVHIPTDIYEGSTIVLNLNWTSLALDEVFKKRBEDP
Db 190 GISMLDAE-----ASPTINDL-LGSALTQSF-----
QY 207 VFGSATGLARYYPASPVDNSRT-PNKID-----LYDVERRP-
Db 215 -----SGKKGHVSKPSLDQQRSCPTCTDSSLNGDFTIYVDNRSPGNVQIVNG
QY 246 ---QG-AASPKDMLILVDVSGVSGVTLKIRTSVSEMLETLDSDDFNVASFNS
Db 270 FAQGLPVPEKIVFVIDVSGSGSKRIQOTREALLKILDVDEDDYDNLFIEST
QY 302 SCFQ-HLVQANVRNKKVLKDAVNNITAKGITDYKGFSAFEQILNINVSRA--
Db 327 TTKDHLVQATPANLKEAKTFVKNIHDOQSMNINDGLKGIEML---NKAREDH
QY 355 NKIIIMLTG-----GEERAOBIFKNYK--DKKVRVFRFSVQGHYERGPQIWMJ
Db 384 TSIIMLTGDDANTGESRPEKIQENVNAIGGKFPFLYNLGF-NLNVNFLETIL
QY 409 YYYEIPSGAIRINTQYLDVLGRPMVLADGKAKQVQWNTVYLDALGL--VI
Db 443 LARIYEDSDANLQIQGYEVAANPLL-----TNVEVEYPENAILDLTI
QY 467 FNIQTGFENKTNLKNQLILGVNGVDVSLIEDIKLTPRTLCPNGYYPFADPNGY
Db 492 F-----YDG-----SEIVVAGRLVDRNDN-----FKADVKGH

631-647. AND CROSS-LINKAGE SITE TO BIKUNIN.

```

Query Match          3.3%; Score 182; DB 1; Length 885;
Best Local Similarity 20.2%; Pred. No. 0.003;
Matches 132; Conservative 107; Mismatches 243; Indels 170; (
QY 27 FPSAVTIKSWDRQBEDLVLTAKTAGVGNQLVDIYEKYQDLYTFVFPNNARQLVEL
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 97 YPGNVKEKEVAKQYEKAVSQGTAG-----LVKA
QY 87 EKLISNRSKAL---VSLAREAKVQAQHWREDPASNEVVYVYNAKDLDLPEKQDS
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 132 EKPTSVNVNAAQSKVTPFELYEBLLRRHKG-----YEWYLVKQPK---
QY 144 RIKPVFTEDANFGRIQSYQAAVHPITDIYEGSTIVLNLNMTSALDVEFKQORE
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 174 LVGHFEIE-----VDIFEPQGISMLDAEASFTINDLL-----

```


STANDARD. PRT: 887 AA.

M N.A.
me-Dawley: TISSUE=Liver;

es E.:
EC-1994) to the EMBL/GenBank/DBJ databases.
: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
: PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
: G THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
: LATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
: L TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
: TV).
: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
: TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
: INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
: NININ, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
: AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
: BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
: TV).
: TY: BELONGS TO THE ITIH FAMILY.
: TV: Containing 1 VWFA domain.

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EMBL; X83231; CAA58233.1; -
InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF_A.
Pfam; PF00092; vwa; 1.
SMART; SM00609; VIT; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
Serine protease inhibitor; Repeat; Signal; Multigene family;
Glycoprotein.
SIGNAL 1 21
PROPEP 22 33
SIGNAL 34 647
CHAIN
PROPEP 648 887
DOMAIN 282 442
CARBOHYD 91 91
CARBOHYD 580 580
CHAIN 647 647
SEQUENCE 887 AA; 99097 MW; 3B9FOFF96D514096 CRC64;

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Very Match	3.3%;	Score 180.5;	DB 1;	Lengthn 887;
1st Local Similarity	18.5%;	Pred. No. 0.0037;		
Matches 173; Conservative	139;	Mismatches 350;	Indels 275;	

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27 FPSAVTIKSWVDKQEDLVTTLAKTAGVNLVDIYEKYQDLYTTPENNARQLVEIF
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
101 VDCSVTKPKRVAOKOYEKAVSQGKTAG----LVKASGRKLEKFTVSVNVAAGSKVII

```

87 EKLLNRSKALVSLAEAKVQAAHQWRED---FASNEVVYYNAKODLDPEKNDSI
||| ||| : | : | : | : | : | :
||| ||| : | : | : | : | : | :

157 EELL-KKNKGYEYWKVQPKQLVRHFEIDAHJFEFGQISNDEH
144 RIKPVFIEDANFGROISYQHAAVHIPTDIYEGSTIVNELNWTSAIDDEVFKKNREI

```

      200  -----DASF-----|||:|
                                     :|:|
                                     |TNDL-LGSALTKSF-----

```

[illegible]

218 -----SGKKGRVSKPGLDQQRSCPTCTDSLLNGDFILVIDVVAEESFONVZ-

[illegible]

QDVSCFQHVLQAVNRNKKVLKDAVNNITAKGITYKKGFSAFEQLLNTVNSRAN
299 : : : : : : : : : : : : : : : : NKAFET

330 --TTWKDHLVKATPANLEEARAFVKNIIDRSMTNIDGLLEGIEMT---

354 -CNKLIIMFIDG GGGG..... : : : :
|::||| |::||| : : : :
385 RSTSIIVMLTDGDANTGESRPEKIQENVNRNAIRGFPLYNLFGNNILYNFLESI

```

408 GYYEIPSGAIRINTQEYLDVLGRPMVLGDKAKQVQWNTNYLDALEGL--VI
      ||| | : | : :
      ||| | : | : :
      ||| | : | : :
      ||| | : | : :

```

445 GFARRIYEDSDASLQLQGFYEEVANPLL-----TNVELEYEFENALHLL

```

466 VFNIIGGFENKRNKRNQVLTQVNSLFGSE
      |  ::  :::: || ::::
494 HF-----YDG-----SEIVAGRLVDRNVDN-----FKADVKG!

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526 NLQPKPKSQBPVTLDFLDLDAELENIDKVEIRNKNMIDGESGEKTF-----RTLVI

527 -----DLTFTEEVDMKEMDAALK-----EQGYIFGDIERLWAYLTITEQJUEE

580 YIDKGNRTYTWLPVNGIDISTA--LVEELIAATLAL
:
575 GDEKENIT-----AAEALS LKYHFVTPLTSMVTTKPEDNEDQTAIADKPGEAA

[REDACTED]

QVFGSATGLARYYPASPWDNSR---TPN-KIDLIDVKRRFWIIQQGGGFADTLLYS 13

CC modified and this statement is not removed. Page 71

RESULT 11	YFBK_ECOLI	STANDARD;	PRT;	575 AA.
ID	YFBK_ECOLI			
AC	P76481;			
DT	01-NOV-1997 (Rel. 35, Created)			
DC	01-NOV-1997 (Rel. 35, last sequence update)			
DD	16-OCT-2001 (Rel. 40, last annotation update)			
DE	Hypothetical protein yfbK.			
DN	YFBK OR B2270.			
GN	<i>Escherichia coli</i> .			
GO	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=X12 / MG1655;			
RC	MEDLINE=97426617; PubMed=3278503;			
EX	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RA	"The complete genome sequence of <i>Escherichia coli</i> K-12.";			
RL	Science 277:1453-1474 (1997).			
CC	-1- SIMILARITY: TO SYNECHOCYSTIS PCC 6803 SL0103.			
CC	-1- SIMILARITY: Contains 1 VWFA domain.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a col.			
CC	between the Swiss Institute of Bioinformatics and the EMBL ou			
CC	the European Bioinformatics Institute. There are no restricti			
CC	use by non-profit institutions as long as its content is i			
CC	modified and this statement is not removed. Usage by and for			
CC	entities requires a license agreement (See http://www.isb-sib.ch			

il to license@sib.ch).
; AAC75330.1; --
64998.
95; yfBK.
02035; WVF_A.
VWA; 1.
; VWA; 1.
34; WFA; 1.
rotein; Complete proteome.
6 394 WFA.
; AA; 63634 MW; 7BB6ALA7A2BE111 CRC64;
2.94; Score 157.5; DB 1; Length 575;
urity 21.6%; Pred.No. 0.047; Indels 105; Gaps 25;
nservative 93; Mismatches 206;
ARQLVIAARDIEKLLSNRSKALVSLAEAKVQAAHOMREDPASNEVYVYNKOD 130
CESQQQSPPTPEQQVLAQAQAIK---EAEQSA---AKALAAQEQVQYSDKQA 75
KND-----SEPGSORIKPVFIEDANFORQISYOHAA---VHIPTDI 172
LQEAPTFAAKAKATHIANEGTARYQQF---DDNPVKVAQNPLATFSLDVTGS 132
IIVUNE-----LNWTSALDEVFKNREEDPSLLMQVFGSATGLARYY 218
RRFLNQGLPPPDARVVEEIVNYFPDWDI---KDKQIPASKPTPFAMRYELA--- 187
WVDSNRPTNKIDLVDRRRPWYIQGAASPKDMLILVDVSGS-VSGLTCLKIRTSVS 277
W-NQRTLLKVDILAKORKSEELPAS---NLVFLIDTSGSMISDERLPTQSSLK 241
TLSDDDDFNVASFNASNAQVSCFOHLVQAVNRNKKVLKQAVNNITAKGITDYKKG 337
ELREQDNIAIVTYAGDSRIA-----LPSISGSHKABINAAIDSLDAESTNGAGL 296
EQLLNNYVRANCKNIIMFTDG-----GEARQEIFENKYNKDKKVRFPFVSQ 391
QOATK-GPIKGGINR-ILLATDGFNVGIDDPKSIEMVKQKRSBVTLSFTGVGN 354
RGPIQWACENKGYEYIPIPSIGAIRINTQEVLDVLRPMVL--AGDKAKQVQ---- 445
TEAMVRIADVNGNYSYIDTLS-----EAQKVLNEMRQMLITVAKDVKAQIEFNP 410
YLDALELGAVITGTLPVFENITQFENKTMKQLILGVGVVD-VSLEDI---KRLT 501
EY---RQIG-----YE-----KQRLRVEHFNNDVNDAGDIGAGKHIT 447
TLCNGYFFALDPNGVYLLHPNLOPKNPKSQE 536
ELTLNGQKASIDKLRYA--PDNKLAKSDKTKE 480
STANDARD; PRT; 946 AA.
59; Q15484;
(Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 42, Last annotation update)
trypsin inhibitor heavy chain H2 precursor (ITI heavy
inter-alpha-inhibitor heavy chain 2) (inter-alpha-trypsin
complex component 1) (Serum-derived hyaluronan-associated
IAP).
IBP2.
; (Human).
; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
; Theria; Primates; Catarrhini; Hominidae; Homo.
; 606;
; NM N.A., AND PARTIAL SEQUENCE.
; 52237; PubMed=2450046;

RA Gebhard W., Schreitmuller T., Hochstrasser K., Wachter E.;
RT "Complementary DNA and derived amino acid sequence of the precursor
RT of one of the three protein components of the inter-alpha-trypsin
RT inhibitor complex.";
RL FEBS Lett. 229:63-67(1988).
RN [2]
RP SEQUENCE OF 384-865 FROM N.A.
RX MEDLINE=89068576; PubMed=2446322;
RA Sallier J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,
RA Benarous R., Okubo I., Kurachi K., Martin J.P.;
RT "Isolation and characterization of cDNAs encoding the heavy chain
RT human inter-alpha-trypsin inhibitor (I alpha TI): unambiguous
RT evidence for multipolypeptide chain structure of I alpha TI.";
RT Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).
RN [3]
RP SEQUENCE OF 384-766 FROM N.A.
RX MEDLINE=89076497; PubMed=2462430;
RA Sallier J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,
RA Martin J.P.;
RT "Human inter-alpha-trypsin inhibitor. Isolation and characterizat
RT of heavy (H) chain cDNA clones coding for a 383 amino-acid sequen
RT of the H chain.";
RL Biol. Chem. Hoppe-Seyler 369:15-18(1988).
RN [4]
RP PARTIAL SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA MEDLINE=88024442; PubMed=2663330;
RA Schreitmuller T., Hochstrasser K., Resinger P.W.M., Wachter E.,
RA Gebhard W.;
RT "cDNA cloning of human inter-alpha-trypsin inhibitor discloses th
RT different proteins.";
RL Biol. Chem. Hoppe-Seyler 368:963-970(1987).
RN [5]
RP SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.
RX MEDLINE=89380192; PubMed=2476436;
RA Engild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;
RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin
RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma.
RT polypeptide chain stoichiometry and assembly by glycan.";
RL J. Biol. Chem. 264:15975-15981(1989).
RN [6]
RP SEQUENCE OF 55-64.
RX TISSUE=Plasma;
RA MEDLINE=93039735; PubMed=1384548;
RA Malki N., Balduyck M., Maes P., Capon C., Mizon C., Han K.K.,
RA Tartar A., Fournet B., Mizon J.;
RT "The heavy chains of human plasma inter-alpha-trypsin inhibitor:
RT isolation, their identification by electrophoresis and partial
RT sequencing. Differential reactivity with concanavalin A.";
RL Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).
RN [7]
RP SEQUENCE OF 55-64 AND 681-702, CROSS-LINK STRUCTURE, AND
RP CARBOHYDRATE-LINKAGE SITES THR-691.
RX MEDLINE=93232026; PubMed=7682553;
RA Engild J.J., Salvesen G., Thøgersen I.B., Valnickova Z.,
RA Pizzo S.V., Hefta S.A.;
RT "Presence of the protein-glycosaminoglycan-protein covalent cross
RT in the inter-alpha-inhibitor-related proteinase inhibitor heavy
RT 2/bikunin.";
RL J. Biol. Chem. 268:8711-8716(1993).
RN [8]
RP SEQUENCE OF 67-101, AND HYALURONAN BINDING.
RX TISSUE=Serum;
RA MEDLINE=94075371; PubMed=7504674;
RA Huang L., Yoneda M., Kimata K.;
RT "A serum-derived hyaluronan-associated protein (SHAP) is the hea
RT chain of the inter-alpha-trypsin inhibitor.";
RL J. Biol. Chem. 268:26725-26730(1993).
RN [9]
RP SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULF
RX TISSUE=Plasma;
RA MEDLINE=94229087; PubMed=7513643;
RA Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,

'56:54 2004

MIC

ournet B., Mizon J.;
lphate covalently cross-links the three polypeptide
-alpha-trypsin inhibitor."
221:881-888(1994).

NKAGE SITES, AND MASS SPECTROMETRY.

6; PubMed=9677337;
on C., Balduyck M., Ricart G., Sautiere P., Mizon J.;
pattern of human inter-alpha-inhibitor heavy chains."
749-756(1998).

NKAGE SITES, AND DISULFIDE BONDS.

0; PubMed=9425062;
ahbek-Nielsen H., Thøgersen I.B., Roepstorff P.,

mal modifications of human inter-alpha-inhibitor;
of glycans and disulfide bridges in heavy chains 1 and

7:408-416(1998).
WAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
JTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
ON SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
TO CELLS UNDERGOING BIOLOGICAL PROCESSES.
-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.
NTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
N, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
ND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
BRIDGE TO THE THEIR C-TERMINAL ASPARTATE.
ROMETRY: MW=76508; METHOD=MALDI; RANGE=55-702.
: BELONGS TO THE ITIH FAMILY.
: Contains 1 VWFA domain.

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profit institutions as long as its content is in no way
his statement is not removed. Usage by and for commercial
res a licensee agreement (see [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)).
ill to license@isb-sib.ch).

CAA30160.1; ALT SEQ.

AAA60558.1; -

AAA59195.1; -

(VHU2

PI9823; -

[67; ITIH2.

1; F:plasma glycoprotein; TAS.

06587; VIT.

002035; VWFA_A.

; vwa; 1.

9; VIT; 1.

7; VWFA; 1.

234; VWFA; 1.

se inhibitor; Repeat; Signal; Multigene family;

glutamic acid; Glycoprotein.

POTENTIAL.

1 18

19 54

55 702

H2.

VWFA.

03 946

08 468

61 284

50 651

18 118

66 666

71 671

73 673

INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN

H2.

VWFA.

VWFA.

VWFA.

VWFA.

VWFA.

VWFA.

VWFA.

VWFA.

VWFA.

VWFA.

VWFA.

VWFA.

VWFA.

VWFA.

FT CARBOHYD 675 675 /FTID-CAR 000215.
FT O-LINKED (GALNAC. . .).
FT /FTID-CAR 000216.
FT O-LINKED (GALNAC. . .).
FT /FTID-CAR 000217.
FT MOD_RES 282 282 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 283 283 GAMMA-CARBOXYGLUTAMIC ACID.
FT BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT CONFLICT 374 374 K -> L (IN REF. 5).
FT CONFLICT 674 674 P -> A (IN REF. 2 AND 3).
FT CONFLICT 705 705 F -> S (IN REF. 2 AND 3).
FT CONFLICT 729 729 N -> D (IN REF. 2 AND 3).
FT CONFLICT 731 731 V -> A (IN REF. 2 AND 3).
SQ SEQUENCE 946 AA; 106436 MW; 1478CF3E8F3BA776 CRC64;

Query Match 2.8%; Score 154.5; DB 1; Length 946;

Best Local Similarity 19.8%; Pred. No. 0.15;
Matches 133; Conservative 106; Mismatches 259; Indels 171; Ga

QY 33 IKSWDKMDELYLAKTAGVGNOLVDIYKQDLYTVEPNNAQOLVETIAARDIEKL
Db 26 LSEFYD--YEDLVEL---APGKQLVAENRRYQSLPGSEEMEEVDQVTLISYKV
QY 93 RSKALVSLALAEKVAQAAHQWRE-----DFASN-----
Db 81 ITSRWATNIOGKVVNNSPQNVVDFVQIPKGAIFSNFSMTVDCGKTFRSSIKETV
QY 123 VYNNAK-----DDLDPKNDSE-----PGSQRIKPFVIEDANFGROISYQH-
Db 141 LYAQAARAKGTAGLVRSALDMENFTEVNLPGAKVQFELHYQVQKMKLGSYEHF
QY 164 -----AAVHIPTDIYEGSTIVNELNWTSLD-----EVFKKNRE-----DPSLLY
Db 201 QPGLAKHLEVVDVWVIEPQGLRFLHVDPTFEGHGFVPSISKQQAHAHVSPKPTVA
QY 209 GSATGLARYTPASPWVDNSRTNPKIDLYDVRPP-----WYQGAAS-----
Db 259 -----RLCPSCR--ETAVDGLVLYDVKREKAGELEVNGYFVHFPAFDNLD!
QY 253 DMLILVDVSGSVGTLKLIKRTSVSEMLETLSDDDFVNVAASNNAQDVSQFHLV
Db 310 NILFVIDVSGSMGVMKQKTVEAMKTLDDLAEDHPSVIDFNQNR--TWNDLLI
QY 313 RNKKVLKADVNNITAKGIDTYKGF---SFAPEQLNLYNVRANCNKIIMLFTDG-
Db 368 TVADAKRYIEKIQPSGGTNINEALLRAIFILNEANNLGLDPSVSLILLVSDGD
QY 366 EERAQELFNKYNKDKKVRVFRFSVGQ-----HNYERGPQMM-----A
Db 428 ELKSLKQKVKENIQDNISLSLGMGFDYDYLKRLSNENHIGIAQRIYGNQDTS
QY 408 GYTYEI--PSIGAIRIN--TQEVLDVL-----GRPMVLG--DKAKQVQWNT
Db 488 KFYNQVSTPLLRNVQFNYPHTSVTDVQNNFNHYFGGSEIVVAGKFDPAK-----
QY 453 ALEGLVITGTLPVFNITGQFNKTNLKNOLLGVMGVDSLEDI---KELTPRF
Db 540 QIE--SVITA-----TSANTQLVLETIAQMDLQDFLSKQKHPDF
QY 509 NGYFATDPNGYVLLHPNLQPKPKSQEPVTLDFDLAELENDIKVEIRNMIDGES
Db 583 LWAYLTIN---QLLAERSLAP-TAAAKRITRSILOMSLDHHTVPLTSLVIENEF
QY 569 FRTLKVSQD 577
Db 639 MLADAPPD 647

RESULT 13

BXCL CLOBO

ID BXCL CLOBO STANDARD; PRT: 1290 AA.

AC P18640;

DT 01-NOV-1990 (Rel. 16, Created)

7:56:54 2004

al. 16, Last sequence update)
 al. 41, Last annotation update)
 toxin type C1 precursor (EC 3.4.24.69) (BONT/C1)
 C1).

ulnium. Clostridia; Clostridiales; Clostridiaceae;

1;

N.A.
 87; PubMed:2204031;
 and M.W., Kurazona H., Binz T., Niemann H., Gill D.M.,
 off M.R.;
 sequence of Clostridium botulinum C1 neurotoxin.";
 Res. 18:4924-4924(1990).

N.A.
 Stockholm / C-ST;
 198; PubMed:2222445;
 li N., Tsuzuki K., Murakami T., Indoh T.,
 akeshi K., Syuto B., Oguma K.;
 nucleotide sequence of the gene coding for botulinum
 in the C-ST phage genome.";
 ys. Res. Commun. 171:1304-1311(1990).

-25.
 Stockholm / C-ST;
 072; PubMed:2450568;
 okosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,
 t of a monoclonal antibody recognizing an antigenic site
 stridium botulinum type B, C1, D, and E toxins and
 .";
 . 56:898-902(1988).

N OF SUBSTRATE.
 966; PubMed:7901002;
 pman E.R., Yamasaki S., Binz T., Niemann H., Jahn R.;
 urotoxin C1 blocks neurotransmitter release by means of
 1/syntaxin.";
 21-4828(1993)
 BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 ; BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
 (DASE THAT CLEAVES SYNTAXIN.

: ACTIVITY: Limited hydrolysis of proteins of the
 cytosol apparatus, synaptobrevins, SNAP25 or syntaxin. No
 action on small molecule substrates.
 : Binds 1 zinc ion per subunit (By similarity).
 DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A
 AIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,
 E-N AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL

N AND TOXIN BINDING, RESPECTIVELY.

LAR LOCATION: Secreted.

NEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF

M NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.

NEOUS: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C

F CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE

PHAGE.

TY: BELONGS TO PEPTIDASE FAMILY M27.

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i Bioinformatics Institute. There are no restrictions on its

-profit institutions as long as its content is in no way

i this statement is not removed. Usage by and for commercial

quires a license agreement (See <http://www.isb-sib.ch/announce/>;

mail to license@isb-sib.ch).

3; CAA47060.1; -

3; CAA51313.1; -

2

DR EMBL; X53751; CAA37780.1; -;
 DR EMBL; D90210; BAA14235.1; -;
 DR EMBL; X62389; CAA44263.1; -;
 DR HSSP; P10845; 3BTA.
 DR MEROPS; M27.002; -;
 DR InterPro; IPR000395; Bontoxilysin.
 DR InterPro; IPR006025; Zn_Mtpeptidse.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; Bontoxilysin.
 DR ProDom; PD001963; Bontoxilysin; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
 KW INIT MET 0
 FT CHAIN 1 448
 FT CHAIN 449 1290
 FT METAL 228 228
 FT ACT SITE 229 229
 FT METAL 232 232
 FT DISULFID 436 452
 FT CONFLICT 84 84
 FT CONFLICT 84 84
 SQ SEQUENCE 1290 AA; 148734 MW; 71FB379F97129E8 CRC64;
 Query Match 2.8%; Score 152; DB 1; Length 1290;
 Best Local Similarity 20.3%; Pred. No. 0.33;
 Matches 205; Conservative 125; Mismatches 346; Indels 334; G;
 QY 106 KVOAAHQWREDFASNEVVYNAKDDLDPEKNDSEPGSQRIK---PVFIEDANFR-
 Db 138 KTRQGNWVKTSINPSVIITG-----PRENIIDPETSTFKLTNNYFAAQEGFAL
 QY 158 -----QISYOHAAVHIPTDIYEGS-----TIVLMELNWTSAIDVEFK---
 Db 193 ISPRFMLTYSNAT-----NDVGEGRFSKSEFCMDPILIMHELN--HAMHNLGYIAI
 QY 199 EDPSSLWQVGSATGLARYYP-----ASPWVDNRTNPKIDLDYVRRPWPYIOGAA
 Db 247 TISSVTSNIFYSQYNVKLEYAEIYAFGGPTID--LIPKARKYFEKALDYRSIP
 QY 254 MLILVDVSG---SVSGLTLKILR-----TSVSEMLETLDSDDFVNVASFNSNAQI
 Db 305 SITTANPSSFNKYIGEYKQKILIRYRFVSVESGEV--TVNRNKFVEL--YNELTQI
 QY 305 QHLVQANVRNKKV-LKDAVNNTAK---GITDYKKGFSAPEQL-----LNVNVI
 Db 361 NYAKIYNQNRKIYLSNVYTPVTANILDDNVDYIQNGFNPKSNLNLVLFMGQNLIS
 QY 352 --ANCKNIIMLFT-----DGGEERAQEIFNK-----YMKD-----KK
 Db 421 RKVNENMLYLFKFKHKAIDG-----RSLYNKTLDCRELLVKNYDLPPIGDISD
 QY 387 FSVGQHYRGRPIQWACENKGYIYELPSIGAIRI--NTQEY--LDVL-----
 Db 476 FLRKDINBETEV-----YYPDNVSVQVILSKNTSEHGQDLDDLYPSIDSE
 QY 431 GRPMVLGAKAKOVQWNTN--VYLDALGLVITGTLPVFNITGQFENKTN-----
 Db 527 GENQVYDNRNTQNDYINSYIYLESQKL-----SDNVEDFTFRSIREALDSAKV
 QY 479 -LKNQILILYMG-----VDVSLEDIKRLTPRFTLCPNGYIFALDPNGVLLHP
 Db 583 TLANKVNAGVQGGFLMWANDVVEFTTILRKDTLDKISDVSAIIP-----YIGF
 QY 531 NPKSQEPVTLDF-----LDAELENDI-----KVEIRNKMIDGESER
 Db 639 NSVRRCNGTFAFAVTGVTILLAPPEFTIPALGAFVYISKVQRNEII-----K
 QY 573 VKSQDERYIDKGNRTYTW-----TFVNGTDYSLALVLPYTSYFYKAKLE
 Db 693 LEORIKKWKD-----SYEMWMTLSRLITQFNNTISYQMYDSL-NYQAGAKAKII
 QY 623 ARSKKGRMKDSETLKP--DNFESGYTFIAPRDYCNLDKISDNNTEFLLNFNEF
 Db 743 LEYKYSDDKENIKSQVENLKNS-----LDVKIS-----EAMNNINKE.

-----DRKTPNPNCSNADLINRVLLDA----- 697
 MLPKVIDELNEFRDNT-----KAKLIN--LTDSEHIIIVGEVDKIKAVNNVF 839
 -----GFTN-----ELVQNYW-----SKQNKIKGVKARFVVTDGGITRVYPKEAGE 738
 NIFSNTNSSLKDIINEFNNINDSKILSLQNRKTLVDTSG-----YNAEYSE 894
 INPETYEDSPYKSLDNDNYFTAPYFNKSGPGAYESGIMVSKAVEIYQGLLK 796
 -----IF--PPDFKLGSSGEDRGKIVITVQENINIVNYSME 935
 [KIDVSWINFTKTSIRDCAGVCDCKNSVDMDCVILDDGGFLMANHD--- 853
 FWRINKWVNLPGYTIID-----SVKNKSGWISGIIISFLVFLTKQNEDEQ 988
 -DYNQIGR-----FFGIDPMLRHLVNIISVAFNKSVDYQSVCE 893
 YDISNAPGNKYNKFFVTVTNMMG---NMKIYNGKLIIDTIKYKE 1035

STANDARD; PRT; 420 AA.

el. 35, Created)
 el. 35, Last sequence update)
 el. 41, Last annotation update)
 rotein all0103.

sp. (strain PCC 6803).
 obacteria; Chroococcales; Synechocystis.
 8;

N.A.
 29; PubMed=8590279;

aka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 bata S.;
 ysis of the genome of the unicellular cyanobacterium
 sp. strain PCC6803. I. Sequence features in the 1 Mb
 up positions 64% to 92% of the genome.";
 1-166(1995).

TO E.COLI YFBK.
 Contains 1 VFMA domain.

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 ail to license@isb-sib.ch).

BAA10635.1; -.

376691.

002035; VFMA.

7; VWA; 1.

234; VFMA; 1.

protein; Complete proteome.

0 AA; 45849 MW; E7111B51478E74F3 CRC64;

2.8%; Score 151.5; DB 1; Length 420;

arity 20.8%; Pred. No. 0.067;

onservative 85; Mismatches 183; Indels 55; Gaps 16;

ILILDVSGSVGLTKLIRTSVSEMLETSLDDFFNVASFNQAQVSCFHLVQA 310

CLVLDHSGSGMDGQPLETVKSAALGLIDRLBEDRLSLVIAFDHRAKIV-----INQ 95

TKVLKDAVNNITAKGITYKGFSPAFQLNLYNVSRANCKNIIMLFTDGGGEAAQ 370

Db 96 QVRNGAIAIAIRLKAEGGTADDEGLKLGIOAAKKEKEDRVS---HIFLLTDGENE
 Qy 371 E-----IFNKYNKDKKVRVFRFSGQHNHYERGPIQWMACENKG---YYEIPISGAIIRI
 Db 153 NDRCLKGTGTVASDYKLIVHTLGFGDH-WNQDVLBAIAASAGSLSIYENPS-EALHT
 Qy 425 EYLDVLGRPMVLADGKAKQVQMTNVYLDALGLG-----LVITGTLVPVNIITQGFENKI
 Db 211 LF-----QRMNSVGLTNAHL-LLELAPQAHAI--VKEVAQVSPETMDLT
 Qy 481 NQLILGVMGVDVSLIEDIKLTPRTLCPCNGYFALDPNGYVLLHPLNLPQKPKKQSE-
 Db 255 NQGAIEEVRGLGDMTDQERV-----LLNLKLDQLPCQHVIGQVIRYDDPASQT
 Qy 537 ----PVLIDFDLDAELENDIKVEIRNKMIDSGSEKTI--FRTLVSQDERYIDKGNRT
 Db 310 SDPLPLTIQ-VQTQYQPSDVTQVQESILTLAKYRQTQIAETKLKAGDRQGAATMLQT
 Qy 591 TPVNGTDSYSLALVPTSYFYIKAKLETITQARSKKGKMKDSETLKP 638
 Db 369 TALQMGDKNGATILQTNA---TRLQSGEDLSEGDREKTRKTRMVSNTLQP 413

RESULT 15

ITH4 PIG STANDARD; PRT; 921 AA.
 AC P79263;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inter-alpha-trypsin inhibitor heavy chain H4 precursor (ITI heavy
 DE chain H4) (Inter-alpha-inhibitor heavy chain 4) (Inter-alpha-trypt
 DE inhibitor family heavy chain-related protein) (IHRP) (Major acute
 DE phase protein) (MAP).
 GN ITIH4 OR IHRP.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1] SEQUENCE FROM N.A., AND SEQUENCE OF 28-36; 695-703 AND 710-722.
 RP TISSUE=Liver;
 RC MEDLINE=96271024; PubMed=8930057;
 RX Ozawa A., Yasue H., Tomita M.;
 RA Hashimoto K., Tobe T., Sumiya J.-I., Sano Y., Choi-Miura N.-H.,
 RT "Primary structure of the pig homologue of human IHRP: inter-alpha-
 RT trypsin inhibitor family heavy chain-related protein.";
 RL J. Biochem. 119:577-584(1996).
 [2]
 RN PRELIMINARY SEQUENCE OF 267-556 FROM N.A.
 RP TISSUE=Liver;
 RC MEDLINE=90371455; PubMed=1697703;
 RX Buchman T.G., Cabin D.E., Vickers S., Deutschman C.S., Delgado E.
 RA "Molecular biology of circulatory shock. Part II. Expression of f
 RT groups of hepatic genes is enhanced after resuscitation from
 RT cardiogenic shock.";
 RL Surgery 108:559-566(1990).
 [3]
 RN SEQUENCE OF 28-54 AND 223-240.
 RP TISSUE=Serum;
 RC MEDLINE=96013138; PubMed=7556597;
 RX Gonzalez-Ramon N., Alava M.A., Sarsa J.A., Pineiro M., Escartin A
 RA Garcia-Gil A., Lampreave F., Pineiro A.;
 RT "The major acute phase serum protein in pigs is homologous to hum
 RT plasma kallikrein sensitive PK-120.";
 RL FEBS Lett. 371:227-230(1995).
 CC -!- FUNCTION: MAY BE INVOLVED IN ACUTE PHASE REACTIONS.
 CC -!- TISSUE SPECIFICITY: Liver-specific.
 CC -!- INDUCTION: LEVELS INCREASE SIGNIFICANTLY AFTER CARDIOGENIC
 CC -!- SHOCK.
 CC -!- PTM: APPEARS TO BE BOTH N- AND O-GLYCOSYLATED (BY SIMILARITY)

7:56:54 2004

us-10-090-827-14.rsp

3D BY PLASMA KALLIKREIN TO YIELD 55- AND 25-KDA

: BELONGS TO THE ITIH FAMILY.
: Contains 1 VFMA domain.
EF 2 SEQUENCE IS INCORRECT DUE TO FRAMESHIFTS AND OTHER
ERRORS.

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AA000024.1; -
AAB46821.1; -
-; NOT_ANNOTATED_CDS.
[C4625. VIT.
006587; VIT.
002035; VWF_A.
; VWA; 1.
; VIT; 1.
; VWA; 1.
134; VWA; 1.
se inhibitor; Repeat; Signal; Multigene family;

1 27
28 921
H4.
VFMA.
N-LINKED (GLCNAC. .) (POTENTIAL).
30 80
N-LINKED (GLCNAC. .) (POTENTIAL).
05 205
N-LINKED (GLCNAC. .) (POTENTIAL).
42 242
N-LINKED (GLCNAC. .) (POTENTIAL).
13 513
N-LINKED (GLCNAC. .) (POTENTIAL).
77 577
HT -> SK (IN REF. 3).
49 50
D -> H (IN REF. 1; AA SEQUENCE).
03 703
1 AA; 102146 MW; E2BF9525DE8D07C CRC64;

2.8%; Score 150.5; DB 1; Length 921;
arity 19.9%; Pred. No. 0.25;
conservative 100; Mismatches 264; Indels 265; Gaps 36;

ALTTL-----FQSLIGSSSEPPSPSAVTKSWDK---MOED--- 43
VLPALLAVLQSTTAHKNIDINIYSLTVDSKVSRAFTVTVSRVKNKSGAVGEATFQ 69
-----LVTLAKTASGVNQLDIVEK--YQDLYT-VEPNNAQLVEIAARDIEKL--- 89
'KKAFTNFMSIDGVTYPCNIKEKAAQEQYSAVARGESAGLVRAATGRKTRQFOVA 129
'SKALVSLALEAEKQVAAHQWREDPASNEVVVYNAKDDLDPEKNDSEPGSQRKVPF 149
'APAAKTFVELVYELLARH-----LGUYELLKTKQPQ-----QLVKHLQ 171
ANFGRO-ISKY-QRAAVHIPTDIYEGSTIVLNE-----LNWTSALDEVFKKNREEDPSL 203
HFEPOGISPLETETESTFMTNELAELTISQNKTKAMIRFPKPTLSQQ-QKSPEQOEV 230
-----MQVFGSATG-----LARYYPASPPVDNSRTPNKIDLYDVRPPWYIQG 247
NFIVRYDVRNRTVVGSGIQIENGVPVHFAPEVW----- 266
PKDMLILVDVSGVSGLTLLKIRTSVSEMLETSLDDDFVNVASPNAGVSCFQHL 307
PKNVIFVIDISGSRGRKIQQTREALIKILGLGSRDQFNLVSPSGEAPR-----RRA 322
NVRNKKVLKDAVNNITAKGTDYKKGFSFAPEQLLNNVSRANCNKI-----IM 359
SAENVEAKSYAAEIHAAQGGTNINDAMLMVQLL-----ERANREELLPARSVTFII 377
DG-----GEERAQEIFNKYNKDKKVRV-----FRPSVGQHNYERGPIQWMA 403

Db 378 LLTGDPTVGETNPSKI-----QKNVREADGQHSFLCFLGFGFDPVPAFLEK-----
QY 404 CENKG-----YY-----YEIPSGAIRINTQBYLDVL-
Db 427 LENGGLARRIYEDSDALQLEDFYQEVANPLRLVAFEPYS-NAVEEVTQDNRFLFF
QY 433 PMVLAG---DKAKQVQWTVNVLDALELGLVITGLTPVENITGQFENKTNLKNQLILG
Db 486 ELVWAGKLRDQSPDV-----LSAKVRGQLHMENTVFWMSRVAEQEAEFLS
QY 487 -----VMGVDSLEDI--KELTPRFTLCPNGYFAIDPNGYVLLF
Db 535 IFHSMERLWAVLTQQLLAQTVSASDAEKKALEARALSLSLNSYFVTPLTLSNVIT
QY 528 QPKNPKSQBPVTLDFDAELENDIKVEIRNKMIDGESGEKTFRTLKVSQDERYDK
Db 595 QBSQVABKP-----VNGNRQGNTHSGHSF-----QFHSV
QY 588 YTWTPVNGTDYSLALVLPYTFYIKAKLEETITQARSKKGMKDSITLKNPFEE
Db 631 SRLTGGSSVD-----PVFS-----HRRGWKGQAQ-----GFEX
QY 648 FIAPR 652
Db 662 -LPPR 665

Search completed: February 20, 2004, 16:56:12
Job time : 15.3006 secs

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n search, using sw model

uary 20, 2004, 16:52:19 ; Search time 18.2804 Seconds
(without alignments)
5450.141 Million cell updates/sec

-10-090-827-14

AGCCLLALTTLFQSLIG.....RLLIQAEQTSDEGNPCDMVK 1036

SUM62

op 10.0 , Gapext 0.5

1308 seqs, 96168682 residues

is satisfying chosen parameters: 283308

th: 0
th: 2000000000

imum Match 0%
imum Match 100%
isting first 45 summaries

IR 76.*

Pir1.*

Pir2.*

Pir3.*

Pir4.*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

seq	length	DB	ID	Description
0.0	1091	2	JH0565	calcium channel al
6.2	1091	2	A44147	calcium channel pr
6.0	1106	1	CHBA2	calcium channel al
9.9	1091	2	T30256	calcium channel al
1.2	734	2	S44617	C50C3.11 protein -
0.5	1148	2	T18770	probable calcium c
3.6	1450	2	C86880	hypothetical prote
3.6	886	2	S54355	inter-alpha-trypsi
3.4	885	2	S30350	inter-alpha-trypsi
3.2	1819	2	D97033	uncharacterized pr
3.0	889	2	JC5576	inter-alpha-trypsi
3.0	2706	2	T28155	variant-specific s
2.9	1984	2	A44396	p-type cation tran
2.9	575	2	D64998	hypothetical prote
2.9	918	2	E90542	lipoprotein (impor
2.9	680	2	A97331	membrane associate
2.8	1516	2	E71619	RAD2 endonuclease
2.8	2364	2	I40884	cytotoxin L - Clo
2.8	946	1	IYHU2	inter-alpha-trypsi
2.8	1315	2	T28679	fibrinogen-binding
2.8	932	2	JC5953	inter-alpha-inhibi
2.8	1291	2	S46431	botulinum neurotox
2.8	1291	2	A49777	botulinum neurotox
2.8	420	2	S76691	hypothetical prote
2.8	1426	2	A99580	hypothetical prote
2.8	921	2	JC4625	inter-alpha-trypsi
2.8	1385	2	D89824	hypothetical prote
2.8	654	2	A69556	methyl-accepting c
2.8	1027	2	B90527	atp-binding protei

proteinase
inter-alpha-
rhoxy prot
DNA-directec
hypothetica
methyl-accet
hypothetica
hypothetica
probable rei
internalin
probable pe
hypothetica
hypothetica
cellulose 1
fibronectin-
ATP-depende

ALIGNMENTS

RESULT 1

JH0565
calcium channel alpha-2b chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug
C:Accession: JH0565
P:Williams, W.E.; Feidman, D.H.; McCue, A.F.; Brenner, R.; Velicelbi,
Neuron 8, 71-84, 1992
A:Title: Structure and functional expression of alpha1, alpha2, and be
A:Reference number: JH0564; MUID:92110010; PMID:1309651
A:Accession: JH0565
A:Molecule type: mRNA
A:Residues: 1-1091 <WIL>
A:Cross-references: GB:M76559; NID:G179761; PIDN:AAA51903.1; PID:G1797
A:Experimental source: basal ganglia
A:Note: Several conflicts are found between GenBank submission, author
C:Comment: This protein is a subunit of the voltage dependent calcium
C:Superfamily: calcium channel alpha-2 chain
C:Keywords: glycoprotein; phosphoprotein
P:1-24/Domain: signal sequence #status predicted <SIG>
F:1-25/1067/Product: calcium channel alpha-2b chain #status predicted <C
F:32,268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by
F:91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by prot
F:92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/E
F:501/Binding site: phosphate (Thr) (covalent) #status predicted
F:833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kine

Query Match	100.0%;	Score	5443;	DB	2;	Length	1091;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	1036;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	MAAGCLLALTTLFQSLIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTAGVNM					
DB	1	MAAGCLLALTTLFQSLIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTAGVNM					
QY	61	YEKQDLYTVFPNNARQLVEIAARDIEKLSNRKALVSLAEAEKVQAAGHOREI					
DB	61	YEKQDLYTVFPNNARQLVEIAARDIEKLSNRKALVSLAEAEKVQAAGHOREI					
QY	121	EVVYNAKDDLDPKNDSEPGSQRIKPVFIEDANFGROIISYOHAAVHIPTDIYEG					
DB	121	EVVYNAKDDLDPKNDSEPGSQRIKPVFIEDANFGROIISYOHAAVHIPTDIYEG					
QY	181	NEIWNSTALDEVFKKNREDEPSLLMQVFGSATGLARYYPASFPWVNSRTPNKIDL					
DB	181	NEIWNSTALDEVFKKNREDEPSLLMQVFGSATGLARYYPASFPWVNSRTPNKIDL					
QY	241	RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDSDDFVNVASFN					
DB	241	RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDSDDFVNVASFN					
QY	301	VSCFQHLVQANVRNKKVLKDAVNNITAKGITYKKGFSAPEQLNLYNVRANCN					

|||||HLVQANVRNKKVLDKDAVNNTAKGIDYKGFSPAFQOLLNYSRANCKIML 360
 |||||BERAQEIPFNKYNKDKKVRVFRFSGVQHNYERGP:QMAACENKGYIYIPIPSIGAIR 420
 |||||BERAQEIPFNKYNKDKKVRVFRFSGVQHNYERGP:QMAACENKGYIYIPIPSIGAIR 420
 |||||YLDVLRPMVLADGAKAKQVQNTNVDLDALEGLVITGTLVPFNITGQENKTNLK 480
 |||||YLDVLRPMVLADGAKAKQVQNTNVDLDALEGLVITGTLVPFNITGQENKTNLK 480
 |||||GVMGVDSVLEIDIKRLTPRFTLCPNGYYFAIDPENGYYVLLHPLNLPKNPKSQBPVTL 540
 |||||GVMGVDSVLEIDIKRLTPRFTLCPNGYYFAIDPENGYYVLLHPLNLPKNPKSQBPVTL 540
 |||||AELNDIKVEIRNKMIDGESGKFTLTKVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
 |||||AELNDIKVEIRNKMIDGESGKFTLTKVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
 |||||PTYSFYIYKAKBETITQARSKKGMKOSSETLKPDMFESGYTFIAPRDYCNLDKI 660
 |||||PTYSFYIYKAKBETITQARSKKGMKOSSETLKPDMFESGYTFIAPRDYCNLDKI 660
 |||||TEFLNMFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQNTWSKORNIKGVKAR 720
 |||||TEFLNMFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQNTWSKORNIKGVKAR 720
 |||||DGGITRVYPKEAGENQENPETYEDSFYKSLDNNDNTVFTAPFNKSGPGAYESGI 780
 |||||DGGITRVYPKEAGENQENPETYEDSFYKSLDNNDNTVFTAPFNKSGPGAYESGI 780
 |||||AVEIYIQGLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVPCDKRNSDVMDCVI 840
 |||||AVEIYIQGLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVPCDKRNSDVMDCVI 840
 |||||GFLLMANHDDVTNOIGRFFGIDPSLMRHLVNI SVYAFNKSVDYQSCEPGAAPKQ 900
 |||||GFLLMANHDDVTNOIGRFFGIDPSLMRHLVNI SVYAFNKSVDYQSCEPGAAPKQ 900
 |||||RSAYVPSVADILQIGWATAAAMSILQOFLSLTFFPRLLLEAVEMEDDDFTASLSKQ 960
 |||||RSAYVPSVADILQIGWATAAAMSILQOFLSLTFFPRLLLEAVEMEDDDFTASLSKQ 960
 |||||TQTOYFFNDKSGVGLDCGNCRSRI PHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020
 |||||TQTOYFFNDKSGVGLDCGNCRSRI PHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020
 |||||TSDGNPCDMVK 1036
 |||||TSDGNPCDMVK 1036
 |||||rotein alpha-2 chain precursor - rat
 |||||: dihydropyridine-sensitive L-type
 |||||im channel alpha-2 chain
 |||||norvegicus (Norway rat)
 |||||34 #sequence_revision 27-Jun-1994 #text_change 20-Aug-1999
 |||||47
 |||||H.; Lee, P.; King, R.G.; Chin, H.
 |||||Sci. U.S.A. 89, 3251-3255, 1992
 |||||n expresses an alternatively spliced form of the dihydropyridine-sensit
 |||||r: A44147; MUID:92228762; PMID:1314383
 |||||47
 |||||nary
 |||||mRNA
 |||||1 <KIM>
 |||||s: GB:M6621; NID:g203954; PIDN:AAA41088.1; PID:g203955
 |||||licium channel alpha-2 chain
 |||||um; glycoprotein; ion channel; transmembrane protein
 |||||96.2%; Score 5234; DB 2; Length 1091;

Best Local Similarity 95.7%; Pred. No. 2.7e-307; Indels 2; Gc
 Matches 992; Conservative 24; Mismatches 19;
 QY 1 MAAGCLLALTTLFQSLIGPSSEBPPFSAVTIKSWVDKQBEDLVTLAKTAGVNOI
 DB 1 MAAGCLLALTTLFQSLIGPSSEBPPFSAVTIKSWVDKQBEDLVTLAKTAGVNOI
 QY 61 YEKYQDLYTVENPNARQVVEIAARDIEKLLSNRSLVLALEAEKVQAAHQRREDI
 DB 61 YEKYQDLYTVENPNARQVVEIAARDIEKLLSNRSLVLALEAEKVQAAHQRREDI
 QY 121 EYVYNAKDDLPENKDSPPGSGORIKPVEIEDANFGROI SYQHAAVHIPTDIYEGS
 DB 121 EYVYNAKDDLPENKDSPPGSGORIKPVEIEDANFGROI SYQHAAVHIPTDIYEGS
 QY 181 NELNWTSSALDEYFKONREDDPSLLVQVFGSATGLARYYPASPWVDSRTPNKIDLYI
 DB 181 NELNWTSSALDEYFKONREDDPSLLVQVFGSATGLARYYPASPWVDSRTPNKIDLYI
 QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLI RTSVSEMLETLDSDDFVNVASFNSI
 DB 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLI RTSVSEMLETLDSDDFVNVASFNSI
 QY 240 RPWYIOGAASPKDMLILVDVSGSVGLTKLI RTSVSEMLETLDSDDFVNVASFNSI
 DB 240 RPWYIOGAASPKDMLILVDVSGSVGLTKLI RTSVSEMLETLDSDDFVNVASFNSI
 QY 301 VSCFOHLVQANVRNKKVLDKDAVNNTAKGIDYKGFSPAFQOLLNYSRANCK
 DB 301 VSCFOHLVQANVRNKKVLDKDAVNNTAKGIDYKGFSPAFQOLLNYSRANCK
 QY 361 FTDGGERAQEI FNKNKDKKVRVFRFSGVQHNYERGP:QMAACENKGYIYIPIPSI
 DB 361 FTDGGERAQEI FNKNKDKKVRVFRFSGVQHNYERGP:QMAACENKGYIYIPIPSI
 QY 421 INTOEYLDVLRPMVLADGAKAKQVQNTNVDLDALEGLVITGTLVPFNITGQENK
 DB 421 INTOEYLDVLRPMVLADGAKAKQVQNTNVDLDALEGLVITGTLVPFNITGQENK
 QY 481 NQLILGVMGVDSVLEIDIKRLTPRFTLCPNGYYFAIDPENGYYVLLHPLNLPKNPKSQE
 DB 481 NQLILGVMGVDSVLEIDIKRLTPRFTLCPNGYYFAIDPENGYYVLLHPLNLPKNPKSQE
 QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTLTKVKSQDERVIDKGNRTYTWTPVNGT
 DB 541 DFLDAELNDIKVEIRNKMIDGESGKFTLTKVKSQDERVIDKGNRTYTWTPVNGT
 QY 600 LALVLPYTSFYIYKAKBETITQARSKKGMKOSSETLKPDMFESGYTFIAPREY
 DB 600 LALVLPYTSFYIYKAKBETITQARSKKGMKOSSETLKPDMFESGYTFIAPREY
 QY 660 LSDNNTFLLNMFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQNTWSKORNI
 DB 660 LSDNNTFLLNMFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQNTWSKORNI
 QY 720 RFPVVTGGITRVYPKEAGENQENPETYEDSFYKSLDNNDNTVFTAPFNKSGPGI
 DB 720 RFPVVTGGITRVYPKEAGENQENPETYEDSFYKSLDNNDNTVFTAPFNKSGPGI
 QY 780 INVSKAVELYIQGLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVPCDKRNSD
 DB 780 INVSKAVELYIQGLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVPCDKRNSD
 QY 840 ILDDGGFLLMANHDDVTNOIGRFFGIDPSLMRHLVNI SVYAFNKSVDYQSCEP
 DB 840 ILDDGGFLLMANHDDVTNOIGRFFGIDPSLMRHLVNI SVYAFNKSVDYQSCEP
 QY 900 QGAGHRSAYVPSVADILQIGWATAAAMSILQOFLSLTFFPRLLLEAVEMEDDDFT
 DB 900 QGAGHRSAYVPSVADILQIGWATAAAMSILQOFLSLTFFPRLLLEAVEMEDDDFT
 QY 960 QSCITETQTOYFFNDKSGVGLDCGNCRSRI PHGEKLMNTNLIFIMVESKGTCP
 DB 960 QSCITETQTOYFFNDKSGVGLDCGNCRSRI PHGEKLMNTNLIFIMVESKGTCP
 QY 1020 IQAEQTSDDGNPCDMVK 1036
 DB 1020 IQAEQTSDDGNPCDMVK 1036

419	IRINTQEVLDVGRPMVLADKAKOVQWNVYLDLDELGLVITGTLVPVNITQPEL	QY
420	IRINTQEVLDVGRPMVLADKAKOVQWNVYLDLDELGLVITGTLVPVNITQPEL	DB
421	IRINTQEVLDVGRPMVLADKAKOVQWNVYLDLDELGLVITGTLVPVNITQFEN	QY
422	IRINTQEVLDVGRPMVLADKAKOVQWNVYLDLDELGLVITGTLVPVNITQFEN	DB
479	LKNQLILGVWGVDSLEDIKELTPRFTLCPNGYYFAIDPNGVYLLHPNLQPK	QY
480	LKNQLILGVWGVDSLEDIKELTPRFTLCPNGYYFAIDPNGVYLLHPNLQPKIGV	DB
531	-----NPKQEPVTLDFDLDELNDIKVEIRNKMIDGESGEKTRTLVKSQ	QY
541	INLKRPRPNVQPKSQEPVTLDFDLDELNDIKVEIRNKMIDGESGEKTRTLVKSQ	DB
580	YIDKGNRTYTWTPVNGTDY-SLALVLPTYSFYIKAKLEETITQARSKKGMKDBET	QY
601	YIDKGNRTYTWTPVNGTDYSSLALVLPTYSFYIKAKLEETITQARY-----SET	DB
639	DNFEESGYTFIAPROYCNDLKIISDNTTEFLINFNEFTDRKTPNPNPCNADLINRVLL	QY
654	DNFEESGYTFIAPROYCSDLKPSDNTTEFLINFNEFTDRKTPNPNPCNTDLINRVLL	DB
699	FTNELVQNYWSKQKNTKGVKARFVVYTDGGITRVYKBAENWQENPETYEDSFYKKE	QY
714	FTNELVQNYWSKQKNTKGVKARFVVYTDGGITRVYKBAENWQENPETYEDSFYKKE	DB
759	DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSW IENFTF	QY
774	DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSW IENFTF	DB
819	RDP CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNQIGREFGIBDPSLMRHLA	QY
834	RDP CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNQIGREFGIBDPSLMRHLA	DB
879	VYAFNKSYYDSVCEGSAAPKQAGHRSAYVPSVADILQIGWATAAASILQOFLI	QY
894	VYAFNKSYYDSVCEGSAAPKQAGHRSAYVPSIADILQIGWATAAASILQOFLI	DB
939	PPRLEAVEMEDDDFTASISKSCITEQTQYFFDNDKSFSGVLDCNGCRIFHGEI	QY
954	PPRLEAAMDMEDDDFTASISKSCITEQTQYFFDNDKSFSGVLDCNGCRIFHVEI	DB
999	TNLIPIWYESKGTCPCDTRLLIIQABQTSOGPNPCDMVK 1036	QY
1014	TNLIPIWYESKGTCPCDTRLLIIQABQTSOGPNPCDMVK 1051	DB

```

RESULT 4
T30256
calcium channel alpha-2-delta-C chain - mouse
C:Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun
C;Accession: T30256
R;Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.
J. Neurosci. 19, 648-691, 1999
A;Title: Molecular diversity of the calcium channel alpha2delta subunit
A;Reference number: Z20794
A;Accession: T30256
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1091 <KLU>
A;Cross-references: EMBL:AJ010949; PIDN:CAA09423.1
A;Experimental source: brain
C;Superfamily: calcium channel alpha-2 chain

Query Match 19.9%; Score 1085; DB 2; Length 1091;
Best Local Similarity 28.7%; Pred. No. 3-5e-57;
Matches 309; Conservative 222; Mismatches 416; Indels 128; G

Qy 3 AGCLALTLTLPQSLLIGPSSEBPPSAVTKSNWDMQEDLVLTAKTASGVNQLV
14 ASALLA-TALLYAALGDVVRESEQIPLSV-VKLWASAFGGEIKSIKAAKYSQGLQIC
63 KYQDLTYVEFPNNARQLVEIARADIEKLLSNRKSALVSLAEKVKVQAQHWREDFI

```

VAITEIDGLQVKKLAKIMEENFHKKSEAVRRLVEAAAEHALKHEFDADL---QY 128
K---DDLDPEKNDSEPSQRIKPVFIEDANFGR-QISYQHAAVHPTDIYEGSTIV 179
VLINERDKCNFLELGEKEFI---LAPNDFHMLPWNISLSVQVPTNMYNKDPAI 185
WTSALDEVFCKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRPFNKIDLYDVR 239
WSESLANKVFVDNDFRDPISLIWQVFGSAKGFQYQGIKWEPE---NGVIAFDCR 242
ITQGAASPKOMLILVDVSGSVGLTILKRTSVSEMLTSLDDDDFVNVAASFNSNAQ 299
ITQAAATSPKVVILVDVSGSMKGURLTAKQTVSSILDTLUGDDDFNIIITYEELH 302
FQ-HLVQAVNENKVKLXDAVNNITAKGITDYKKGFSFAPEQLLNNVNSRAN---CN 355
LNGTLVQADRNTKEHFREHLDKLPAGIGMLDIALNEAFNILLSDFNHTQGSICS 362
PTDGEERAAQBIFNKNY-KDKKVRVFRFSGVQHNYERGPIOWACENKGYIYEP 414
ITDGAVIDTDTIFAKYNPDKRVIIFYLIGREAAFPADNLKMWACANKGFFQIS 422
IRINTQEYLDVLRPMLAGKAKQOVNTNYLD-----ALELGLVI---TGT 463
VQENWVEYLHVLSRPKVI--DQEDHVWTEAYIDSTLPQAKLADDQGLVMTTVA 480
NITGQFENKTNILKNQILIGWGVDSLEDDIKRLTPRTLCPNGYYPALDNGVLL 523
S---KQNETRSGK-ILLGVGTDPVFKELKTTPKYGGLHGVAFAITWNGYILT 535
QP---KNPQSQB--VTLDFDLAELENDIKVEIRNMKIDBSGSEKTFRTILVKSQDE 578
RPIYBEGKKRRKPEYSVDLSEVWEHDDV-LNANVNRKTGK--FSMEVK---588
KGKRLVMTNDYYTIDIKTTPFSLGVALSRGHGKYFF-----RGNVT 634
KGKRT-----YTTPVNGTDSLALVLT-YSFYIKAKLEETITQARSKKHKM 631
LKPDNTEESGYTFIAPDYN-DLAKISDNTEFLANFNEFIDRKTNNPNSCNADLI 690
L--HDLEHPDVSIADEWSYCNLDLHPEHRLHLSQLEAIKLYLKGEK-LLQCDXELI 691
LDAGFTNELVONYWS-----KQNIKGKARFVVTDGITVRYP-----733
FDA-VYSAPEAWTSLALNKSNSDKGEVAFGLTRTGLSKRLNLFVGAELTNQD 750
GENWQENPTEYDSFYKSLDN--DNYVTAPY----FNKSGPAYESGIMVSKAV 786
GDKENIFNADHFFPLMYRAAEQTAGSFVYS1PFSTGTWNKS-----NVVTAFTSI 804
QGKLLKPAVGIKIDVNSMIENFTKTSIRDPACGAPVCDCKRNSDVMDCVILDDGGF 846
DERKSPVVAAGVQMKLEFFORKFWTASRQCASLDGKCSISCDDETVCVCLDINGF 864
INHDYTTNQIGRPFGEIDPSLMRHLNMSIVAFNKSVDYQSVECPGAAPQGAHRS 906
3--EDYT-QTGDFFGEVEGAVNKKLTWGSFKITLYDYQAMCR---ANKSESDSAH 918
PSVADILQIGWATAAASILLQFLLSITPEPRLLAEVEMEDDDFTASLSK-----QS 961
DYPKAFI-----SAAKIMTELVLFLVEP-----NLCSWHSDWTAKAKQLTLEP 968
EQOTQVFDNDKSFSGVLDGNCNSRIFPGEKLMNTNLIIFIVWSKGTCPCDT 1016
FVDAFVSEFTIKETTGNTACRPSKSFYI001PSNLFMVVWS--SCLCES 1021

```
- Caenorhabditis elegans
habditis elegans
95 #sequence revision 20-Feb-1995 #text_change 30-Jun-2001
```

[illegible]

RESULT 6
Tl8770
probable calcium channel protein - *Caenorhabditis elegans*
C.Species: *Caenorhabditis elegans*
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct
C.Accession: Tl8770; T25249
R:Sulston, J.

D97033
 uncharacterized protein, probably surface-located [imported] - Clostri
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep
 C:Accession: D97033
 R,Nolling, J.; Brston, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.
 J. Dairy, M.D.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Produ
 A:Reference number: A96900; PMID:21359325; PMID:21359325
 A:Accession: D97033
 A:Status: preliminary
 A:Molecule type: DNA

inhibitor heavy chain 3 precursor - human
[C3; inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor heavy
chain (man)
#sequence revision 20-Feb-1995 #text change 04-Feb-2000
S34123, S02141; D34245; A39079; S50133; B53642; A59167
Barrat-Mehrpour, M.; Thiberville, L.; Bost, F.; Sesbouee, R.; Martin,
J., 771-776, 1993
inter-alpha-trypsin inhibitor-precursor heavy chain cDNA and deduced amino-
acid sequence
S30350; MUID:93215656; PMID:7681778

IA
30U1>
EMBL:X67055; NID:9288562
3L Data Library, June 1992
S34123

NA
X', 312-343, 'R', 345-885 <BOU2>
EMBL:X67055; NID:9288562; PIDN:CAA47439.1; PID:9288563
4.; Bourguignon, J.; Sesbouee, R.; Mattei, M.G.; Passage, E.; Salier,
P., 147-154, 1989
na inter-alpha-trypsin inhibitor is encoded by four genes on three ch
S02141; MUID:89137072; PMID:2465147

red with conceptual translation

NA
'G', 358-845, 'H', 847-885 <DIAL>
'EMBL:X14690; NID:935464; PIDN:CAA32821.1; PID:g35465
ogersen, I.B.; Pizzo, S.V.; Salvessen, G.
15975-15981, 1989
f inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-al
A92736; MUID:89380192; PMID:2476436

ENG1>
ENGL>
lvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V.
747-751, 1991
n 4-sulfate covalently cross-links the chains of the human blood prot
A39079; MUID:91093267; PMID:1898736

'otein
<ENG2>
'M'; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesbouee, R.; Muschio-Bon
eta 1219, 551-554, 1994
entation of the inter-alpha-trypsin inhibitor heavy chain H1 and H3 g
'S50132; MUID:95002176; PMID:7522574

ity
NA
DIA2>
'EMBL:X75318
'Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.
423-7429, 1994
arthritis-associated hyaluronan binding protein, forms a stable compl
'A53642; MUID:94271799; PMID:7516184
2
rotein
'X' <WIS>
arvang, K.L.; Ploug, M.
5-200, 1998
ate as covalent crosslink in human inter-alpha-trypsin inhibitor: a no
'S02431; MUID:88167187; PMID:2450785
7
rotein
'GEKEQAVDT' <JES>
alpha-inhibitor, this protein is covalently cross-linked by chondroitin

GDB:120109; OMIM:146650

A;Accession: T28155
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA

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re: strain IT 4/25/5

3.0%; Score 161; DB 2; Length 2706;
rity 18.2%; Pred. No. 0.74;
nservative 137; Mismatches 345; Indels 338; Gaps 46;
QEDLVTLAKTAGSNQVLDIVYKQDYLYTVEPNNA-----RQL 78
AEFECTRKI-----KLENNKCEKD---EPNNKYCSGDHCKRTYLDKNTIF 358
RDIEKLSNRKALVSLALRAEKVQAHAHQWREDPASNEVYVYNAKDDLPDKNS 138
PRCENACSNYTK-----WISIQKQPKQK--YNNEI---KIKTNINNENDK 408
---PGSORIKPVTEDANFGQISYQAAVHIPTDIVEGSTIVLNLNWTSALE 191
LDKKGYSTIN--TFLESUNHGKQC-----DN 438
REEDPSLLWQVFGSATGLARYYPASP-----WVDNSRTPNKI 233
KTNFKNL--ETFGP-----SGYCEACPIYGVKCSNEKCTPVTENENSNRLPTDT 493
RRRPWYTOGAASPKDMLILVDVSGVSGITLKLRTSVSEMLETLSDDDDFVNAS 293
N-----ATNIDMLVNDGIGNAI-----515
QDVSCFOHLVQAVNRKK-----VLKDAVNNITAKGIDYKKGPSFAPEQLL 345
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RANCKNIIMLFTDGEERAQEIFNKYNKDKKRVFRFVSGQHNVERGPIOMACE 405
DHNRLK-----EKIDVICIKENINENICIKCKTN-----CE 610
YEIPSIGAIRI-----NTQYLDVLRPMVLADGKAKQVQWNTVYLDALGLVIT 461
ILEKKEAWDKINQHNQKHMIFILYPIWITGFYEK--ITFPNDFKALE-----DV 665
/ENITQOFENKMLKNQILGVNGVDVSLIEDIKRLTPRFLCNGYFYAIDPNGVY 521
/LDTLKECQD--THCKTEKIRSI--DVDLIKEIISWLQNKIEVCKS--HHEDRHEYC 721
VLOPKNPKSOEPVTLDFDLAELENDIKVEIRNRKMDGESGEXT-----FRT 571
JILPKSVDDDEDD--BEVDEEKESSQTTKRN--ISQGGTKSASCVKGACAIKVG 775
JDBRYID-----KGNRTVTM-----TPVNGTD-----YSLALVLPYSF 609
KSNGSIDNCAKNRKKNQWQCKNXTFDVNGEVCMPPRRKSICTHNLTEBQTKNK 835
--YIKAKLET--ITQARSKGKMKDSTLK-----PDNFEF--SGVTFTIAPDYC--N 656
EAFIKAAKETNLLMDYKNDKNEABELLKKGIKIPEDFMIMFTYFGDFDPCLEN 895
---KISDNTTEFLINFEIDRK-----TPNPNPC--NADLINRVLLDAGFTNEL 703
DVDYKVKINVKVFNSSKRGFKKIDPENWNNNGPQIWNGLCALIHADTKDSIKN 955
-----W-----SKQNKIKGVKARFV 723
KYEVKITLAKDGSNGMTLSEFAKPKFLRMFVWYDDYCKERQKYLTEVASTCKS 1015
ITRV-----YKPEAGENWQENPETYEDSFYKRSLDN-----DNTV-- 762
QLKCDRCGNKNCDBYKMYRKKKEBNMLQDYKDKRNGKIDGKPIGIIKVDYVL 1075
-----FTAPYFNKSGPGVSGIWMVSKAVEIYIQGLLKPAVVVGIIKIDVNSWI-- 810
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1076 ANAKBYLKKKTASCTVSSGKAQNSATEEVKKNIELLSEEQY-----YDADQY

811 -----ENFTKTSIRDPCAGPVCDCK-----RNSDVMDCVIL 841

1127 TKFIHDDKYSKISGRSNCCGLNSDAKKNKIKWRNSDEKDYAPL 1169

RESULT 13

A44396

p-type cation translocating ATPase - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum

C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jun-1993

C:Accession: A44396

R:Krishna, S.; Cowan, G.; Meade, J.C.; Wells, R.A.; Stringer, J.R.; Rob J. Cell Biol. 120, 385-398, 1993

A:Title: A family of cation ATPase-like molecules from Plasmodium falciparum

A:Reference number: A44396; MUID:93132070; PMID:8421054

A:Accession: A44396

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-1984 <KRI>

A>Note: sequence extracted from NCBI backbone (NCBIP:122678)

Query Match 2.9%; Score 159; DB 2; Length 1984;

Best Local Similarity 17.1%; Pred. No. 0.59;

Matches 179; Conservative 144; Mismatches 359; Indels 366; Gaps

QY 58 VDIYKYQDLYVVEPNNAQLVEIAARDIEKLLSNR-----SKALVSLAL

DB 128 INVY-RYNTSYIISSS-----ELVPGDIYEIKNNMTIPCDTIIILSGSVTNGHMLJ

QY 107 VQAQHWRDDPASNEVYVYNAKDDLPDKND-----SEPGSORIKPVEDANFGI

DB 181 V-PIHKERLPFEGNAIINKNKYDSNDEKDYLRINYNNHASINMIKRNHLIBETLGI

QY 161 YQAAVHIPTDIVEGSTIVLNLNW--TSALDEVFKKREEDPSLLWQVFGSATGLAI

DB 240 EYKSNTH-----DLSNKKLCYINNTYDDVHMKGNKD

QY 220 ASPWVDNSRTPNKIDLYDVRRPWYTOGA--ASPKDMLILVDVSGVSGITLKLIRTI

DB 273 ---YNNNNNNKKKKNNLN---FVKGTVINSNLLY-----

QY 279 MLETLSDDDFVNVASFNQADVSCFOHLVQAVNRKVKVLKDAVNNITAKGIDYK

DB 304 -----DDKIGVNIPE---DDVNNMKH--KFNORININYNKDNTNL-----EYN

QY 339 FAFEQLLNVNVRANCKIIMLFTDGEERAQEIFNKYNKDKKRVFRFVSGQHN

DB 346 YIYDCLLKVKVEAISQKNKIY-----SNEDINKY-----

QY 399 IOWMACENKGYEYIPIPSIGAIRINTQYLDVLRPMVLG-----DK

DB 375 ----MLYGGYVLSLYNINKIKYNNKEENRILGL-VIKTGFITTKGRIVNNILYHK

QY 445 QWTVNYLDALGLGVITGTLPVNIITQFENKTNLKNQLILG-----

DB 430 NLINDSYKFLII-LIYALFSVFILYITLSNNEYTHIILKCLDIITDAIPALP

QY 488 MGVDVSLIEDIKRLTPRFLCNGYYPEA-----IDPNGYVLLHPNLQ-----PKN

DB 489 VGISIAISRLKKKPSISCLCPHKINAGQINTWVDFKTG-TLIENNLOFIIITON

QY 536 EPVTLDFDLAELENDIKVEIRNRKMDGESGEXTFRTLVKQSDERYIDKGNRTYTW

DB 548 NMLS-DFIHLK-----EMNTESYIHSKDDNMHNKN-----

QY 596 TDYSLALVLPYSYIYKAKLETITQARSKGKMKD-----SETLKPDNE

DB 578 -----SIISYYIKDNMKNLHTSSK-KKSIKTSRNFVQTIKSCLDJQHYI

QY 646 YTFIAPDYCNDLKISDNN--TEFLN-----FNEF--IDRKTPNPNPCNADLINR

NTTYCNDLHINDSTCSSYLLNSETKDAYCEYYNIDH-----LCD-----INKKND 678
ELVONYSKQKNIKGVKARFVTTGGITRVYPKEAGENWQENPETYEDSFYKRSI 756
ELMGKYSKNELMGKTIKNELM-----GKYSKNEL 712
VFTAPYFNKSGPGAVESGIMVSKAVEIYIOGKLKPAVVG-----IKIDVNSWI 810
---MGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNEL 765
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IDYNDYPCD---YNCNCCNDTYHRLVYHNKNSFNIPPEKNKSYNNISHIKI 822
-----FGEIDSLMRHLVNSVAF-----NKSYDYQ 889
FEALACHTLSKVNKNKMGVLEILMFNTNCDMLNNSFIKEKKNCSDYDQ 882
GAAPKQAGHRSAYVPSVADILQIGWATAAASILQOFLSLTPRILLEAVEME 949
DGNKNGANDERCHLNN-----NLVSYNILKRF----- 912
TASLSKOSCTEOTQYFFDNDKS 977
SRLQMSVIVKST-YGNNDNN 937

in b2270 - Escherichia coli (strain K-12)
chia coli
7 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
8 Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co-
au, B.; Shao, Y.
1462, 1997
ete genome sequence of Escherichia coli K-12.
8 A64720; MUID:97426617; PMID:9278503
ary; nucleic acid sequence not shown; translation not shown
NA
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rce: GB:AE000317; GB:U00096; NID:91788605; PIDN:AACT5330.1; PID:91788606;
rce: strain K-12, substrain MG1655

2.9%; Score 157.5; DB 2; Length 575;
arity 21.6%; Pred. No. 0.1; 206; Indels 105; Gaps 25;
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LQEAFTFAAAKAKATHIANPCTARYQOF---DDNPVQVQAQNPATSLDVTGS 132
TIVLNE-----LNWTSALDEVFKNREEDPSLLWQVFGSATGLARY 218
TRFLNQGLLPPDPAVRVEIVNFFSDNDI--KDKQSIKASKPIPFAMRYELA--- 187
WYDNRTPNKIDLYDVRPWPYIOGAASPOMLILVDVSGS--VGLTLKLIKRTSVS 277
W-NEQRTLLKVLILAKDKRSELPAS---NLVFLIDTSGMSIDSLRPLIQSSILK 241
3TLDSDDFNVASFNQAQVSCFQHLVQANVKNKVLKDVANNITAKGIDYKKG 337
KELREQDNIATVYAGDSRIA-----LPSISGSHKABINAAIDSLDAEBSGTGAGL 296
FEQLLNVNVRANCNKLIMLPTDG-----GEERAQEIFNKYNKDKVRVFRFSVQ 391
YQQAATK-GFTKGGINR--ILLATDGDENVGIDDPKPSIESWYKKQRESGVILTSTGVGN 354

392 HNYERGPIQWMAKCNKGYIYEIPSIGAIRINTQEVLDVLGRPMVL--AGDKAKQV-
355 SNYNEMAMVRIADVGNNGNSYIDTILS-----EAKVLNSEMOMLITVAKDVQAQIEI
446 WTNVYLDALDELGLVITGTLPEVNITGQFENKTNLKNQLILGVMGVD--VSLEDI---I
411 WTEY---RQIG-----YE-----KQLRVEHFHNDVNDVADGIGAGI
502 PRFTLCPNGYFFAIDPNGVYLLHPNLOPKPKSQE 536
448 LLFELTLNGOKASIDKLRYA--PDNKLAKSDKTK 480
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E90542
lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-
C;Accession: E90542
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissot
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathog
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: E90542
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-918 <KUR>
A;Cross-references: GB:AL445566; PID:914089658; PIDN:CAC13418.1; GSPDB
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU 2450
A;Genetic code: SGC3

Query Match 2.9%; Score 156.5; DB 2; Length 918;
Best Local Similarity 20.0%; Pred. No. 0.25; 229; Indels 161; G
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305 QHLVQANVRKVKV-----LKDAVNNTAKGITDYKKGFSFAFEQQLNKNVSRANCK
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361 FTDGGEERAQIEFNKYNKDKV---RVFRFSVQGHYERGIQWMAKCNKGYIYEI
146 -TDG---SMNIIIVLAKONGVLEKFKIT-----GLLSEL
418 AIRINTQEVLDVLGRPMVLADGKAKQVQWTVNYLDLGLVITGTL-
182 DONLK---VDVPKNENILASSIVEVEQITNE-----KISLSTQGVKVPSTFDLTKY
468 NITQFENKTNLKNQLILGVMG-----VDVSLSDIKR--LTPRFTL-CPNGYIYF
233 HVLSHDDKGLKIRVLSAKSKTSKDFDYTIQFQSFLEDRISLAKQGVNKL
519 GYVLLHPNLOPKPKSQEPTVLDLDALENDIKVEIRNKMIDGESGEKTRTLV
292 ---IISLQLLPSSASSED--KLVNLSAYDISVPDGLKFNFSVFEAKQGT-
579 RYIDKGNRTYTPVNGTDYSALVLPYSPYIKAKLEETITQARSKKGMKDSH
339 ---DKGVLTQITQINGTRTTEEVKLDIQTENILKRYLDETLIKLIDSV--VLKKN
638 ---PDNFEESGYTFIAPRDYCNLDKISDNNTBFLNLFNEF-IDRKTPNNPNSCNADLL
394 SLPSLSEVKEI---ENWQNEIELLSDSKAKINVKNEFQVSVSTSANPEYN---
695 LDAGFTNE-----LVQNYMSKQNIKGVKARF--VVTGGITRVYP---KEAGI
443 IDGSLNVEVRISRDGIVQVTKRLSGLTKLDANLPDVVAKANVSNQLPGLKAKD
743 NPETYE-DSF-----YKRSLDN---DNVVTAPY---FNKSGPGI
503 GEKTFSTDSFELKFKPNKAKENNSILNLYKLSLENVKLNKFNFSQGVFDVFTKGTGI

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VEIYIQQKLL-----KPAVVGIKIDVNSWIENFTKTSIRDPGAG 824
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ITTFKKOVLFRDPOYRYVEDNDHFHKAIALTTKMRNEFIKK----- 610

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RNSDV 835
:|:
}ENDDL 620

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February 20, 2004, 16:59:26
зесв
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

1 search, using sw model

quary 20, 2004, 16:48:25 ; Search time 11.5951 Seconds
(without alignments)
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10-090-827-15

3
AGCLLALTLTQSLIG.....PDVCFDNNVLEDYDCGVS 1063

SUM62

cp 10.0 , Gapext 0.5

863 seqs, 47026705 residues

s satisfying chosen parameters: 127863

th: 0

th: 2000000000

nimum Match 0%

ximum Match 100%

string first 45 summaries

issProt_41.*

the number of results predicted by chance to have a
than or equal to the score of the result being printed,
d by analysis of the total score distribution.

SUMMARIES

ry	ch	length	DB	ID	Description
0	1	1091	1	CIC2 HUMAN	P54289 homo sapien
3	1	1091	1	CIC2 RAT	P54290 rattus norv
1	1	1106	1	CIC2 RABIT	P13806 corytolagus
0	1	1249	1	Y103 SYNY3	P13874 caenorhabdi
5	1	886	1	ITH3_MOUSE	O61704 mus musculu
3	1	885	1	ITH3 HUMAN	O66033 homo sapien
2	1	887	1	ITH3 RAT	O63416 rattus norv
9	1	886	1	ITH3 MESAU	P97280 mesocricetu
9	1	1829	1	DPOL THEST	O33845 thermococcu
8	1	1956	1	ATX1_PLAFA	O04956 plasmodium
8	1	575	1	YFBK_ECOLI	P76481 escherichia
8	1	946	1	ITH2 HUMAN	P19823 homo sapien
7	1	1290	1	EXCI_CLOBO	P18640 clostridium
7	1	420	1	Y103 SYNY3	O55874 synchocyst
7	1	921	1	ITH4_PIG	P79263 sus scrofa
7	1	654	1	MCPQ_BACSU	P54576 bacillus su
7	1	930	1	ITH4_HUMAN	O14624 h inter-alp
6	1	964	1	DPOL CBEPV	P30319 choriostoneu
6	1	1087	1	YXNK_CLOTH	P38535 clostridium
6	1	946	1	ITH2 MESAU	P97279 mesocricetu
5	1	1169	1	SMC_METJA	O59037 methanococc
5	1	1251	1	RBP2_PLAVB	O02668 sus scrofa
5	1	935	1	ITH2_PIG	P16154 clostridium
5	1	2710	1	TOXA_CLODI	O25490 manduca sex
5	1	3305	1	APLP MANSE	P13423 bacillus an
5	1	764	1	PAG_BACAN	P38198 saccharomyc
5	1	1513	1	STU1_YEAST	P16480 bacillus th
5	1	1180	1	C4AA_BACTI	O99715 homo sapien
5	1	3063	1	CAIC_HUMAN	O61703 mus musculu
4	1	946	1	ITH2_MOUSE	P52340 human herpe
4	1	2077	1	TEGU_HSV6U	O51737 borrelia bu
4	1	862	1	MUTS_BORBU	P07248 saccharomyc
4	1	1323	1	ADRI_YEAST	

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35	132.5	2.4	929	1	CAIC_NOTVI	Q91145 notop
36	132.5	2.4	1679	1	Y109_YEAST	P40457 sacch
37	132	2.4	697	1	YE9C_SCHPO	O13773 schiz
38	131.5	2.3	1018	1	YCL4_METJA	Q58611 metha
39	131	2.3	1634	1	DPOL_METJA	Q58295 metha
40	131	2.3	1658	1	YMG7_YEAST	Q03661 sacch
41	130.5	2.3	987	1	YD94_METJA	Q58789 metha
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43	129	2.3	1244	1	Y307_MYCFU	P75342 mycop
44	128.5	2.3	1254	1	UBPC_YEAST	P39538 sacch
45	128	2.3	1113	1	Y140_MYCFU	P75033 mycop

ALIGNMENTS

RESULT 1
CIC2 HUMAN
ID CIC2 HUMAN STANDARD; PRT; 1091 AA.
AC P54289;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta
DE subunits precursor.
GN CACNA2D1 OR CACNL2A OR CCHL2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92110010; PubMed=1309651;
RA Williams M.E., Feldman D.H., McCue A.F., Brenner R.,
RA Velicelebi G., Ellis S.B., Harpold M.M.;
RT "Structure and functional expression of alpha 1, alpha 2, and beta
RT -subunits of a novel human neuronal calcium channel subtype";
RL Neuron 8:71-84(1992).
CC - FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT RO
CC - EXCITATION-CONTRACTION COUPLING.
CC - SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUN
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE A
CC AORTA TISSUES.
CC - PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED
CC A PRECURSOR FORM (BY SIMILARITY).
CC - SIMILARITY: TO OTHER SPECIES' ALPHA-2 SUBUNIT.
CC - SIMILARITY: Contains 1 VFMA domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a coll
CC between the Swiss Institute of Bioinformatics and the EMBL out
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CC modified and this statement is not removed. Usage by and for c
CC entities requires a license agreement (See <http://www.isb-sib.ch/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M76559; AAA51903.1; --
CC PIR; JH0565; JH0565.
CC Genew; HGNC:1399; CACNA2D1.
CC MIM; 114204; --
CC GO; GO:0005891; C-voltage-gated calcium channel complex; TAS.
CC GO; GO:0015270; P-dihydropyridine-sensitive calcium channel a..
CC GO; GO:0006832; P-small molecule transport; TAS.
CC InterPro; IPR004010; Cache.
CC InterPro; IPR002035; VWF_A.
CC Pfam; PF02743; Cache; 1.
CC Pfam; PF00092; vwa; 1.
CC SMART; SM00327; VWA; 1.
CC PROSITE; PS0234; VWF_A; 1.

Transmembrane; Ion transport; Voltage-gated channel;
1; Glycoprotein; Phosphorylation; Signal.
1 24 POTENTIAL.
5 944 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT
5 1091 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY
SIMILARITY).
6 469 POTENTIAL.
16 930 POTENTIAL.
17 1086 POTENTIAL.
13 430 VWFA.
12 92 N-LINKED (GLCNAC. .) (POTENTIAL).
16 136 N-LINKED (GLCNAC. .) (POTENTIAL).
14 184 N-LINKED (GLCNAC. .) (POTENTIAL).
14 324 N-LINKED (GLCNAC. .) (POTENTIAL).
18 348 N-LINKED (GLCNAC. .) (POTENTIAL).
15 475 N-LINKED (GLCNAC. .) (POTENTIAL).
15 585 N-LINKED (GLCNAC. .) (POTENTIAL).
14 594 N-LINKED (GLCNAC. .) (POTENTIAL).
53 663 N-LINKED (GLCNAC. .) (POTENTIAL).
59 769 N-LINKED (GLCNAC. .) (POTENTIAL).
12 812 N-LINKED (GLCNAC. .) (POTENTIAL).
76 876 N-LINKED (GLCNAC. .) (POTENTIAL).
33 883 N-LINKED (GLCNAC. .) (POTENTIAL).
73 973 N-LINKED (GLCNAC. .) (POTENTIAL).
36 986 N-LINKED (GLCNAC. .) (POTENTIAL).
31 501 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
33 833 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
91 AA; 123183 MW; 284E13E29A47837 CRC64;
100.0%; Score 5599; DB 1; Length 1091;
arity 100.0%; Pred. No. 0;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
CLIALTLTQLSLIGSSSEPPPSAVTIKSWDKQEDLVTLAKTASGVNQLVDI 60
CLIALTLTQLSLIGSSSEPPPSAVTIKSWDKQEDLVTLAKTASGVNQLVDI 60
QDLVTPNNARQLVETAAEDIEKLNRSKALVSLALEKVKQAQHWREDFASN 120
QDLVTPNNARQLVETAAEDIEKLNRSKALVSLALEKVKQAQHWREDFASN 120
YNAKDDLDPEKNDSEPSQRIKPVFIEDANFGRQISYCHAAVHIPTDIYEGSTIVL 180
YNAKDDLDPEKNDSEPSQRIKPVFIEDANFGRQISYCHAAVHIPTDIYEGSTIVL 180
WTSALDEVFKKQREDEPSLLMQVFGSATGLARYYPASPWNDSRTPNKIDLYDVR 240
WTSALDEVFKKQREDEPSLLMQVFGSATGLARYYPASPWNDSRTPNKIDLYDVR 240
IQGAASPKDMLILVDVSGVSGLTILKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300
IQGAASPKDMLILVDVSGVSGLTILKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300
QHLVQANVRNKKVLDKADANNITAKGIDTYKKGFSPAFQQLLNYSRANCNKIIML 360
QHLVQANVRNKKVLDKADANNITAKGIDTYKKGFSPAFQQLLNYSRANCNKIIML 360
XGEERAQEIIPNKYKDKKVRFRFSQGHNYERGPQIOWMACENKGYIYIPISGAIR 420
XGEERAQEIIPNKYKDKKVRFRFSQGHNYERGPQIOWMACENKGYIYIPISGAIR 420
YELVDLGRPMVLGAKQVQWNTVYLDALGLVITGTLPVFNITGQFENKTNLK 480
YELVDLGRPMVLGAKQVQWNTVYLDALGLVITGTLPVFNITGQFENKTNLK 480
LLGVMGVDSLEDIKRLTPRTLCPNGYYPADIPNGVYLLHPLNPKNPQSPVTL 540
LLGVMGVDSLEDIKRLTPRTLCPNGYYPADIPNGVYLLHPLNPKNPQSPVTL 540
DAELNDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRTYTWPNVNGTDYSL 600
DAELNDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRTYTWPNVNGTDYSL 600

601 ALVLPITYSYIIKAKLEETITQARSKKGMKQSETLKPDNPFESGTYTPIAPRDYCN
601 ALVLPITYSYIIKAKLEETITQARSKKGMKQSETLKPDNPFESGTYTPIAPRDYCN
661 SNNTEFLNFEFIDRKTTPNPNPCNADLNINVLDDAGFTNVLQVNSKQKNIK
661 SNNTEFLNFEFIDRKTTPNPNPCNADLNINVLDDAGFTNVLQVNSKQKNIK
721 FVVTGGITRVVPKAGENQWENPETEYDSFYKRSLDNDNNTYVTFAPYFNKSGPGAY
721 FVVTGGITRVVPKAGENQWENPETEYDSFYKRSLDNDNNTYVTFAPYFNKSGPGAY
781 MYSKAVEIYIQGLKLPVAVVGKIDVNSWIENTFTKTSIRDPCAGPVDCCKRNSDVM
781 MYSKAVEIYIQGLKLPVAVVGKIDVNSWIENTFTKTSIRDPCAGPVDCCKRNSDVM
841 LDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKS YDYOSVCEPGA
841 LDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKS YDYOSVCEPGA
901 GAGHRSAVPSVADIIQIGWATAAAWSILQQFLSLTPRLLLEAVEMEDDDFTAS
901 GAGHRSAVPSVADIIQIGWATAAAWSILQQFLSLTPRLLLEAVEMEDDDFTAS
961 SCITEQYQFPDNDKSPSGVLDCGNCRIIFHGEKLMNTNLIIFIMVESKGTCPDCT
961 SCITEQYQFPDNDKSPSGVLDCGNCRIIFHGEKLMNTNLIIFIMVESKGTCPDCT
1021 QASQTSQGNPCDMVKOPRYRKGPDVCFDNNVLEDDYDCCGVS 1063
1021 QASQTSQGNPCDMVKOPRYRKGPDVCFDNNVLEDDYDCCGVS 1063
RESULT 2
CIC2_RAT STANDARD; PRT; 1091 AA.
ID_CIC2_RAT
AC P54290;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta
DE subunits precursor.
GN CACNA2D1 OR CACNA2A OR CCHL2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92228762; PubMed=1314383;
RA Kim H.L., Kim H., Lee P., King R.G., Chin H.;
RT "Rat brain expresses an alternatively spliced form of the
RT dihydropyridine-sensitive L-type calcium channel alpha 2 subunit.
RL Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).
CC -|- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT RC
CC EXCITATION-CONTRACTION COUPLING
CC -|- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUN
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=2 isoforms are produced;
CC Name=1;
CC IsoId=P54290-1; Sequence=Displayed;
CC -|- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSE
CC A PRECURSOR FORM (BY SIMILARITY).
CC -|- SIMILARITY: TO OTHER SPECIES' ALPHA-2 SUBUNIT.
CC -|- SIMILARITY: Contains 1 VWFA domain.
CC This SWISS-PROT entry is copyright. It is produced through a col
CC between the Swiss Institute of Bioinformatics and the EMBL ou

HAADMEDDDFTASMSKQSCITEQYQFFDNDKSGFSGVLDGCGNCSRIHFVEXLKN 1013
 IMVESKGTCPDTRLLIQAEQTSQDGNPCDMVQPRYKGPDPVCFNNVLEDTD 1058
 IMVESKGTCPDTRLLIQAEQTSQDGNPCDMVQPRYKGPDPVCFNNVLEDTD 1073

1063

1078

STANDARD; PRT; 1249 AA.

; F34373;

el. 28, Created)

el. 42, Last sequence update)

el. 42, Last annotation update)

ent calcium channel unc-36 precursor (Uncoordinated

72 OR C50C3.9/C50C3.10/C50C3.11.

elegans.

azoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

eloderinae; Caenorhabditis.

9;

N.A.

N2;

18; PubMed:7906398;

scough R., Anderson K., Baynes C., Berks M., Coulson A.,

urton J., Connell M., Copsey T., Cooper J., Fraser A.,

ar S., Du Z., Durbin R., Favello A., Hillier L., Jier M.,

ones M., Green P., Hawkins J., Halseter N.,

Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,

roy C., Rifken L., Roopra A., Saunders D., Showkhen R.,

ion N., Smith A., Smith M., Sonhammer E., Staden R.,

Jerry-Mieg J., Thomas K., Vaudin M., Vaughan K.,

Watson A., Weinstock L., Wilkinson-Sproat J.,

tiguous nucleotide sequence from chromosome III of C.

38 (1994).

-2002) to the EMBL/GenBank/DBJ databases.

TISSUE SPECIFICITY.

; Sanchez B.M., Kenyon C.J.;

ing sensitivity to serotonin in *Caenorhabditis elegans*."

May act as an auxiliary subunit of the UNC-2 voltage-

ium channel which appears to trigger calcium-activated

pathways that control the serotonin response. Inhibiting

sensitivity of the vulval muscles results in egg laying

may act in both neurons and muscle cells to enhance motor

SPECIFICITY: Descendants of the cells AB and AB.p (that give

early all nonpharyngeal neurons), descendants of pi (that

to body muscle) and cell lineages that give rise to the

juvenile motor neurons.

Y: Contains 1 VWFA domain.

OT entry is copyright. It is produced through a collaboration

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DR EMBL; L14433; AAA27971.3; --
 DR PIR; S44617; S44617.
 DR WormPep; C50C3.9; CE32168.
 DR InterPro; IPR004010; Cache.
 DR InterPro; IPR002035; VWFA.
 DR Pfam; PF02743; Cache; 1.
 DR Pfam; PF00092; vwa; 1.
 DR SMART; SM00327; VWFA; 1.
 DR PROSITE; PS0234; VWFA; 1.
 DR Behavior; Ionic channel; Ion transport; Voltage-gated channel;
 KW Calcium channel; Signal; Glycoprotein.
 FT SIGNAL 1 19
 FT CHAIN 20 1249
 FT DOMAIN 250 479
 FT CARBOHYD 100 100
 FT CARBOHYD 140 140
 FT CARBOHYD 146 146
 FT CARBOHYD 302 302
 FT CARBOHYD 520 520
 FT CARBOHYD 558 558
 FT CARBOHYD 757 757
 FT CARBOHYD 838 838
 FT CARBOHYD 903 903
 FT CARBOHYD 923 923
 FT CARBOHYD 1130 1130
 FT SEQUENCE 1249 AA; 144375 MW; 533FF6059D375FB2 CRC64;

Query Match 13.0%; Score 727.5; DB 1; Length 1249;
 Best Local Similarity 23.1%; Pred. No. 1e-35;
 Matches 284; Conservative 201; Mismatches 467; Indels 275; Gc

QY 47 LAKTAGVNLVDIYEKQDLYTVPNNARQVETAAARDIEKLSNRS---KALV
 DB 36 MKETFSKISHETILKQYKLVSEEFQDPRAELKSKKHRIEDYLVKRSOFAYKAKI
 QY 103 EAEKQAAHQWREDFASNEVYVYNAKDDLDPEK-NDSEPGSORIKP-----VFIE
 DB 94 EARSVRNDSTVNDPQSKSFIRFMSAKQNGDGTIYESNHLGKRLKYNKTSFNLQ
 QY 156 -GRQSYQAAVHIPTDIYEGSTIVLNLNWTSLADVEFKKREEDPSLLMQVFGSI
 DB 154 YLPTSSVSSAVHIPTPLDYDRNEDLLRKIDW-SDIDAVYRTNRETKOLAFQFCSI
 QY 215 ARYPASPWW-DNSRTPNKIDYVRRRPWYITQGAASPKDMLILVDVSSVSLTIL
 DB 213 MRYTPAASWFDNQ--DEHLDLFDCTNTEWYINSATNSKNVILMLDMSGMLGQRY
 QY 274 TSVSEMLETLSDDDFVNVASFNNA---QOVSCFQHLVQANVKNKKVLDVANNIT
 DB 271 QTTEATLETLSHNDYFNITFTSKNTFLDGCNGTNGLLQATMRNKKALREKMDTYQ
 QY 331 TDYKKGFSFAFQQLNLYNSV-----
 DB 331 AEYKALPLAFSVLLDLKGSVALYTKEMSMSANATNEYQFHELPHEVLAATKQ
 QY 351 -----RANKUIMLPDGGERAQEIFNKYNKKKVRVRSVGVQHNVERG
 DB 391 INNGGDNNGRACENVIMLITDGNAPYAKKIFDMYNADKKVRVFTFLVGDDEADFEN
 QY 402 MACENKGYEIEPSIGAIRINTQVYL-----DVLGRPMVLGADKAKOVQWNTVYIDA
 DB 451 MACNNGYMHVHANMADVDEKIHHRMRGRVVRHYKESGQLS---WWTGVYRER
 QY 458 L--VITGLPVPNITQGFENKTN-----LNQLILG
 DB 508 RPEIPAEVPIITQSGFAMVKNKMSRRKIRLQKSEARSRMFVTVTVSYPIVNETPMG
 QY 491 DVSLIEDIKRTPRTLCPNGYYPFADNGVYLLHPNLQPKNP-----KSEPVTLDF
 DB 568 NIPLTEVAQKSHPANIGSKSYFFMLDQNGFVMTHPQLRPIDPFTKYHKQNNNDL
 QY 545 -----AELENDIKVEIRNMKIDGESGEKTFRLV

CC	ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC	BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1,
CC	AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AN
CC	BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUN
CC	TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
CC	-I- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROI
CC	4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
CC	SIMILARITY).
CC	-I- SIMILARITY: BELONGS TO THE ITHH FAMILY.
CC	-I- SIMILARITY: Contains 1 VWFA domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a coll
CC	between the Swiss Institute of Bioinformatics and the EMBL out
CC	the European Bioinformatics Institute. There are no restriction
CC	use by non-profit institutions as long as its content is in
CC	modified and this statement is not removed. Usage by and for c
CC	entities requires a license agreement (See http://www.isb-sib.ch/
CC	or send an email to license@isb-sib.ch).
CC	-----
CC	EMBL; X70393; CAA49843.1; --
DR	PIR; S54355; S54355
DR	MGD; MGI:96620; Ithh3.
DR	InterPro; IPR006587; VIT.
DR	InterPro; IPR002035; VWF_A.
DR	Pfam; PF00092; vwa; 1.
DR	SMART; SM00609; VIT; 1.
DR	SMART; SM00327; VWA; 1.
DR	PROSITE; PS50234; VWFA; 1.
DR	Serine protease inhibitor; Repeat; Signal; Multigene family;
KK	Glycoprotein.
KK	SIGNAL 1 18
FT	PROPEP 19 30
FT	CHAIN 31 646
FT	PROPEP 647 886
FT	DOMAIN 279 439
FT	CARBOHYD 88 88
FT	CARBOHYD 577 577
FT	BINDING 646 646
FT	SEQUENCE 886 AA: 98977 MW: 15955308CF5030A CRC64:
SQ	

THE UNIVERSITY OF CHICAGO

I I K A S C P K T E F E T V S N V A G S K V T E

DB 98 YPGNVKKEVAQKQYENAVSQKTAG-----LVASGRKWEATVQVNVVIGGKRAV

04 87 EKILSNRSKALVSLAEAEKVQAAHQWREDFASNEVVYNAKDDLDPKNDSEPGC

[illegible]

Db 154 EELL-KRNKGKYMVLKVQPKQLVRHFEID-----AHIFEF--

147 RUEBPDANECPBOTSVOHAAVHTPTDIVEGSTTVI.NELNWTSADEVFKKNREEDPS

QY I47 FVFIBDANFONQICIGITRVAUUIIDTIFOSZ : LKABN-1

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Db      190 GISMLDAE-----ASFITNDL-LGSALTKSF-----

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QY 207 VFGSATGLARYYPASPWDNSRT-PNKID-----LYDVRRRP-----

215 -----SCKKGHVSEKPSLDOORSCTCTPSLLNGDEFTIVYDVNRESPGNVQIVNG:

----- CTZ -----

246 ---QG--AASPDKMLILVDVSGSVSGLTCLKIRTSVSEMLETLSDDDFVNVASFNSI

-----KII DOWKEDNYI NETI.EST.

Db 270 FAPQGLPVPKNI VFVLDVSGSMGKRIQQIKREALDKI DDDVNEDEEITNTLEED

302 SCFO-HLVOANVRNKKVLKDAVNNITAKGITYKKGFSFAFEQLLNYNVSRAN---

[illegible]

Db 327 TTTWKDHLVQATPANLKEAKTFVKNIHDQSMNTNINDGLLKGIEML-----NKAREDHIT

SECRET
REF ID: A66582

QY 355 NKILMLFIDG---GEERAQELFNKINK--DKAAVKLRIDVQGANLDRSELEHNE

db
384 TSIIIMLTGDANTGESRPEKIQENVRNAIGGKFPYLNLFGLFG-NNLNYNFLETIAI

2
1

N.A.
a-Dawley; TISSUE=Liver;
s E.;
C-1994) to the EMBL/GenBank/DBJ databases.
MAY ACT AS A CARRIER OF HYALURONIN IN SERUM OR AS A
ROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
ION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
Y).

Qy	239	QDVSCFOHLVQAVNRNKKVKLXDAVNNTAKGITYKKGFSAFPOLLNVNVRAN-
Db	330	--TTWKDHLVKATPANLEEARAFYKNTDRDSMTINDLLRGIEML---NKAREDH
Qy	334	-CNKTIIMLFTDG---GEERAQEIFENKYNKDKKVRVFRFSVG-OHNYERGPIOMMA
Db	335	RSTSLVMLTGDGDTANGESRPEKIQENVRNAIRCKFFLYNLGFGNNLVNPFLESIA
Qy	408	GYTIEPSIGAIRINTQBYLDVLRGPMVLADGKAKQVQWTVNYLDALIELGL--VIT
Db	445	GFARRIYEDSDASLQLQGFYBEVANPFL---TNVELEYEPENAILDLTR
Qy	466	VPNITGQFENKTNLKNQLILGVMGVDYSLEDIKRLTPRFTLCPNGYFFAIDPNGVYV
Db	494	HP-----YDG-----SEIVVAGRLVDRNVN-----FKADVKVGHG

Belongs to the cation transport ATPases family (P-type subfamily V.

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AA46646.1: -
 01757: ATPase E1-E2.
 01494: ATPase P-type; 7.
 54: ATPase E1 E2; 1.
 55: Membrane; Phosphorylation; Magnesium; ATP-binding.
 1 35 CYTOPLASMIC (POTENTIAL).
 2 58 POTENTIAL.
 3 61 EXTRACELLULAR (POTENTIAL).
 4 80 POTENTIAL.
 5 407 CYTOPLASMIC (POTENTIAL).
 6 427 POTENTIAL.
 7 440 EXTRACELLULAR (POTENTIAL).
 8 462 POTENTIAL.
 9 1818 CYTOPLASMIC (POTENTIAL).
 10 1837 POTENTIAL.
 11 1845 EXTRACELLULAR (POTENTIAL).
 12 1863 POTENTIAL.
 13 1881 CYTOPLASMIC (POTENTIAL).
 14 1905 POTENTIAL.
 15 1928 EXTRACELLULAR (POTENTIAL).
 16 1952 POTENTIAL.
 17 1956 CYTOPLASMIC (POTENTIAL).
 18 496 PHOSPHORYLATION (BY SIMILARITY).
 19 1760 MAGNESIUM (BY SIMILARITY).
 20 1764 MAGNESIUM (BY SIMILARITY).
 21 251 POLY-ASN.
 22 256 POLY-LYS.
 23 941 POLY-ASN.
 24 1347 POLY-LYS.
 25 1372 POLY-ASN.
 26 1684 POLY-ASN.
 27 230285 MW; AE708AA899009335 CRC64;

2.8%; Score 159; DB 1; Length 1956;
 Identity 17.1%; Pred. No. 0.23;
 Conservative 144; Mismatches 359; Indels 366; Gaps 45;

KYQDLYTVEPNARQLVEIARDIEKLSNR-----SKALVSLALEAEK 106
 RYNTSYISS-----ELVPGDIYEIKNNWTIPCDITILSGVTMSEHMLTGES 152
 QWREDFASNEVYVYNAKDDLPKND-----SEPGSQRIKPVFIEDANFGQIS 160
 KERLPFGNALINKNNKYSNDEKDDYLRIYNNHASINMKRNLIEBTICKKOR 211
 VHIPTDIYEGSTIVLNELW-TSALDEVFQKQREEDPSLLMQVFGSATGLARYYP 219
 TH-----DLCSMNKLCYINNTYDDVHMKNKMD-----244
 TNSRTPNKIDLYDVERRRPWYIOGA-ASPKDMLILVDVSGSVGLTLKLTIVSVE 278
 INNNNNKKKKKNNLN-----FVKGTYINNDLLY-----275
 SDPDFNVVASFNASNAQDVSCFOHLVQANVRNKKVLKDAVNNITAKGTYDKKGS 338
 ---DDKIGVNIPE---DDVNNMKH--KFNQRIYNNKDTNNL-----EYNNKRR 317
 LNNVSVRANCKIIMLFTDGEERAQEIFNKIKDKKVRFRFVGQHNVERGP 398
 LLLKVEAISQKNKIIV-----SNEDINKY-----346

399 IQWMACENKGYEYIPSGAIRINTOBYLDVGRPMVLAG-----DKA
 347 ---MLYGGTVLSLYNINKYNNKEENRILGL-VIKTGFITTKGKIVNNILYHK
 445 QMTNYYLDALGLVIGTLPVFNITQGFENKTNLKNQILGL-----
 402 NLINDSYKFLII-LIIVALPSVILLYITLSNNYTHIIKICLDIITDAIPALPT
 488 MGVDVSLIEDIKRLTPRFTLCPNGYVFA-----IDPNGYVLLHPNLQ-----PKNP
 461 VGIISALRSKKKFSISCLCPKINIAGINTWVFDKTG-TLNNLOFQIGIITONK
 536 EPVTLDFDAELNDIKVEIRNMIDGSGKTRTTLVKQODERYIDKGNRTYWTTP
 520 NWLS-DFTHIK-----EMNTESYIHSKDDNNHKN-----
 596 TDYSLALVLPYSFYIYKAKLEETITQARSKGGKMKD-----SETLKPNFE
 550 -----SIISYYIKNNKNLHTSK-KKSTIKERSNLFVQTIKSCLLKDHVYK
 646 YFTIAPRDYCNLDKISDNN-TEFLIN-----FNEF--IDRKTNNPNSCNADLINRV
 600 KEYTNNYTCNDLHNDSTCSSYLLNSETKDAYCEYNIIDH-----LCD--INKK
 697 AGFTNELVONYMSKQKNIKGVKARPVVDGGITRVYPKEAGENWOENPETYEDSFYK
 651 INSKNELMGYSKNELMGKTIKNELM-----GKYSK
 757 DNDNVFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVG-----IKIDVK
 685 -----MGYSKNELMGYSKNELMGYSKNELMGYSKNELMGKTIKNQVGVDTK
 811 ENFTKTSIRD-PCAGPVCDCKRNSDVMDCV-----ILDDGGFLLMANHDDYTNOIGRF
 738 MNCNDYNDYPCD---YNCNCCNDYTHLEVHNKONSFWIPPEKNKSYNNISEE
 863 -----FGEIDPSLMRHLVNIISVAF-----NKS
 795 NYPLLFALACCHTSLSKNKGMDVLEILMFNTNCDMLINNNSFIIEKKKNCSS
 890 SVCBGAAPKQAGHSAYVPSVADILQIGWATAAASILQOELLSLTFPRLLEAI
 855 KI---DGDKNIGANDERCHLNN-----NLVSYNILKRF-----
 950 DDDFTASLSKQSCITEQYQYFDDNDSKS 977
 885 ---EFQSRLOQMSVIVKST-YGNNDNN 909

RESULT 11
 YPFBK_ECOLI
 ID YPFBK_ECOLI STANDARD; PRT; 575 AA.
 AC P76481;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein yfbb.
 GN YPFBK OR B2270
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINS=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474 (1997).
 CC -!- SIMILARITY: TO SYNECHOCYSTIS PCC 6803 SLL0103.

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 8: ail to license@isb-sib.ch).
 9: -----
 10: 1; AAC75330.1; -;
 11: 364998;
 12: 395; yfbk.
 13: 02035; VWFA_A.
 14: 1; vwa; 1.
 15: 7; VWA; 1.
 16: 234; VWFA; 1.
 17: protein; Complete proteome.
 18: 16 394 VWFA.
 19: 5 AA; 63634 MW; 78B6A1A77A2BE111 CRC64;
 20: -----
 21: 2.8%; Score 157.5; DB 1; Length 575;
 22: arity 21.6%; Pred. No. 0.047; Indels 105; Gaps 25;
 23: conservative 93; Mismatches 206;
 24: ARQLVEIARDIDIKLLSNRSKALVSLALEAEKQAAHQWREDFASNEVVVYNAKDD 130
 25: KESQQQPSPTTEQVLAAQAAIK---EAEQSAAA---AKALAQCEVQVQYSDKQA 75
 26: KND-----SFGSORIKPVIEDANFGROI SYQHA---VHIPTDI 172
 27: LQEAPTFAAAKAKATHIANPGTARYQOF---DDNPKVQAQNPATFSLDVTGTS 132
 28: IIVLINE-----LNWTSALDVFKNREEDPSLLMQVFGSATGLARYY 218
 29: RRFLNQGLPPDPADRVREIVNYPSPDWI---KDKQSIKPKPIPPFAWVELA--- 187
 30: WVDNRSPTNKIDLYDVRRRPWIYQGAASPKMDLILVDVSGS-VSLGLTLKIRTSVS 277
 31: ELREQDNIATVYAGDSRIA-----LPSISGSHKAEINAAIDSLDAGSTNGGAGL 296
 32: EQLLNYSVRANCKNIIMLTG-----GEAAQEIFNKYKDKKVRVFRFSVGQ 391
 33: QQATK-GFIKGGIIR-ILLATDGFNVGIDDPKSIENSVKQSGVLTSTFGVGN 354
 34: RGPIQWACENKGYEYIETPSIGAIRINTQYLDVIGRPML--AGDKAKQVQ---- 445
 35: EAMVRIADVGNVSYIDTLES---EAQKVLNEMRQMLITVAKDKVKAQIEFNPA 410
 36: YLDALEGLVLTGTLPVNITGCPENKTNLKNQLILGVMGVD-VSLEDI---KELT 501
 37: Y---RQIG-----YE-----KRLRVEHFNNNDVNDAGDIGAKGKIT 447
 38: LCPNGYYPAIDPBGVYLLHPLNQPNKPSQE 536
 39: ILTLNGKASIDKLYA---PDNKLAKSDTKYE 480
 40: -----
 41: STANDARD; PRT; 946 AA.
 42: 39; Q15484;
 43: (Rel. 17, Created)
 44: (Rel. 17, Last sequence update)
 45: (Rel. 42, Last annotation update)
 46: trypsin inhibitor heavy chain H2 precursor (ITI heavy
 47: inter-alpha-inhibitor heavy chain 2) (Inter-alpha-trypsin
 48: complex component II) (Serum-derived hyaluronan-associated
 49: AP).
 50: -----

GN ITIH2 OR IGHEP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=88152237; PubMed=2450046;
 RA Gebhard W., Schreitmuller T., Hochstrasser K., Wachter E.;
 RT "Complementary DNA and derived amino acid sequence of the precurs-
 RT of one of the three protein components of the inter-alpha-trypsin
 RT inhibitor complex";
 RL FEBS Lett. 229:63-67(1988).
 RN [2]
 RP SEQUENCE OF 384-865 FROM N.A.
 RX MEDLINE=88068576; PubMed=2446322;
 RA Salier J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,
 RA Benarous R., Ohkubo I., Kurachi S., Kurachi K., Martin J.P.;
 RT "Isolation and characterization of cDNAs encoding the heavy chain
 RT human inter-alpha-trypsin inhibitor (I alpha II): unambiguous
 RT evidence for multipolypeptide chain structure of I alpha II.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).
 RN [3]
 RP SEQUENCE OF 384-766 FROM N.A.
 RX MEDLINE=89076497; PubMed=2462430;
 RA Salier J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,
 RA Martin J.P.;
 RT "Human inter-alpha-trypsin inhibitor. Isolation and characterizat
 RT of heavy (H) chain cDNA clones coding for a 383 amino-acid sequen
 RT of the H chain.";
 RL Biol. Chem. Hoppe-Seyler 369:15-18(1988).
 RN [4]
 RP PARTIAL SEQUENCE FROM N.A.
 RX TISSUE=Liver;
 RA MEDLINE=88024442; PubMed=3663330;
 RA Schreitmuller T., Hochstrasser K., Resinger P.W.M., Wachter E.,
 RA Gebhard W.;
 RT "cDNA cloning of human inter-alpha-trypsin inhibitor discloses th
 RT different proteins.";
 RL Biol. Chem. Hoppe-Seyler 368:963-970(1987).
 RN [5]
 RP SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.
 RX MEDLINE=89380192; PubMed=2476436;
 RA Englund J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;
 RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin
 RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma.
 RT polypeptide chain stoichiometry and assembly by glycan.";
 RL J. Biol. Chem. 264:15975-15981(1989).
 RN [6]
 RP SEQUENCE OF 55-64.
 RX TISSUE=Plasma;
 RA MEDLINE=9303735; PubMed=1384548;
 RA Malki N., Balduyck M., Maes P., Capon C., Mizon C., Han K.K.,
 RA Tartar A., Fournet B., Mizon J.;
 RT "The heavy chains of human plasma inter-alpha-trypsin inhibitor:
 RT isolation, their identification by electrophoresis and partial
 RT sequencing. Differential reactivity with concanavalin A.";
 RL Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).
 RN [7]
 RP SEQUENCE OF 55-64 AND 681-702. CROSS-LINK STRUCTURE, AND
 RX CARBOHYDRATE-LINKAGE SITES THR-691.
 RA MEDLINE=93232026; PubMed=7682553;
 RA Englund J.J., Salvesen G., Thøgersen I.B., Valnickova Z.,
 RA Pizzo S.V., Hefta S.A.;
 RT "Presence of the protein-glycosaminoglycan-protein covalent cross
 RT in the inter-alpha-inhibitor-related proteinase inhibitor heavy c
 RT 2/pikunin.";
 RL J. Biol. Chem. 268:8711-8716(1993).
 RN [8]
 RP SEQUENCE OF 67-101, AND HYALURONAN BINDING.
 RX TISSUE=Serum;
 RA MEDLINE=94075371; PubMed=7504674;
 RA Huang L., Yoneda M., Kimata K.;

d hyaluronan-associated protein (SHAP) is the heavy
ter alpha-trypsin inhibitor.";
268:26725-26730(1993).

-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.

7; PubMed=7513643;
on C., Baldyck M., Sautiere P., Kouach M.,
Gurnet B., Mizon J.;
phate covalently cross-links the three polypeptide
alpha-trypsin inhibitor.";
1. 221:881-888(1994).

INKAGE SITES, AND MASS SPECTROMETRY.

6; PubMed=9677337;
on C., Baldyck M., Ricart G., Sautiere P., Mizon J.;
pattern of human inter-alpha-inhibitor heavy chains.";
1:749-756(1998).

INKAGE SITES, AND DISULFIDE BONDS.

10; PubMed=9425062;
abek-Nielsen H., Thøgersen I.B., Roepstorff P.,

mal modifications of human inter-alpha-inhibitor:
of glycans and disulfide bridges in heavy chains 1 and

1:408-416(1998).

MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
TEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
ON SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
TO CELLS UNDERGOING BIOLOGICAL PROCESSES.

-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
N, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
VD PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
BRIDGE TO THEIR C-TERMINAL ASPARTATE.

ROMETRY: MW=76508; METHOD=MALDI; RANGE=55-702.

: BELONGS TO THE ITIH FAMILY.

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CAA30160.1; ALT_SEQ.

AAA60558.1; -

AAA59195.1; -

VHU2.

P19823; -

67; ITIH2.

; F: plasma glycoprotein; TAS.

06587; VIT.

02035; VWF_A.

VW2; 1.

; VIT; 1.

; VWA; 1.

34; VWFA; 1.

e inhibitor; Repeat; Signal; Multigene family;

utamic acid; Glycoprotein.

1 18

9 54

5 702

3 946

8 468

INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN

H2.

3 946

8 468

FT	DISULFID	261	264			
FT	DISULFID	650	651			
FT	CARBOHYD	118	118			
FT						N-LINKED (GLCNAC. . .) (COMPLEX) .
FT						/FTid=CAR_000140.
FT	CARBOHYD	666	666			O-LINKED (GALNAC. . .) (PARTIAL) .
FT						/FTid=CAR_000214.
FT	CARBOHYD	671	671			N-LINKED (GLCNAC. . .) .
FT	CARBOHYD	673	673			O-LINKED (GALNAC. . .) .
FT						/FTid=CAR_000215.
FT	CARBOHYD	675	675			O-LINKED (GALNAC. . .) .
FT						/FTid=CAR_000216.
FT	CARBOHYD	691	691			O-LINKED (GALNAC. . .) .
FT						/FTid=CAR_000217.
FT	MOD RES	282	282			GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD RES	283	283			GAMMA-CARBOXYGLUTAMIC ACID.
FT	BINDING	702	702			CHONDROITIN 4-SULFATE, CROSS-LINK SIT.
FT	CONFLICT	374	374			K -> L (IN REF. 5).
FT	CONFLICT	674	674			P -> A (IN REF. 2 AND 3).
FT	CONFLICT	705	705			F -> S (IN REF. 2 AND 3).
FT	CONFLICT	729	729			N -> D (IN REF. 2 AND 3).
FT	CONFLICT	731	731			V -> A (IN REF. 2 AND 3).
SQ	SEQUENCE	946 AA;	106436 MM;			1478CF3BF3BA776 CRC64;

Query Match 2.8%; Score 154.5; DB 1; Length 946;

Best Local Similarity 19.9%; Pred. No. 0.15;
Matches 133; Conservative 106; Mismatches 259; Indels 171; Ga

QY	33	IKSVNDKQEDLVTLAKTAGVGNOLVDIYKQDLYTVEPNARQLVEIAARDIEKL				
Db	26	LSEFVD---YEDLVEL---APGQFLVAENRYQKSLPGESEEMEEVDQVLYSKV				
QY	93	RKALVSLALEAKKQAAHWRRE-----DFASN-----				
Db	81	ITSRMTTIQSKVNNSPQNVVDVQIPKGAFISNFSMTVDGKTPRSSIKKKTV				
QY	123	VYNNAK-----DDLDPKNDSE-----PGSQRKIPFIEDANFGRIQISYOH-				
Db	141	LYAQARAKGTAGLVRRSALDMENFRTEVNVLPKAKVQFELHYQEVKWKILGSEYHR				
QY	164	---AAVHIPDIDYEGSTIVLNLNWTSLD-----EVFKKNREE-----DPSLLW				
Db	201	QGRLEKLEVDVWVIEPQGLRFLHVPDTPFGHFGVPIVSKGQQAHVSPKPTVAG				
QY	209	GSATGLARYYPASPVDNSTRPNKIDLYDVRRRP-----WYIOGAAS-----				
Db	259	-----RICHSCR---ETAVDGELVLDVKREKAGELEVFGYVHFVFFADNLDL				
QY	253	DMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNNAQDVSCFQHLVC				
Db	310	NILFVIDVSGSMGVMKQTVEMAKTILDDLRAEDHFSVIDPNQIR--TWNRDLIS				
QY	313	RNKKVLDAVNNITAKGITDYKKGKGF---SFAPEQLNLYNVSRANCKIIMLPTDG--				
Db	368	TQVADAKRYIEKI QPSGGTINNEALLRAIFILNEANNLGLDDPNVSLIILVSDGDF				
QY	366	BERAQEIFNKYNKDKKVRVFRFSVQO-----HNYERGPQIWM-----AC				
Db	428	ELKLSKI QKNVKENIQDNISLPSLGWGFVDYDFLKLRSNENHGAQRIYGNQDTSE				
QY	408	GYYYEI--PSIGAIRIN--TOEYLDVL-----GRPMVLGAG--DKAKQVQWTV				
Db	488	KFYNOVSTPLLRNVQNPYPTSVTDVQNNFNHYFGSGSEIVVAGKFPDAK-----				
QY	453	ALELGLVITGLTPVENITGQFENKTNLKNQLITLVGMGVDSVLEDI-----KRLTPRFT				
Db	540	QIE--SVITA-----TSANTQLVLETLAQWDDLQDFLSKDKHADPDT				
QY	509	NGYYFAIDPNPGYVLLHPNLQPKNPKSQBPVTLDFLDLAELNDIKVEIRNKMIDGSGC				
Db	583	LWAYLTIN---QLLAERSLAP--TAAAKRRITRSILQMSLDHHIVTPLTSLVIENBAC				
QY	569	FRTLKVSQD 577				

PPQD 647

STANDARD; PRT; 1290 AA.

el. 16, Created)
 el. 16, Last sequence update)
 el. 41, Last annotation update)
 otxin type C1 precursor (EC 3.4.24.69) (BoNT/C1)
 C1).

Cl).
 tulinum.
 icutes; Clostridia; Clostridiales; Clostridiaceae;

1;

N.A.
 {87; PubMed=2204031;
 und M.W., Kurazona H., Binz T., Niemann H., Gill D.M.,
 off M.R.;
 quence of Clostridium botulinum C1 neurotoxin.";
 Res. 18:4924-4924(1990).

N.A.

Stockholm / C-ST;
 {98; PubMed=2222445;
 jii N., Tazuke K., Murakami T., Indoh T.,
 akeshi K., Syuto B., Oguma K.;
 nucleotide sequence of the gene coding for botulinum
 in the C-ST phage genome.";
 yb. Res. Commun. 171:1304-1311(1990).

-25.

Stockholm / C-ST;
 {72; PubMed=2450068;
 kosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,
 : of a monoclonal antibody recognizing an antigenic site
 stridium botulinum type B, C1, D, and E toxins and
 .";
 . 56:898-902(1988).

N OF SUBSTRATE.

366; PubMed=7901002;
 man E.R., Yamasaki S., Binz T., Niemann H., Jahn R.;
 rotoxin C1 blocks neurotransmitter release by means of
 l/syntaxin.";
 21-4828(1993).

BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
 DASE THAT CLEAVES SYNTAXIN.

ACTIVITY: Limited hydrolysis of proteins of the
 ytois apparatus, synaptobrevins, SNAP25 or syntaxin. No
 action on small molecule substrates.

Binds 1 zinc ion per subunit (By similarity).
 DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A
 IN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,
 N- AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
 AND TOXIN BINDING, RESPECTIVELY.

AR LOCATION: Secreted.

BOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF

NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.
 BOUS: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C
 CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE
 HAGE.

Y: BELONGS TO PEPTIDASE FAMILY M27.

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EMBL; X66433; CAA47060.1; -
 EMBL; X72793; CAA51313.1; -
 EMBL; X53751; CAA37780.1; -
 EMBL; D90210; BAA14235.1; -
 EMBL; X62389; CAA44263.1; -
 HSSP; F10845; 3ETA.
 MEROPS; M27.002; -

InterPro; IPR000395; Bontoxilysin.
 InterPro; IPR006025; Zn.MTpeptidase.
 Pfam; PF01742; Peptidase M27; 1.
 PRINTS; PR00760; BONTOKILYSIN.
 ProDom; PD001963; Bontoxilysin; 1.
 PROSITE; PS00142; ZINC_PROTEASE; 1.
 Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
 INIT MET 0

FT CHAIN	1	448	BOTULINUM NEUROTOXIN C1, LIGHT-CHAIN
FT CHAIN	449	1290	BOTULINUM NEUROTOXIN C1, HEAVY-CHAIN
FT METAL	228	228	ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE	229	229	BY SIMILARITY.
FT METAL	232	232	ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID	436	452	INTERCHAIN (PROBABLE).
FT CONFLICT	84	84	P -> T (IN REF. 2).
SQ	SEQUENCE	1290 AA; 148734 MW; 71FBE379F97129E8 CRC64;	

Query Match 2.7%; Score 152; DB 1; Length 1290;

Best Local Similarity 20.3%; Pred. No. 0.33;

Matches 205; Conservative 125; Mismatches 346; Indels 334; G;

QY 106 KVCQAHHQWREDPASNEVYNAKDDLDPKNDSEPGSQRIK---PVFIEDANFGR-
 DB 138 KTFQGNWVKVGSINPSVIITG-----PRENIIDPETSTFKLTNNTFAAQGEFGAL-
 QY 158 -----QISVQHAHVIPTDIYEGS-----TIVLEINWTSALDEVFK---
 DB 193 ISPRFMLTYSNAT-----NDVGEGRFSKSEFCMDPILILAHLELN--HAMHLYGIAI
 QY 199 EDFSLIHWQPGSATGLARYYP-----ASPMVDNSRTPNKIDLYDVRPPWYIOGAA
 DB 247 TISSVTSNIFYSQVNVKLEYAEIYAFGGPTID--LIPKSARKYFEKALDYYSIA
 QY 254 MLILVDVSG---SVSGLTLLAIR-----TSVSEMLETSLDDDFVNVASFNSNAQD
 DB 305 SITTANPSSFNKYGKYEKQKLRKYRVVSSGSEV--TVNRKFFVEL--YNELTQI
 QY 305 QHLVQANVRNKV-LKDAVNNITAK---GITYKKGFSPAFQL-----LNYNVSR
 DB 361 NYAKIYNVQRKIYLSNVYTPVTANILDDNVYDIQNGFNIPKGNLNLVLFMGQNLNR
 QY 352 --ANCKNIMLFT-----DGGERAQEIFNK-----YMKO-----KKV
 DB 421 RKNVPENMLYTFKFKHAKIDG-----RSYKNTKDCRELLVKNTDLPFGIDISDV
 QY 387 FSVGQHYRGPQIOMMACENKGYEYIIPSGAIRI--NTQY--LDVL-----
 DB 476 FLRCKDINEETEV-----YYPDNVSDVDQVLSKNTSEHGQLDLYPSIDSES
 QY 431 GRPMVLADKAKQVQWVN--VYLDALGLGVITGTLFPVFNITGTFENKTN-----
 DB 527 GENQVFYDNRNTQVNDYLSNYLYLESQKL-----SDNVEDFTFTRSIEBALONSAKVY
 QY 479 -LKNQLILGWG-----VDVSLIEDIKRLTPRFTLCPNGYIFAIDPNGVYLLHPN
 DB 583 TLANKVAGVQGGFLMWANDVVEDFTTNILRKOTLDKISDVSAIIP-----YIGPA
 QY 531 NPKSQEPVTLDF-----LDAELENDI-----KVEINKNMIDGESGKT
 DB 639 NSVERGNFTEAFATVGTVILLAPPEFTIPALGAFVIYSKVQVERNEII-----KT

te phase serum protein in pigs is homologous to human
ein sensitive PK-120.";
:227-230(1995).

MAY BE INVOLVED IN ACUTE PHASE REACTIONS.

CIFICITY: Liver-specific.

LEVELS INCREASE SIGNIFICANTLY AFTER CARDIOGENIC

RS TO BE BOTH N- AND O-GLYCOSYLATED (BY SIMILARITY).

ED BY PLASMA KALLIKREIN TO YIELD 55- AND 25-KDA

: BELONGS TO THE ITIH FAMILY.

: Contains 1 VWFA domain.

EF.2 SEQUENCE IS INCORRECT DUE TO FRAMESHIFTS AND OTHER

ERRORS.

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il to license@isb-sib.ch).

AAD00024.1; --

AAB46821.1; --

;; NOT_ANNOTATED_CDS.

IC4625.

IO6587; VIT.

IO2035; VWFA_A.

vwa; 1.

; VIT; 1.

; VWA; 1.

;34; VWFA; 1.

se inhibitor; Repeat; Signal; Multigene family;

1 27

18 921

INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN

H4.

70 428

80 80

95 205

12 242

3 513

77 577

19 50

73 703

AA; 102146 MW; E2BF95925DE8D07C CRC64;

2.7%; Score 150.5; DB 1; Length 921;

arity 19.9%; Pred.No. 0.25;

nservative 100; Mismatches 264; Indels 265; Gaps 36;

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SKALVSLALAEKQVAAHQWREDFASNEVYVNAKDDLDPEKNDSEPGSORIKVPF 149

PAKVTTELVEYELLARH-----LGVYELLKIQPQ-----QLVKHLQ 171

NFGHQ-LSY-QHAAVHIPTDIYEGSTIVLNE-----LWNTSALDEVFKKNEEDPSL 203

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-----WQVFGSATG-----LARYYPASFPWVDNSRTPNKKIDLYDVRBPWYIQG 247

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KDMLILVDVSGSVSLTLKILRTSVSEMLETLSDDDFWNVASFNSAQDVSCFQHL 307

Db 267 SAIPKNVIFVIDTSGMGRKIQQOTREALIILKLDGSRDQPNLVSFSGEAPR-----

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Db 323 VAASAENVEEAKSYAAETHAQGTININDAMLMAVQLL-----ERANRELLPARSVT

QY 360 LETDG-----GEERAQEIYKYNKDKKVRV-----PFSVGQHNVERGPIC

Db 378 LITDGDPTVGETNPSKI-----QKNVREADQGHSLFCLGPGFDVVPYAFLEK----

QY 404 CENKG-----YY-----YEIPSIGAIRINTQEYLDVL-

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Db 662 -LPPR 665

Search completed: February 20, 2004, 16:56:17

Job time : 16.5951 secs

6:26:18 2004

us-10-090-827-14.rapb

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1 search, using sw model

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the number of results predicted by chance to have a
than or equal to the score of the result being printed,
by analysis of the total score distribution.

SUMMARIES

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0	1063	14	US-10-090-827-15	Sequence 15, Appl
0	1091	9	US-09-875-423-4	Sequence 4, Appl
0	1091	14	US-10-162-012-17	Sequence 17, Appl
0	1091	14	US-10-090-827-16	Sequence 16, Appl
0	1091	15	US-10-162-102-17	Sequence 17, Appl
3	1086	15	US-10-375-253-49	Sequence 49, Appl
0	1084	15	US-10-375-253-53	Sequence 53, Appl
8	1036	14	US-10-090-827-7	Sequence 7, Appl
8	1063	14	US-10-090-827-8	Sequence 8, Appl
8	1069	14	US-10-090-827-9	Sequence 9, Appl
8	1091	14	US-10-090-827-5	Sequence 5, Appl
6	1103	15	US-10-375-253-47	Sequence 47, Appl
2	1079	15	US-10-375-253-51	Sequence 51, Appl
2	1018	14	US-10-090-827-13	Sequence 13, Appl

16	5316	97.7	1091	15	US-10-375-253-20	Sequence 2
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19	2907.5	53.4	1145	14	US-10-116-949-4	Sequence 4
20	2886.5	53.0	1076	14	US-10-116-949-6	Sequence 6
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23	1085	19.9	1091	15	US-10-162-102-18	Sequence 1
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26	1084	19.9	1091	15	US-10-162-102-15	Sequence 1
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ALIGNMENTS

RESULT 1
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; Sequence 14, Application US/10090827
; Publication No: US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 subu
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090.827
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-14

Query Match	100.0%	Score 5443;	DB 14;	Length 1036;
Best Local Similarity	100.0%;	Pred. No. 0;		
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Location US/10090827
IS20030073132A1
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ar-Lambert
[ON: Method for the screening of alpha 2 delta-1 subunit
[ON: binding ligands
179
TION NUMBER: US/10/090,827
DATE: 2002-03-06
ON NUMBER: US/09/397,549
TE: 1999-09-16

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; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 1063
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-15

Query Match      100.0%; Score 5443; DB 14; Length 1063;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gc

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3DGNPCDMVK 1036
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0981657A1

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JN: 21784, A NOVEL HUMAN CALCIUM CHANNEL

JN: FAMILY MEMBER AND USES THEREOF

10448-059001

ION NUMBER: US/09/875,423

ATE: 2001-06-05

NUMBER: US 60/209,257

3: 2000-06-05

NOS: 6

2 for Windows Version 4.0

sapiens

100.0%; Score 5443; DB 9; Length 1091;

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nservative 0; Mismatches 0; Indels 0; Gaps 0;

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HLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAPFQLLNYSRANCNKIIML 360

HLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAPFQLLNYSRANCNKIIML 360

EERAQEIFNKYNKDKKVVFRFSYGOHNYERGPIQWACENKGYIYIPISGAIR 420

EERAQEIFNKYNKDKKVVFRFSYGOHNYERGPIQWACENKGYIYIPISGAIR 420

YLDVLRPMVLADKAKQVQWNTNYLDALEGLVITGTLPVFNITGOFENKTNLK 480

YLDVLRPMVLADKAKQVQWNTNYLDALEGLVITGTLPVFNITGOFENKTNLK 480

GVMGVDVSLDILKLTFRFTLCPNGYYFAIDPNGYVLLHPNLQPNPKSPQEPVTL 540

GVMGVDVSLDILKLTFRFTLCPNGYYFAIDPNGYVLLHPNLQPNPKSPQEPVTL 540

541 DFLDAELNDIKVIRNKMIDGESSEKTFRTLVSQDERYIDKGNRTYTWTVPNGTD

541 DFLDAELNDIKVIRNKMIDGESSEKTFRTLVSQDERYIDKGNRTYTWTVPNGTD

601 ALVLPYTSFYIYKAKLBETITQARSKKGKMKDSETLKPDNFEESGYTFIARPDYCN

601 ALVLPYTSFYIYKAKLBETITQARSKKGKMKDSETLKPDNFEESGYTFIARPDYCN

661 SDNTEFLLNENEFIDRKTNNPSCNADLINRVLLDAGFTNELLVQNYWSKQKNIKGV

661 SDNTEFLLNENEFIDRKTNNPSCNADLINRVLLDAGFTNELLVQNYWSKQKNIKGV

721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKXSLDNNDNTVFTAPYFNKSGPGAYE

721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKXSLDNNDNTVFTAPYFNKSGPGAYE

781 MYSKAVEIYIOGKLLKPAVIGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVM

781 MYSKAVEIYIOGKLLKPAVIGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVM

841 LDDGGFLLMANHDDYTNOIGRFFGEIDPDLMLRHLVNIISVYAFNKSVDYQSVCEPGAA

841 LDDGGFLLMANHDDYTNOIGRFFGEIDPDLMLRHLVNIISVYAFNKSVDYQSVCEPGAA

901 GAGHRSAYVPSVADILQIGWATAAAWSILQOFLLSLTFPRLLLEAVEMEDDDFTASL

901 GAGHRSAYVPSVADILQIGWATAAAWSILQOFLLSLTFPRLLLEAVEMEDDDFTASL

961 SCITEQTOYFFDNDSKSPGVLDCGNCRSRI FHGKLMNTNLI FIMVESKGTCPDTR

961 SCITEQTOYFFDNDSKSPGVLDCGNCRSRI FHGKLMNTNLI FIMVESKGTCPDTR

1021 QAEQTS DGNPCDMVK 1036

1021 QAEQTS DGNPCDMVK 1036

RESULT 4

US-10-162-012-17

; Sequence 17, Application US/10162012

; Publication No. US20030051660A1

; GENERAL INFORMATION:

; APPLICANT: Curtis, Rory A.J.

; APPLICANT: Silos-Santiago, Immaculada

; APPLICANT: Gu, Wei

; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY M

; FILE REFERENCE: 10448-190001

; CURRENT APPLICATION NUMBER: US/10/162,012

; PRIOR FILING DATE: 2002-06-04

; PRIOR APPLICATION NUMBER: US 60/209,845

; PRIOR FILING DATE: 2000-06-06

; PRIOR APPLICATION NUMBER: US 09/875,321

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: PCT/US01/18340

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: US 60/209,257

; PRIOR FILING DATE: 2000-06-05

; PRIOR APPLICATION NUMBER: US 09/875,423

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: PCT/US01/18398

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/209,238

; PRIOR FILING DATE: 2000-06-05

; PRIOR APPLICATION NUMBER: US 09/875,363

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: PCT/US01/18247

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/227,068

; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: US 09/928,530

; PRIOR FILING DATE: 2001-08-13

; PRIOR APPLICATION NUMBER: PCT/US01/25475

; PRIOR FILING DATE: 2001-08-15

ON NUMBER: US 60/226,770
 TE: 2000-08-21
 ON NUMBER: US 09/934,421
 TE: 2001-08-21
 ON NUMBER: PCT/US01/26096
 TE: 2001-08-21
 ON NUMBER: US 60/279,281
 TE: 2001-03-28
 ON NUMBER: US 10/109,029
 TE: 2002-03-28
 ON NUMBER: PCT/US02/09728
 TE: 2002-03-28
 ON NUMBER: US 60/290,288
 TE: 2001-05-11
 ON NUMBER: US (not assigned)
 TE: 2002-05-13
 D NOS: 48
 EQ for Windows Version 4.0

sapiens

100.0%; Score 5443; DB 14; Length 1091;
 arity 100.0%; Pred. No. 0;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;

CLLALTLTQLSLLIGPSSPEPPSAVTIKSWVDKMOEDLVTLAKTAGVNLVDI 60
 CLLALTLTQLSLLIGPSSPEPPSAVTIKSWVDKMOEDLVTLAKTAGVNLVDI 60
 JDLVTEPNARQVLAARDIEKLLNRSKALVSLALEAEKVQAAHOWREDFASN 120
 JDLVTEPNARQVLAARDIEKLLNRSKALVSLALEAEKVQAAHOWREDFASN 120
 YNAKDDLPKNDSEPGSQIKPVFIEDANFGQISYQHAHVHIPTDIYEGSTIVL 180
 YNAKDDLPKNDSEPGSQIKPVFIEDANFGQISYQHAHVHIPTDIYEGSTIVL 180
 ATSALDEVFKNREEDPSLLWQVFGSATGLARYYPASPWVDNRTNPKIDLYDVR 240
 ATSALDEVFKNREEDPSLLWQVFGSATGLARYYPASPWVDNRTNPKIDLYDVR 240
 IQGAASPDKMLILVDVSGSVGLTLKILRTSVSEMLETLSDDDFVNVSFNSAQD 300
 IQGAASPDKMLILVDVSGSVGLTLKILRTSVSEMLETLSDDDFVNVSFNSAQD 300
 JHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSAPEQLLNYNVRANCKIIML 360
 JHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSAPEQLLNYNVRANCKIIML 360
 JBERAQEIFNKYNKKVRVFRFSVQGHNYERGPQWMAKNGYIYEIPSIGAIR 420
 JBERAQEIFNKYNKKVRVFRFSVQGHNYERGPQWMAKNGYIYEIPSIGAIR 420
 JYLDVLRPMVLADGAKQVQWNTNVLDLLEGLVITGTLVPENITQGFENKTLK 480
 JYLDVLRPMVLADGAKQVQWNTNVLDLLEGLVITGTLVPENITQGFENKTLK 480
 JYMGVDVSLDILKRLTPRTLCNPGYFAIDPNGVYLLHPNLQPNKPSQEPVTL 540
 JYMGVDVSLDILKRLTPRTLCNPGYFAIDPNGVYLLHPNLQPNKPSQEPVTL 540
 JELENDIKVEIRNMKIDGESGKTRTLVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
 JELENDIKVEIRNMKIDGESGKTRTLVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
 JYTSFYIYKAKLETTIQAASKGKMDSETLKPDPFESGYTFIAPROYCNDLKI 660
 JYTSFYIYKAKLETTIQAASKGKMDSETLKPDPFESGYTFIAPROYCNDLKI 660
 JEPFLNFEFIDRKTNNPNSCNADLNRVLLDAGFTNELVQNYWSKQKNIKGKAR 720

Db 661 SDANTEFLNPNFIDRKTNNPNSCNADLNRVLLDAGFTNELVQNYWSKQKNIKG
 QY 721 FVVTDDGIGITRVYKPEAGENQENPETYEDSFYKESLONDNYVFTAPYFNKSGPGAY
 Db 721 FVVTDDGIGITRVYKPEAGENQENPETYEDSFYKESLONDNYVFTAPYFNKSGPGAY
 QY 781 MVSKAVEIYIQGKLLKPAVVIGIKIDVNSWIENFTKTSIRDPACGVPVDCCKRNSDVW
 Db 781 MVSKAVEIYIQGKLLKPAVVIGIKIDVNSWIENFTKTSIRDPACGVPVDCCKRNSDVW
 QY 841 LDGCGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSQYDYQSVCEPGA
 Db 841 LDGCGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSQYDYQSVCEPGA
 QY 901 GAGHRSAYVPSVADILQIGWATAAASIIQQFLLSITFPRLLEAVEMEDDDFTAS
 Db 901 GAGHRSAYVPSVADILQIGWATAAASIIQQFLLSITFPRLLEAVEMEDDDFTAS
 QY 961 SCITEQTQYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLI FIMVESKGTCPCDT
 Db 961 SCITEQTQYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLI FIMVESKGTCPCDT
 QY 1021 QAEQTSQGNPCDMVK 1036
 Db 1021 QAEQTSQGNPCDMVK 1036

RESULT 5
 US-10-090-827-16
 ; Sequence 16, Application US/10090827
 ; Publication No. US20030073132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert
 ; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 sub
 ; FILE REFERENCES: 179
 ; CURRENT APPLICATION NUMBER: US/10/090,827
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US/09/397,549
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: Patencin ver. 2.1
 ; SEQ ID NO 16
 ; LENGTH: 1091
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-090-827-16

Query Match 100.0%; Score 5443; DB 14; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1036; Conservative 0; Mismatches 0; Indels 0; G

QY 1 MAAGCCLLALTTLTQLSLLIGPSSPEPPSAVTIKSWVDKMOEDLVTLAKTAGVNC
 Db 1 MAAGCCLLALTTLTQLSLLIGPSSPEPPSAVTIKSWVDKMOEDLVTLAKTAGVNC
 QY 61 YEKYQDLYTVEPNARQVLAARDIEKLLNRSKALVSLALEAEKVQAAHOWREDI
 Db 61 YEKYQDLYTVEPNARQVLAARDIEKLLNRSKALVSLALEAEKVQAAHOWREDI
 QY 121 EYVYNAKDDLPKNDSEPGSQIKPVFIEDANFGQISYQHAHVHIPTDIYEGS
 Db 121 EYVYNAKDDLPKNDSEPGSQIKPVFIEDANFGQISYQHAHVHIPTDIYEGS
 QY 181 NELNWTSADEVFKNREEDPSLLWQVFGSATGLARYYPASPWVDNRTNPKIDLYI
 Db 181 NELNWTSADEVFKNREEDPSLLWQVFGSATGLARYYPASPWVDNRTNPKIDLYI
 QY 241 RPYWYIQGAASPKDMLILVDVSGSVGLTLKILRTSVSEMLETLSDDDFVNVSFNS
 Db 241 RPYWYIQGAASPKDMLILVDVSGSVGLTLKILRTSVSEMLETLSDDDFVNVSFNS

'DGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
 'DGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
 'JAVEIYIQGLKLPKAVVGIKIDVNSWIENTFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
 'JAVEIYIQGLKLPKAVVGIKIDVNSWIENTFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
 'JGFLMANHDDYTNOIGRFFGEBIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
 'JGFLMANHDDYTNOIGRFFGEBIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
 'RSAYVPSVADILQIGWATAAASILQOFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960
 'RSAYVPSVADILQIGWATAAASILQOFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960
 'EQTOYFFNDKSKSGVLDCGNCRSRI FHGEKLMNTNLI FIMVESKGTCPCTRLLI 1020
 'EQTOYFFNDKSKSGVLDCGNCRSRI FHGEKLMNTNLI FIMVESKGTCPCTRLLI 1020
 'TSDGPNPCDMVK 1036
 'TSDGPNPCDMVK 1036

lication US/10375253

US20040018510A1

ION:

SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES

ION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

ION: METHODS

SD9813DA

TION NUMBER: US/10/375,253

DATE: 2003-02-27

ON NUMBER: 08/450,273

TE: 1995-05-25

ON NUMBER: 08/404,354

TE: 1995-02-15

ON NUMBER: 07/914,231

TE: 1992-07-13

ON NUMBER: 08/314,083

TE: 1994-09-28

ON NUMBER: 07/914,231

TE: 1992-07-13

ON NUMBER: 07/603,751

TE: 1990-11-09

ON NUMBER: 08/290,012

TE: 1994-08-11

ON NUMBER: 08/149,097

TE: 1993-11-05

ON NUMBER: 08/105,536

TE: 1993-08-11

ON NUMBER: 08/149,097

TE: 1993-11-05

Application data removed - See File Wrapper or PALM.

D NOS: 65

EQ for Windows Version 4.0

a

arity 99.3%; Score 5403.5; DB 15; Length 1086;

onservative 0; Mismatches 0; Indels 5; Gaps 1;

CLIALTLTQSLIGSPSEPPPSAVTIKSWVDMQEDLVTLAKTASGVNQLVDI 60

CLIALTLTQSLIGSPSEPPPSAVTIKSWVDMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLTYVEPNNAQLVEIARADIEKLSNRKALVSLALEAEKVQAAHQWREI
 Db 61 YEKYQDLTYVEPNNAQLVEIARADIEKLSNRKALVSLALEAEKVQAAHQWREI
 QY 121 EVVYNKADDDLPKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEG
 Db 121 EVVYNKADDDLPKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEG
 QY 181 NELNWTSDALDVEFKKNREDEPSLLWQVFGSATGLARYYPASVWNSRTPNKIDLI
 Db 181 NELNWTSDALDVEFKKNREDEPSLLWQVFGSATGLARYYPASVWNSRTPNKIDLI
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTFLKIRTSVSEMLETSLDDDDFVNVSFNE
 Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTFLKIRTSVSEMLETSLDDDDFVNVSFNE
 QY 301 VSCQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAPEQLLNYNVSRANCN
 Db 301 VSCQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAPEQLLNYNVSRANCN
 QY 361 FTDGGEERAQEI FNKYNKDKKVRFRFSVGOHNYERGP IOMMACENKGYIYEI PSI
 Db 361 FTDGGEERAQEI FNKYNKDKKVRFRFSVGOHNYERGP IOMMACENKGYIYEI PSI
 QY 421 INTOEYLDVLGRPMVLADGKAKQVQWNTNVLDALELGLVITGTLPVFNITQGFNF
 Db 421 INTOEYLDVLGRPMVLADGKAKQVQWNTNVLDALELGLVITGTLPVFNITQGFNF
 QY 481 NQLILGVWGVDSLEDIKRLTPFTLCPNGYYPFAIDPNGYVLLHPNLOPKPKSQE
 Db 481 NQLILGVWGVDSLEDIKRLTPFTLCPNGYYPFAIDPNGYVLLHPNLOPKPKSQE
 QY 541 DFLDAELENDIKVEIRNMIDGSGEKTFTLVKSQDERYIDKGNRTVTWTPVNGI
 Db 541 DFLDAELENDIKVEIRNMIDGSGEKTFTLVKSQDERYIDKGNRTVTWTPVNGI
 QY 596 ALVLTYSFYIYKAKLEETITQARSKGKMDSETLKPDPNPEESGYTFIAPRDYCN
 Db 596 ALVLTYSFYIYKAKLEETITQARSKGKMDSETLKPDPNPEESGYTFIAPRDYCN
 QY 661 SDNNTFLLNPNFIDRKTNNPSCNADLINRVLLDAGTNNELVQNYWSKQKNIKG
 Db 661 SDNNTFLLNPNFIDRKTNNPSCNADLINRVLLDAGTNNELVQNYWSKQKNIKG
 QY 721 FVVTDDGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAY
 Db 721 FVVTDDGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAY
 QY 776 MVSKAVEIYIQGLKLPKAVVGIKIDVNSWIENTFTKTSIRDPKAGVPCDCKRNSDVM
 Db 776 MVSKAVEIYIQGLKLPKAVVGIKIDVNSWIENTFTKTSIRDPKAGVPCDCKRNSDVM
 QY 841 LDDGGFLMANHDDYTNOIGRFFGEBIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGA
 Db 841 LDDGGFLMANHDDYTNOIGRFFGEBIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGA
 QY 901 GAGHSAYVPSVADILQIGWATAAASILQOFLLSLTPRLLLEAVEMEDDDFTAS
 Db 901 GAGHSAYVPSVADILQIGWATAAASILQOFLLSLTPRLLLEAVEMEDDDFTAS
 QY 961 SCITEQTOYFFNDKSKSGVLDCGNCRSRI FHGEKLMNTNLI FIMVESKGTCPCDT
 Db 961 SCITEQTOYFFNDKSKSGVLDCGNCRSRI FHGEKLMNTNLI FIMVESKGTCPCDT
 QY 1021 QABQTS DGNPCDMVK 1036
 Db 1016 QABQTS DGNPCDMVK 1031

RESULT 8

US-10-375-253-53

; Sequence 53, Application US/10375253

; Publication No. US20040018510A1

ION:
ALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
ION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ION: METHODS

SD9813DA

ION NUMBER: US/10/375,253

DATE: 2003-02-27

ION NUMBER: 08/450,273

TE: 1995-05-25

ION NUMBER: 08/404,354

TE: 1995-02-15

ION NUMBER: 07/914,231

TE: 1992-07-13

ION NUMBER: 08/314,083

TE: 1994-09-28

ION NUMBER: 07/914,231

TE: 1992-07-13

ION NUMBER: 07/603,751

TE: 1990-11-09

ION NUMBER: 08/290,012

TE: 1994-08-11

ION NUMBER: 08/149,097

TE: 1993-11-05

ION NUMBER: 08/105,536

TE: 1993-08-11

ION NUMBER: 08/149,097

TE: 1993-11-05

Application data removed - See File Wrapper or PALM.

ION NOS: 65

IQ for Windows Version 4.0

99.0%; Score 5386.5; DB 15; Length 1084;

Identity 99.2%; Pred. No. 0;

inservative 0; Mismatches 1; Indels 7; Gaps 1;

LLALTLTFLQSLIGPSSPEPPSAVTIKSWDKMQEDLVTAKTASGVNQLVDI 60

LLALTLTFLQSLIGPSSPEPPSAVTIKSWDKMQEDLVTAKTASGVNQLVDI 60

DLTYTVPNNARQLVEIARDIEKLSNRKALVSLALEAEKVQAAHQRDPASN 120

DLTYTVPNNARQLVEIARDIEKLSNRKALVSLALEAEKVQAAHQRDPASN 120

NAKDDLPKNDSEPGSQRIKPVFTEDANFGRQISYQHAHVHPTDIYEGSTIVL 180

NAKDDLPKNDSEPGSQRIKPVFTEDANFGRQISYQHAHVHPTDIYEGSTIVL 180

TSALDEVKKREEDPSLLQWVFGSATGLARYYPASPMVDNSRTNKKIDLDVRR 240

TSALDEVKKREEDPSLLQWVFGSATGLARYYPASPMVDNSRTNKKIDLDVRR 240

QGAASPKDMLIIVDSGVSGLTLLKIRTSVSEMLETLSDDDFVNVSFNSNAQD 300

QGAASPKDMLIIVDSGVSGLTLLKIRTSVSEMLETLSDDDFVNVSFNSNAQD 300

HLVQANVRNKKVLKADVNNITAKGTTDYKGFSPAFQQLNLYNVSANCKIIML 360

HLVQANVRNKKVLKADVNNITAKGTTDYKGFSPAFQQLNLYNVSANCKIIML 360

IERAQEIKFNKNDKKVRFVSQHNHYERGPIQWACENKGYIETPSGAIR 420

IERAQEIKFNKNDKKVRFVSQHNHYERGPIQWACENKGYIETPSGAIR 420

YLDVLGRPMVLADGKAKOVQWNTVYLDLGLVITGLPVFNITQGENKTNLK 480

YLDVLGRPMVLADGKAKOVQWNTVYLDLGLVITGLPVFNITQGENKTNLK 480

QWGMVDVSLIEDIKRUTPRFTLCPNGYYPFAIDPNGYVLLHPNLQPKNPKSQBFVTL 540

Db 481 NQILGVMGVDSLEDIKRLTFRFTLCPNGYYPFAIDPNGYVLLHPNLQPKNPKSQE
Qy 541 DFLDAELENDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGT
Db 541 DFLDAELENDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGT
Qy 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFIAPRDYCN
Db 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFIAPRDYCN
Qy 661 SDNTEFLNFEFIDRKTPNPNFSCNADLINRVLLDAGFTNELVQNVWSKQKNIKG
Db 654 SDNTEFLNFEFIDRKTPNPNFSCNADLINRVLLDAGFTNELVQNVWSKQKNIKG
Qy 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNRYVFTAPYFNKSGPGAY
Db 714 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNRYVFTAPYFNKSGPGAY
Qy 781 MVS KAVEIYIQGLKLPVAVVGIKIDVNSWIENTFTKTSIRDPACAGPVCDCRNSDVM
Db 774 MVS KAVEIYIQGLKLPVAVVGIKIDVNSWIENTFTKTSIRDPACAGPVCDCRNSDVM
Qy 841 LDDGGFLMANHDDYTNQIGRFFGEIDPDLMLRHLVNI SVYAFNKS YDYQSVCEPGA
Db 834 LDDGGFLMANHDDYTNQIGRFFGEIDPDLMLRHLVNI SVYAFNKS YDYQSVCEPGA
Qy 901 GAGHRAYVPSVADIIQIGHWATAAAWSILQOFLSLTFFPRLEAVEMEDDDFTAS
Db 894 GAGHRAYVPSVADIIQIGHWATAAAWSILQOFLSLTFFPRLEAVEMEDDDFTAS
Qy 961 SCITEQTYFFDNDKSFSGVLDGNCNCRIFHGEKLMNTNLIIFIMVESKGTCPCDT
Db 954 SCITEQTYFFDNDKSFSGVLDGNCNCRIFHGEKLMNTNLIIFIMVESKGTCPCDT
Qy 1021 QAEQTS DGNPCDMVK 1036
Db 1014 QAEQTS DGNPCDMVK 1029

RESULT 9

US-10-090-827-7

; Sequence 7, Application US/10090827

; Publication No. US20030073132A1

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert

; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 sub

; FILE REFERENCE: 179

; CURRENT APPLICATION NUMBER: US/10/090,827

; PRIOR FILING DATE: 2002-03-06

; PRIOR APPLICATION NUMBER: US/09/397,549

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 1036

; TYPE: PRT

; ORGANISM: Sus scrofa

US-10-090-827-7

Query Match 98.8%; Score 5380; DB 14; Length 1036;

Best Local Similarity 98.7%; Pred. No. 0;

Matches 1023; Conservative 6; Mismatches 7; Indels 0; G

Qy 1 MAAGCLLALTTLTFLQSLIGPSSPEPPSAVTIKSWDKMQEDLVTAKTASGVNQI

Db 1 MAAGCLLALTTLTFLQSLIGPSSPEPPSAVTIKSWDKMQEDLVTAKTASGVNQI

Qy 61 YEKYQDLYTVEPNNARQLVEIARDIEKLSNRKALVSLALEAEKVQAAHQRREDI

Db 61 YEKYQDLYTVEPNNARQLVEIARDIEKLSNRKALVSLALEAEKVQAAHQRREDI


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FFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNIISVYAFNKSVDYOSVCEPGAAPKQ 900
|||||
FFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNIISVYAFNKSVDYOSVCEPGAAPKQ 900
|||||
SAYVPSVADIIQIGHWATAAASIIQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
|||||
SAYVPSIADIIHIGWATAAASIIQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
|||||
|QTQFFDNDKSFSGVLDGCGNCSRIHFHGEKLMNTNLIIFIMVESKGTCTPCDTRLII 1020
|||||
|QTQFFDNDKSFSGVLDGCGNCSRIHFHGEKLMNTNLIIFIMVESKGTCTPCDTRLII 1020
|||||
SDGNPCDMVK 1036
SDGNPCDMVK 1036

cation US/10090827
S20030073132A1
ON:
x-Lambert
ON: Method for the screening of alpha 2 delta-1 subunit
ON: binding ligands
179
ION NUMBER: US/10/090, 827
DATE: 2002-03-06
N NUMBER: US/09/397, 549
E: 1999-09-16
NOS: 21
In Ver. 2.1

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crofa

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98.8%; Score 5380; DB 14; Length 1069;
rity 98.7%; Pred. No. 0;
nservative 6; Mismatches 7; Indels 0; Gaps 0;

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LLALTLTLFQSLIIGPSSEBPPPSAVTIKSWVDKMQEDLVTLAKTAGSNQVLVDI 60
|||||
LLALTLTLFQSLIIGPSSEBPPPSAVTIKSWVDKMQEDLVTLAKTAGSNQVLVDI 60
|||||
|DLYTVEPNARQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDPASN 120
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|DLYTVEPNARQVLEIAARDIEKLLSNRSKALVRLALEAEKVQAAHQRDPASN 120
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|||||
TSALDEVEKKREEDPSLLWQVFGSATGLARYYPASPWDNSRTPNKIDLDVRR 240
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TSALDEVEKKREEDPSLLWQVFGSATGLARYYPASPWDNSRTPNKIDLDVRR 240
|||||
QGAASPDKMLILVDVSGVSGLTLLKIRTSVSEMLETLSDDDFVNVAFSNNAQD 300
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|||||
HLVQANVRKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCKIIML 360
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HLVQANVRKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCKIIML 360
|||||
HEERAQEIIFKNYKDKKRVFPFVSCOHYERGPQIOWMACENKGYIYEIPSGAIR 420
|||||
HEERAQEIIFAKYKDKKRVFTFVSGOHYDRGPQIOWMACENKGYIYEIPSGAIR 420
|||||
YLDVLGRPWLAGDKAKQVQWNTNVYLDLDALEGLVITGTLPVFNITGQENKTNLK 480
|||||
YLDVLGRPWLAGDKAKQVQWNTNVYLDLDALEGLVITGTLPVFNITGQENKTNLK 480
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QY 481 NQILIGVMGVDSLEIDKELTFRFTLCPNGYFFAIDPENGTVLLHPLNLPKNPKSQE
Db 481 NQILIGVMGVDSLEIDKELTFRFTLCPNGYFFAIDPENGTVLLHPLNLPKNPKSQE
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSDERYIDKGNRTYTWTPVNGT
Db 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSDERYIDKGNRTYTWTPVNGT
QY 601 ALVLPYSPYIYKAKLEETITQARSKKGMKQSETLKPDPFESGYTFIAPRDYCN
Db 601 ALVLPYSPYIYKAKLEETITQARSKKGMKQSETLKPDPFESGYTFIAPRDYCN
QY 661 SDNNTTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNKIKG
Db 661 SDNNTTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNKIKG
QY 721 FVVTGGITRVYPKKEAGENWQENPETYEDSFYKRSILDNDNYFTAPYFNKSGFGAYI
Db 721 FVVTGGITRVYPKKEAGENWQENPETYEDSFYKRSILDNDNYFTAPYFNKSGFGAYI
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPGAGPVCDCKRNSDVM
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPGAGPVCDCKRNSDVM
QY 841 LDDGGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNIISVYAFNKSVDYOSVCEPGA
Db 841 LDDGGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNIISVYAFNKSVDYOSVCEPGA
QY 901 GAGHSAYVPSVADIIQIGHWATAAASIIQQFLLSLTFPRLLLEAVEMEDDDFTAS
Db 901 GAGHSAYVPSIADIIHIGWATAAASIIQQFLLSLTFPRLLLEAVEMEDDDFTAS
QY 961 SCITEQTYFFDNDKSFSGVLDGCGNCSRIHFHGEKLMNTNLIIFIMVESKGTCTPCDTI
Db 961 SCITEQTYFFDNDKSFSGVLDGCGNCSRIHFHGEKLMNTNLIIFIMVESKGTCTPCDTI
QY 1021 QAEQTSDBGPNPCDMVK 1036
Db 1021 QAEQTSDBGPNPCDMVK 1036

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RESULT 12

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US-10-090-827-5
; Sequence 5, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 sub
; TITLE OF INVENTION: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-090-827-5

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Query Match 98.8%; Score 5380; DB 14; Length 1091;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1023; Conservative 6; Mismatches 7; Indels 0; G

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QY 1 MAAGCLLALTLTLFQSLIIGPSSEBPPPSAVTIKSWVDKMQEDLVTLAKTAGSNQI
Db 1 MAAGCLLALTLTLFQSLIIGPSSEBPPPSAVTIKSWVDKMQEDLVTLAKTAGSNQI
QY 61 YEKYQDLYTVEPNARQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEI

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-----NPKSQBPVTLDFDAELENDEIKVEIRNKMIDGESGKTFRTLVKSQDERYI 581
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TYTWPVNGTDSIALVLPYVSFYIYKAKLEETITQARSKKGMKQSETLKPONF 641
TYTWPVNGTDSIALVLPYVSFYIYKAKLEETITQARY-----SETLKPONF 653
TFIAPRDYCNLDKISDNNTFLNMFNFIORKTENNPSNADLINRVLLDAGFTN 701
TFIAPRDYCNLDKISDNNTFLNMFNFIORKTENNPSNADLINRVLLDAGFTN 713
YMSKQKNIKGKARFVVTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNY 761
YMSKQKNIKGKARFVVTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNY 773
YFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDP 821
YFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDP 833
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CDCRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPISLMRHLVNI SVYA 893
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DYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWWATAAAWSILQOFLLSLTTPR 953
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EMEDDDTASLSKOSCSITEQYTFDNDKSFSGVLDCGNCRSIFHGEKLMNTNL 1013
ESKGTCCDRLLIQAEQTSQGNPCDMVK 1036
|||||
ESKGTCCDRLLIQAEQTSQGNPCDMVK 1048

ication US/10375253

S20040018510A1

ON:

ALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES

ON: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

ON: METHODS

SD9813DA

ION NUMBER: US/10/375,253

ATE: 2003-02-27

N NUMBER: 08/450,273

E: 1995-05-25

N NUMBER: 08/404,354

E: 1995-02-15

N NUMBER: 07/914,231

E: 1992-07-13

N NUMBER: 08/314,083

E: 1994-09-28

N NUMBER: 07/914,231

E: 1992-07-13

N NUMBER: 07/603,751

E: 1990-11-09

N NUMBER: 08/290,012

E: 1994-08-11

N NUMBER: 08/149,097

E: 1993-11-05

N NUMBER: 08/105,536

E: 1993-08-11

N NUMBER: 08/149,097

E: 1993-11-05

Application data removed - See File Wrapper or PALM.

NOS: 65

Q for Windows Version 4.0

? LENGTH: 1079
? TYPE: PRT
? ORGANISM: Human
US-10-375-253-51

Query Match 98.2%; Score 5347; DB 15; Length 1079;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1023; Conservative 0; Mismatches 1; Indels 12; Gs

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DB	1	MAAGCLLALTTLFOSLIGSSSEPPFSAVTIKSWVDKMOEDIVTLAKTAGVNOI
QY	61	YEKYODLTVPENNARQOLVEIARDEIKLLSNRSKALVSLALEAEKVQAAHQWREDE
DB	61	YEKYODLTVPENNARQOLVEIARDEIKLLSNRSKALVSLALEAEKVQAAHQWREDE
QY	121	EVVYNKADDDLPENKNDSEPGSQRIKPVFIEDANFGROIISYOHAAVHIPTDIYEGST
DB	121	EVVYNKADDDLPENKNDSEPGSQRIKPVFIEDANFGROIISYOHAAVHIPTDIYEGST
QY	181	NELNWTSADEVFYKKNREDEPSLLQVFGSATGLARYYPASPWVNSRTPNKIDLYI
DB	181	NELNWTSADEVFYKKNREDEPSLLQVFGSATGLARYYPASPWVNSRTPNKIDLYI
QY	241	RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRTSVSEMLETSLDDDFVNVASFNSN
DB	241	RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRTSVSEMLETSLDDDFVNVASFNSN
QY	301	VSCFOHLVQAVNRNKKVKADAVNNITAKGITYKKGSPFAFQOLLNLYNVRANCNKI
DB	301	VSCFOHLVQAVNRNKKVKADAVNNITAKGITYKKGSPFAFQOLLNLYNVRANCNKI
QY	361	FTDGGEEARAQEIFNKYNKKVVRVRFVSGQHNVERGPQIOWMACENKGYVYIETIC
DB	361	FTDGGEEARAQEIFNKYNKKVVRVRFVSGQHNVERGPQIOWMACENKGYVYIETIC
QY	421	INTQEYLDVLGRPMVLADGKAKQVQWTVNYLDALGLGLVITGTLPVFNITGQFENKI
DB	421	INTQEYLDVLGRPMVLADGKAKQVQWTVNYLDALGLGLVITGTLPVFNITGQFENKI
QY	481	NQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHHPNLOPNKPSQEE
DB	481	NQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHHPNLOPNKPSQEE
QY	541	DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGTI
DB	541	DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGTI
QY	601	ALVLPYTSFYIYKAKLEETITQARSKKGMKQSETLKPONFEESGYTFTAPRDYCN
DB	596	ALVLPYTSFYIYKAKLEETITQARY-----SETLKPONFEESGYTFTAPRDYCN
QY	661	SDNTEFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNLTAPYFNKSKQKNIKGV
DB	649	SDNTEFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNLTAPYFNKSKQKNIKGV
QY	721	FVVTDDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYE
DB	709	FVVTDDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYE
QY	781	MYSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPKAGPVCDCRNSDVM
DB	769	MYSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPKAGPVCDCRNSDVM
QY	841	LDGGLFLMANHDDYTNOIGRFFGEIDPISLMRHLVNI SVYAFNKSQYQSVCEPGAA
DB	829	LDGGLFLMANHDDYTNOIGRFFGEIDPISLMRHLVNI SVYAFNKSQYQSVCEPGAA
QY	901	GAGHRSAYVPSVADILQIGWWATAAAWSILOQFLLSLTTPRLLLEAVEMEDDDFTASL
DB	889	GAGHRSAYVPSVADILQIGWWATAAAWSILOQFLLSLTTPRLLLEAVEMEDDDFTASL

6:26:18 2004

us-10-090-827-15.rapb

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YQYFFDNDSKSPGVLDCGNCRSRIIPHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
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ication US/10162012
320030051660A1
DN: Rory A.J.
s-Santiago, Inmaculada
ve
DN: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
[0448-190001
ION NUMBER: US/10/162,012
ATE: 2002-06-04
V NUMBER: US 60/209,845
3: 2000-06-06
V NUMBER: US 09/875,321
3: 2001-06-06
V NUMBER: PCT/US01/18340
3: 2001-06-06
V NUMBER: US 60/209,257
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V NUMBER: US 09/875,363
3: 2001-06-05
V NUMBER: PCT/US01/18247
3: 2001-06-05
V NUMBER: US 60/227,068
3: 2000-08-22
V NUMBER: US 09/928,530
3: 2001-08-13
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3: 2001-08-15
V NUMBER: US 60/226,770
3: 2000-08-21
V NUMBER: US 09/934,421
3: 2001-08-21
V NUMBER: PCT/US01/26096
3: 2001-08-21
V NUMBER: US 60/279,281
3: 2001-03-28
V NUMBER: US 10/109,029
3: 2002-03-28
V NUMBER: PCT/US02/09728
3: 2002-03-28
V NUMBER: US 60/290,288
3: 2001-05-11
V NUMBER: US (not assigned)
3: 2002-05-13
NOS: 48
Q for Windows Version 4.0

sapiens

100.0%; Score 5599; DB 14; Length 1091;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Ga
QY 1 MAACCLALATLTLFQSLIGSSSEPPPSAVTIKSWVDKMQEDLVTAKTASGVNOL
DB 1 MAACCLALATLTLFQSLIGSSSEPPPSAVTIKSWVDKMQEDLVTAKTASGVNOL
QY 61 YEKQDLYTVPEPNNARQVLAARDIEKLLSNRSGKALVSLAEAKVQAAHQWREDF
DB 61 YEKQDLYTVPEPNNARQVLAARDIEKLLSNRSGKALVSLAEAKVQAAHQWREDF
QY 121 EVVYNAKODLDPEKNDSEPGSORIKPVFIEDANFGRQISYQHAHVHIPTDIYEGST
DB 121 EVVYNAKODLDPEKNDSEPGSORIKPVFIEDANFGRQISYQHAHVHIPTDIYEGST
QY 181 NELNMTSALDEVFKKREEDPSLLWQVFGSATGLARYYPASPVWVDSNRTPKNDILYD
DB 181 NELNMTSALDEVFKKREEDPSLLWQVFGSATGLARYYPASPVWVDSNRTPKNDILYD
QY 241 RPWTIOGAASPKDMLILVDVSGSVSGTLTKLIRTSVSEMLETLDSDDDFVNVASFNSN
DB 241 RPWTIOGAASPKDMLILVDVSGSVSGTLTKLIRTSVSEMLETLDSDDDFVNVASFNSN
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNTVNSRANCNKI
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNTVNSRANCNKI
QY 361 FTDGGERAQRIFNKYNKDKKVRFRFSVGHNYERGPIONMACENKGYEYIPISIG
DB 361 FTDGGERAQRIFNKYNKDKKVRFRFSVGHNYERGPIONMACENKGYEYIPISIG
QY 421 INTOEYLDVLGRPMVLADGKAKQVQWNTNVYLDLLEGLVITGTLPVFNITQGFENKT
DB 421 INTOEYLDVLGRPMVLADGKAKQVQWNTNVYLDLLEGLVITGTLPVFNITQGFENKT
QY 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLOPKPKSQEP
DB 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLOPKPKSQEP
QY 541 DFLDAELENDIKVEIRNMIDGESSEKTERFLVKSQDERYIDKGNRTYTWTVPVNGTD
DB 541 DFLDAELENDIKVEIRNMIDGESSEKTERFLVKSQDERYIDKGNRTYTWTVPVNGTD
QY 601 ALVLPTYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEESGYTFIAPRDYCN
DB 601 ALVLPTYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEESGYTFIAPRDYCN
QY 661 SDNTEFLINFEFIDRKTNNPCNADLINRVLLDAGFTNELVQNYWSKQNKIKGV
DB 661 SDNTEFLINFEFIDRKTNNPCNADLINRVLLDAGFTNELVQNYWSKQNKIKGV
QY 721 FVVTDDGGITRVYPKEAGENWOENPETYEDSYKXSLDNDNVFTAPYFNKSGPGAYE
DB 721 FVVTDDGGITRVYPKEAGENWOENPETYEDSYKXSLDNDNVFTAPYFNKSGPGAYE
QY 781 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWBNFTKTSIRDPACAGPVCCKRNSDVM
DB 781 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWBNFTKTSIRDPACAGPVCCKRNSDVM
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAA
DB 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAA
QY 901 GAGHRSAYVPSVADILQIGWATAAAWSILQOFLSLTFFPRLLAEVEMEDDDFTASL
DB 901 GAGHRSAYVPSVADILQIGWATAAAWSILQOFLSLTFFPRLLAEVEMEDDDFTASL
QY 961 SCITEQTOYFFDNDSKSPGVLDCGNCRSRIIPHGEKLMNTNLIIFIMVESKGTCPDTR
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QY 1021 QAEQTSQSGPNFCDMVKQPRYKRGPDVCFDNNVLEDTDCGGVS 1063

6:26:18 2004

us-10-090-827-15.rapb

SDGPNPCDMVKQPRYKRGPDVCFDNNVLEDTDCGGVS 1063

ication US/10090827

320030073132A1

DN:

r-Lambert

DN: Method for the screening of alpha 2 delta-1 subunit

DN: binding ligands

179 ION NUMBER: US/10/090,827

ATE: 2002-03-06

N NUMBER: US/09/397,549

E: 1999-09-16

NOS: 21

In Ver. 2.1

sapiens

100.0%; Score 5599; DB 14; Length 1091;

rity 100.0%; Pred. No. 0;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

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LLALTLFOSLLIGPSSEPPFSAVTKISWVDMQEDLVTLAKTASGVNQLVDI 60

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DLTVFENNAQOLVEIARIDIEKLLSNRKAIVSLALEAEKVOAAHQRDFASN 120

NAKDDLPEKNDSPFGSQRIKPVIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180

NAKDDLPEKNDSPFGSQRIKPVIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180

TSALDEVFKNREEDPSLLNQVFSATGLARYYPASPWVNSRTPNKIDLYDVR 240

TSALDEVFKNREEDPSLLNQVFSATGLARYYPASPWVNSRTPNKIDLYDVR 240

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QGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETLSDDDFVNVASFNSNAQ 300

HLVQANVRNKKVLKDAVNNITAKGITYKGFSPAFQOLLNINVSFRANCKIIML 360

HLVQANVRNKKVLKDAVNNITAKGITYKGFSPAFQOLLNINVSFRANCKIIML 360

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EERAQEIFNKYNDKKVVRFPFSGQNYERGPQIOMWACENKGYIIPSTIGAIR 420

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YLDVLRPMVLADGKAKQVQNTVYLDALGLVITGTLPVFNITGQFENKTNLK 480

GVMGVDVSLIEDIKLTPFTLCPNGYYPADPNQVYLLHPNLPKNPKSQBPVTL 540

GVMGVDVSLIEDIKLTPFTLCPNGYYPADPNQVYLLHPNLPKNPKSQBPVTL 540

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ELENDIKVEIKNMDGSGEKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600

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TYSFYIKAKLEETITQARSKKGMKQSEITLKPDPNFESGYTFIAPRDYCNLDKI 660

EFLNLFNEFIDRKTNNPSCNADLINRVLLDAGFTNQLVQVWSKQKNGVKAR 720

661 SDNTEFLNFEFIDRKTNNPSCNADLINRVLLDAGFTNQLVQVWSKQKNGV

721 FVVTDDGGITRVYKPEAGENWQENPETVEDSPYKRSNDNDNVFTAPYENKSGPGAYE

721 FVVTDDGGITRVYKPEAGENWQENPETVEDSPYKRSNDNDNVFTAPYENKSGPGAYE

781 MVSKAVEIYIQGKLLKPAVVGKIDVNSWIBNFTKTSIROPCAGVPVCDCKRNSDVM

781 MVSKAVEIYIQGKLLKPAVVGKIDVNSWIBNFTKTSIROPCAGVPVCDCKRNSDVM

841 LDDGGFLMANHDDYTNOIGRPFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPAA

841 LDDGGFLMANHDDYTNOIGRPFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPAA

901 GAGHRSAYVPSVADILQIGWWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASL

901 GAGHRSAYVPSVADILQIGWWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASL

961 SCITEQTOYFFDNDKSKFSFVLDGCGNSRIFHGEKLMNTNLIIFIMVESKGTCPDTR

961 SCITEQTOYFFDNDKSKFSFVLDGCGNSRIFHGEKLMNTNLIIFIMVESKGTCPDTR

1021 QAEQTSQDGNPCDMVKQPRYKRGPDVCFDNNVLEDTDCGGVS 1063

1021 QAEQTSQDGNPCDMVKQPRYKRGPDVCFDNNVLEDTDCGGVS 1063

RESULT 5

US-10-162-102-17

; Sequence 17, Application US/10162102

; Publication No. US2003023236A1

; GENERAL INFORMATION:

; APPLICANT: Curtis, Rory A.J.

; APPLICANT: Silos-Santiago, Inmaculada

; APPLICANT: Gu, Wei

; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY M

; FILE REFERENCE: 10448-190001

; CURRENT APPLICATION NUMBER: US/10/162,102

; CURRENT FILING DATE: 2003-04-04

; PRIOR APPLICATION NUMBER: US 60/209,845

; PRIOR FILING DATE: 2000-06-06

; PRIOR APPLICATION NUMBER: US 09/875,321

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: PCT/US01/18340

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: US 60/209,257

; PRIOR FILING DATE: 2000-06-05

; PRIOR APPLICATION NUMBER: US 09/875,423

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: PCT/US01/18398

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/209,238

; PRIOR FILING DATE: 2000-06-05

; PRIOR APPLICATION NUMBER: US 09/875,363

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: PCT/US01/18247

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/227,068

; PRIOR FILING DATE: 2000-08-22

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 1091

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-162-102-17

Query Match 100.0%; Score 5599; DB 15; Length 1091;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps

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LAALTTLFQSLILGPSSEPPPSAVTIKSWVDKMOEDLVTLAKTASGVNQLVDI 60
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; Publication No. US20040018510A1
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; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: SD9813DA
; CURRENT APPLICATION NUMBER: US/10375,253
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354
; PRIOR FILING DATE: 1995-02-15
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 08/314,083
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 07/603,751
; PRIOR FILING DATE: 1990-11-09
; PRIOR APPLICATION NUMBER: 08/290,012
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: 08/105,536
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; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 1086
; TYPE: PRT
; ORGANISM: Human
US-10-375-253-49

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DB 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFEQQLNNVNSRANCNKI
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DB 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVGOHNYERGPIONMACENKGYEYIIPSIG
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 JS20040018510A1
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 BALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
 ION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ION: METHODS
 SD9813DA
 ION NUMBER: US/10/375,253
 DATE: 2003-02-27
 ON NUMBER: 08/450,273
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 ON NUMBER: 07/914,231
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 ON NUMBER: 08/290,012
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 ON NUMBER: 08/149,097
 TE: 1993-11-05
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 TE: 1993-08-11

PRIOR APPLICATION NUMBER: 08/149,097
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 SEQ ID NO 53
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3	0	1086	15	US-10-375-253-49	Sequence 49, Appl
0	0	1084	15	US-10-375-253-53	Sequence 53, Appl
8	0	1063	14	US-10-090-827-8	Sequence 8, Appl
8	0	1069	14	US-10-090-827-9	Sequence 9, Appl
8	0	1091	14	US-10-090-827-5	Sequence 5, Appl
6	0	1103	15	US-10-375-253-47	Sequence 47, Appl
3	0	1079	15	US-10-375-253-51	Sequence 51, Appl
7	0	1091	15	US-10-375-253-20	Sequence 20, Appl
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19	3004.5	53.7	1145	14	US-10-116-949-4	Sequence 4
20	2983.5	53.3	1076	14	US-10-116-949-6	Sequence 6
21	1119.5	20.0	1091	9	US-09-875-423-5	Sequence 5
22	1119.5	20.0	1091	14	US-10-162-012-18	Sequence 18
23	1119.5	20.0	1091	15	US-10-162-012-18	Sequence 18
24	1114.5	19.9	1091	9	US-09-875-423-2	Sequence 2
25	1114.5	19.9	1091	14	US-10-162-012-15	Sequence 15
26	1114.5	19.9	1091	15	US-10-162-102-15	Sequence 15
27	1109	19.8	1114	12	US-10-257-174-35	Sequence 35
28	1097	19.6	1075	12	US-10-257-174-34	Sequence 34
29	1076	19.2	1090	10	US-09-833-222A-10	Sequence 10
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31	462.5	8.3	223	13	US-10-005-168-2	Sequence 2
32	360	6.4	1274	16	US-10-380-727-8	Sequence 8
33	350	6.3	1223	10	US-09-964-256A-2	Sequence 2
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35	286	5.1	75	15	US-10-264-049-3575	Sequence 35
36	272	4.9	51	9	US-09-864-761-44281	Sequence 44
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38	190	3.4	35	9	US-09-864-761-38318	Sequence 38
39	187	3.3	74	14	US-10-029-386-28507	Sequence 28
40	185	3.3	35	9	US-09-864-761-36461	Sequence 36
41	182	3.3	885	9	US-09-828-423-5	Sequence 5
42	180.5	3.2	497	15	US-10-334-143-23	Sequence 2
43	171.5	3.1	888	12	US-10-282-122A-57155	Sequence 5
44	167	3.0	796	15	US-10-369-493-18214	Sequence 1
45	161	2.9	1829	15	US-10-435-766-13	Sequence 1

ALIGNMENTS

RESULT 1
US-10-090-827-15
; Sequence 15, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 subu
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 1063
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-15

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Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1063;	Conservative	0;	Mismatches	0;
			Indels	0;
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6:26:18 2004

us-10-090-827-15.rapb

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cation US/09875423

0081657A1

ON:

S, Rory A.J.

ON: 21784, A NOVEL HUMAN CALCIUM CHANNEL

ON: FAMILY MEMBER AND USES THEREOF

10448-059001

TON NUMBER: US/09/875, 423

ATE: 2001-06-05

IN NUMBER: US 60/209,257

E: 2000-06-05

; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-423-4

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps

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ication US/10162102
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 N: RORY A.J.
 3: Santiago, Inmaculada
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N: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
 L0448-190001
 ION NUMBER: US/10/162,102
 ATE: 2003-04-04
 V NUMBER: US 60/209,845
 3: 2000-06-06
 V NUMBER: US 09/875,321
 3: 2001-06-06
 V NUMBER: PCT/US01/18340
 3: 2001-06-06
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100.0%; Score 5599; DB 12; Length 1091;
 city 100.0%; Pred. No. 0;
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RESULT 4

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 ; Sequence 17, Application US/10162012
 ; Publication No. US20030051660A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Rory A.J.
 ; APPLICANT: Silos-Santiago, Inmaculada
 ; APPLICANT: Gu, Wei
 ; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY M
 ; FILE REFERENCE: 10448-190001
 ; CURRENT APPLICATION NUMBER: US/10/162,012
 ; CURRENT FILING DATE: 2002-06-04
 ; PRIOR APPLICATION NUMBER: US 60/209,845
 ; PRIOR FILING DATE: 2000-06-06
 ; PRIOR APPLICATION NUMBER: US 09/875,321
 ; PRIOR FILING DATE: 2001-06-06

GenCore version 5.1.6
copyright (c) 1993 - 2004 Compugen Ltd.

n search, using sw model

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10-090-827-15

9
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SUM62

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ith: 0

rch: 2000000000

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than or equal to the score of the result being printed,
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SUMMARIES

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1.0	1091	9	US-09-875-423-4	Sequence 4, Appl
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1.0	1091	15	US-10-162-012-17	Sequence 17, Appl
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1.0	1084	12	US-10-375-253-53	Sequence 53, Appl
1.8	1063	15	US-10-090-827-8	Sequence 8, Appl
1.8	1069	15	US-10-090-827-9	Sequence 9, Appl
1.8	1091	15	US-10-090-827-5	Sequence 5, Appl
1.6	1103	12	US-10-375-253-47	Sequence 47, Appl
1.3	1079	12	US-10-375-253-51	Sequence 51, Appl
1.7	1091	12	US-10-375-253-20	Sequence 20, Appl
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29	462.5	8.3	1223	14	US-10-005-168-2	Sequence
30	350	6.3	1223	11	US-09-964-256A-2	Sequence
31	350	6.3	1223	12	US-10-146-733-44	Sequence
32	286	5.1	75	12	US-10-264-049-3575	Sequence
33	272	4.9	51	9	US-09-864-761-4281	Sequence
34	270	4.9	53	9	US-09-864-761-38267	Sequence 3
35	190	3.4	35	9	US-09-864-761-38318	Sequence 3
36	187	3.3	74	12	US-10-029-386-28507	Sequence
37	185	3.3	35	9	US-09-864-761-36461	Sequence 3
38	182	3.3	885	9	US-09-828-423-5	Sequence 5
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ALIGNMENTS

RESULT 1

US-10-090-827-15
; Sequence 15, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 sub
; FILE OF INVENTION: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1993-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 1063
; TYPE: PPT
; ORGANISM: Homo sapiens
US-10-090-827-15

Query Match	100.0%	Score 5599;	DB 15;	Length 1063;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1063;	Conservative	0;	Mismatches	0; Indels 0; G
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DB	1	MAAGCCLALTLTFLQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQI		
QY	61	YEKYQDLYTFVFNNAQVIEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRREDI		
DB	61	YEKYQDLYTFVFNNAQVIEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRREDI		
QY	121	EVVYVYNAKDDLPKNDSEPGSQRIKPVIEDANFGQISYQHAHVHIPTDIYEGS		
DB	121	EVVYVYNAKDDLPKNDSEPGSQRIKPVIEDANFGQISYQHAHVHIPTDIYEGS		
QY	181	NELNMTSALDEYFKKNREEDPSLLMQVFGSATGLARYYPASPMWNSRTPNKIDLYI		

1 NUMBER: PCT/US01/18340
 2: 2001-06-06
 1 NUMBER: US 60/209,257
 1: 2000-06-05
 1 NUMBER: US 09/875,423
 1: 2001-06-05
 1 NUMBER: PCT/US01/18398
 1: 2001-06-05
 1 NUMBER: US 60/209,238
 2: 2000-06-05
 1 NUMBER: US 09/875,363
 3: 2001-06-05
 1 NUMBER: PCT/US01/18247
 3: 2001-06-05
 1 NUMBER: US 60/227,068
 3: 2000-08-22
 1 NUMBER: US 09/928,530
 3: 2001-08-13
 1 NUMBER: PCT/US01/25475
 3: 2001-08-15
 1 NUMBER: US 60/226,770
 3: 2000-08-21
 1 NUMBER: US 09/934,421
 3: 2001-08-21
 1 NUMBER: PCT/US01/26096
 3: 2001-08-21
 1 NUMBER: US 60/279,281
 3: 2001-03-28
 1 NUMBER: US 10/109,029
 3: 2002-03-28
 1 NUMBER: PCT/US02/09728
 3: 2002-03-28
 1 NUMBER: US 60/290,288
 3: 2001-05-11
 1 NUMBER: US (not assigned)
 NOS: 48
 E: 2002-05-13
 Q for Windows Version 4.0

sapiens

rity 100.0%; Score 5599; DB 15; Length 1091;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 LLALTLTLFQSLIGPSSEPPPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
 LLALTLTLFQSLIGPSSEPPPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
 DLYTVEPNARQVLEIARDIEKLLSNRSKALVSLALEAEKVAQAAHQWREDPASN 120
 DLYTVEPNARQVLEIARDIEKLLSNRSKALVSLALEAEKVAQAAHQWREDPASN 120
 NAKDDLPEKNDSEPGSRIKPVFIEDANFGQISYQAAVHIPTDIYEGSTIVL 180
 NAKDDLPEKNDSEPGSRIKPVFIEDANFGQISYQAAVHIPTDIYEGSTIVL 180
 TSALDEVKQREDEPDLNQVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240
 TSALDEVKQREDEPDLNQVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240
 CGAASPCKDMLILVDVSGVSGITLKLIRTSVSEMLETLSDDDFVNVSFNSNAQD 300
 CGAASPCKDMLILVDVSGVSGITLKLIRTSVSEMLETLSDDDFVNVSFNSNAQD 300
 JHLVQANVNKKVLDXAVNNITAKGITYDKKGFSAFQELLNYSRANCKIIML 360
 JHLVQANVNKKVLDXAVNNITAKGITYDKKGFSAFQELLNYSRANCKIIML 360
 JEEERAQEIFNKYNKOKKVRFRFSVQGHNYERGPIQWMACENKGYIYEISIGAIR 420

Db 361 FTDCGEERAQEIFNKYNKOKKVRFRFSVQGHNYERGPIQWMACENKGYIYEISIG
 QY 421 INTOEYLDVLRPMVLAGDKAKOVQWNTNVYLDALGLVITGTLPVFNITQGFENKI
 Db 421 INTOEYLDVLRPMVLAGDKAKOVQWNTNVYLDALGLVITGTLPVFNITQGFENKI
 QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHPNLOPKPKSQEP
 Db 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHPNLOPKPKSQEP
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTERLVKSQDERYIDKGNRTYTTWTPVNGTD
 Db 541 DFLDAELENDIKVEIRNKMIDGESGEKTERLVKSQDERYIDKGNRTYTTWTPVNGTD
 QY 601 ALVLPTYSFYIYKAKLEETITQARSKKGKMKDSETLKPDNFEESGYTFIAPRDYCN
 Db 601 ALVLPTYSFYIYKAKLEETITQARSKKGKMKDSETLKPDNFEESGYTFIAPRDYCN
 QY 661 SDNNTFEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELYQNYWSKQKNIKGV
 Db 661 SDNNTFEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELYQNYWSKQKNIKGV
 QY 721 FVVTDDGGITRVYPKEAGENWOENPETVEDSFYKSLDNDNVFTAPYFNKSGPGAYE
 Db 721 FVVTDDGGITRVYPKEAGENWOENPETVEDSFYKSLDNDNVFTAPYFNKSGPGAYE
 QY 781 MVSKAVEIYIQGLLKPAVVGIKIDVNSWIEFNFTKTSIRDPGAGVPCDCKNSDVM
 Db 781 MVSKAVEIYIQGLLKPAVVGIKIDVNSWIEFNFTKTSIRDPGAGVPCDCKNSDVM
 QY 841 LDDGGFLLMANHDDYTNOIGRPFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAA
 Db 841 LDDGGFLLMANHDDYTNOIGRPFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAA
 QY 901 GAGHRSAYVPSVADILQIGWATAAANSILOQFLISLTFPRLLHAVERNEDDDFTASL
 Db 901 GAGHRSAYVPSVADILQIGWATAAANSILOQFLISLTFPRLLHAVERNEDDDFTASL
 QY 961 SCITTEQTYFFDNDKSKSPGVLDCGNCRSRI FHGEKLMNTNLIPIFVSKSGTCPCDTR
 Db 961 SCITTEQTYFFDNDKSKSPGVLDCGNCRSRI FHGEKLMNTNLIPIFVSKSGTCPCDTR
 QY 1021 QAEQTSDEPNCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063
 Db 1021 QAEQTSDEPNCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063

RESULT 5

US-10-090-827-16
 ; Sequence 16, Application US/10090827
 ; Publication NO. US20030073132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert
 ; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 subu
 ; TITLE OF INVENTION: binding ligands
 ; FILE REFERENCE: 179
 ; CURRENT APPLICATION NUMBER: US/10/090,827
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US/09/397,549
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 16
 ; LENGTH: 1091
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-090-827-16

Query Match 100.0%; Score 5599; DB 15; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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LAALTLTLFQSLILIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGVGNQVLVDI 60
LAALTLTLFQSLILIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGVGNQVLVDI 60
OLYTVENNAROLVETIARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEDFASN 120
OLYTVENNAROLVETIARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEDFASN 120
VAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180
VAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180
TSALDVFVKKREDEPSLLMQVFGSATGLARYYPASPVNDNSRTPNKIDLYDVR 240
TSALDVFVKKREDEPSLLMQVFGSATGLARYYPASPVNDNSRTPNKIDLYDVR 240
XGAASPKDMLILVDVSGSVSLGLTKLIRTSVSEMLETLSDDDFVNVSFNSNAQD 300
XGAASPKDMLILVDVSGSVSLGLTKLIRTSVSEMLETLSDDDFVNVSFNSNAQD 300
ILVQANVRNKKVLKDAVNNITAKGIDTYKKGFSAFEQQLLNYSRANCNKIIML 360
ILVQANVRNKKVLKDAVNNITAKGIDTYKKGFSAFEQQLLNYSRANCNKIIML 360
ZERAQEIFNKYNKDKKVRFRFVSGQHNVERGPIQWMAKCNKGYIYEIPSIGAIR 420
ZERAQEIFNKYNKDKKVRFRFVSGQHNVERGPIQWMAKCNKGYIYEIPSIGAIR 420
LDVLGRPMVLADGKAKQVQWTVNYLDALGLVITGTLPVFNITGQFENKTNLK 480
LDVLGRPMVLADGKAKQVQWTVNYLDALGLVITGTLPVFNITGQFENKTNLK 480
YVNGDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLPKPKSQEPVTL 540
YVNGDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLPKPKSQEPVTL 540
ZLENDIKVEIRNKMIDGESSEKTRFLVKSQDERYDKGNRTYTWTVPNGTDYSL 600
ZLENDIKVEIRNKMIDGESSEKTRFLVKSQDERYDKGNRTYTWTVPNGTDYSL 600
TYSFYIKAKLETTITQARSKKGMKDSSETLKPDPNFEESGYTFIAPRDYCNLDKI 660
TYSFYIKAKLETTITQARSKKGMKDSSETLKPDPNFEESGYTFIAPRDYCNLDKI 660
FLILNFEFIDRKTNNPSCNADLINRVLLDAGFTNELVQNYWSKQNKIKGVKAR 720
FLILNFEFIDRKTNNPSCNADLINRVLLDAGFTNELVQNYWSKQNKIKGVKAR 720
XGTRVYPKEAGENWQENPETYEDSFYKRSLDNDNTVFTAPYPNKSGPGAYESGI 780
XGTRVYPKEAGENWQENPETYEDSFYKRSLDNDNTVFTAPYPNKSGPGAYESGI 780
TEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAPVCDCKENSVDMDCVI 840
TEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAPVCDCKENSVDMDCVI 840
TLLMANHDDYTQIGRAFFGEIDPSLMRHLVNIISVYAFNKSQYDYQSCVCEGAPKQ 900
TLLMANHDDYTQIGRAFFGEIDPSLMRHLVNIISVYAFNKSQYDYQSCVCEGAPKQ 900
IAYVPSVADILQIGWATAAAMSILQOFLLSLTFPRLLBAVEMEDDDFTASLSKQ 960
IAYVPSVADILQIGWATAAAMSILQOFLLSLTFPRLLBAVEMEDDDFTASLSKQ 960
JTCYFFDNDKSPSGVLDCCNCSRI FHGEKLMNTNLI FIMVESKGTCPDCTRLII 1020
JTCYFFDNDKSPSGVLDCCNCSRI FHGEKLMNTNLI FIMVESKGTCPDCTRLII 1020
JGPNPCDMVKQPRYKRGPDVCFDNNVLEDYTDCCGVGS 1063
JGPNPCDMVKQPRYKRGPDVCFDNNVLEDYTDCCGVGS 1063
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RESULT 6
US-10-375-253-49
; Sequence 49, Application US/10375253
; Publication No. US20040018510A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: SD9813DA
; CURRENT APPLICATION NUMBER: US/10375,253
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354
; PRIOR FILING DATE: 1995-02-15
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 08/314,083
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 07/603,751
; PRIOR FILING DATE: 1990-11-09
; PRIOR APPLICATION NUMBER: 08/290,012
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: 08/105,536
; PRIOR FILING DATE: 1993-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 1086
; TYPE: PRT
; ORGANISM: Human
US-10-375-253-49
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Query Match 99.3%; Score 5559.5; DB 12; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1058; Conservative 0; Mismatches 0; Indels 5; Gaps 0

Qy 1 MAACCLALTLTLFQSLILIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGVGNQVL
Db 1 MAACCLALTLTLFQSLILIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGVGNQVL

Qy 61 YEKYQDLYTVENNAROLVETIARDIEKLLSNRSKALVSLALEAEKVQAAHQRDE
Db 61 YEKYQDLYTVENNAROLVETIARDIEKLLSNRSKALVSLALEAEKVQAAHQRDE

Qy 121 EVVYNNAKDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHPTDIYEGST
Db 121 EVVYNNAKDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHPTDIYEGST

Qy 181 NELNWTSALEDEVFKKREDEPSLLMQVFGSATGLARYYPASPVNDNSRTPNKIDLYD
Db 181 NELNWTSALEDEVFKKREDEPSLLMQVFGSATGLARYYPASPVNDNSRTPNKIDLYD

Qy 241 RPYIOGAASPDKMLILVDVSGSVSLGLTKLIRTSVSEMLETLSDDDFVNVSFNSN
Db 241 RPYIOGAASPDKMLILVDVSGSVSLGLTKLIRTSVSEMLETLSDDDFVNVSFNSN

Qy 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSAFEQQLLNYSRANCNKI
Db 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSAFEQQLLNYSRANCNKI

Qy 361 FTDGGERAQBIEFNKYNKDKKVRFRFVSGQHNVERGPIQWMAKCNKGYIYEIPSIG
Db 361 FTDGGERAQBIEFNKYNKDKKVRFRFVSGQHNVERGPIQWMAKCNKGYIYEIPSIG

Qy 421 INTOBYLDVLGRPMVLADGKAKQVQWTVNYLDALGLVITGTLPVFNITGQFENKTI
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|||||
YLDVLRPMVLADGAKQVQWTVNYLDALGLVITGTLPVFNITGQFNKTNLK 480
GVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPNPKSQEPVTL 540
GVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPNK-----EPVTL 535
ELENDIKVEIRNKMIDGESGKTRFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
ELENDIKVEIRNKMIDGESGKTRFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 595
TYSFYIKAKLEETITQARSKGKMKOSETLKPONFESGYTFIAPRDYCNLDKI 660
TYSFYIKAKLEETITQARSKGKMKOSETLKPONFESGYTFIAPRDYCNLDKI 655
EFLNPNFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
EFLNPNFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 715
GGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 780
GGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 775
VEIYIQGLLKPAAVGIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840
VEIYIQGLLKPAAVGIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVMDCVI 835
FLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAFNKSVDYOSVCEPGAPKQ 900
FLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAFNKSVDYOSVCEPGAPKQ 895
SAYVPSVADIIQIGWATAAAWSIIQQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960
SAYVPSVADIIQIGWATAAAWSIIQQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 955
QTQYFFDNDSKFSGLVDCGNCRI FHGEKLMNTNLI FIMVESKGTCTCDTRLII 1020
QTQYFFDNDSKFSGLVDCGNCRI FHGEKLMNTNLI FIMVESKGTCTCDTRLII 1015
SDGNPNCDMVQKPRYRKGPVDFCDNNVLEDYTDGCGVS 1063
SDGNPNCDMVQKPRYRKGPVDFCDNNVLEDYTDGCGVS 1058

```

ication US/10375253

IS20040018510A1

ON:

ALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES

ON: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

ON: METHODS

SD9813DA

TON NUMBER: US/10/375, 253

ATE: 2003-02-27

N NUMBER: 08/450, 273

E: 1995-05-25

N NUMBER: 08/404, 354

E: 1995-02-15

N NUMBER: 07/914, 231

E: 1992-07-13

N NUMBER: 08/314, 083

E: 1994-09-28

N NUMBER: 07/914, 231

E: 1992-07-13

N NUMBER: 07/603, 751

E: 1990-11-09

N NUMBER: 08/290, 012

E: 1994-08-11

N NUMBER: 08/149, 097

E: 1993-11-05

N NUMBER: 08/105, 536

E: 1993-08-11

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; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 1084
; TYPE: PRT
; ORGANISM: Human
US-10-375-253-53

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Query Match      99.0%; Score 5542.5; DB 12; Length 1084;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1055; Conservative 0; Mismatches 1; Indels 7; Gc

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QY 1 MAAGCLLALTLTLFOSLALIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTAGSVNQL
DB 1 MAAGCLLALTLTLFOSLALIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTAGSVNQL
QY 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKQVAAHQWREDE
DB 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKQVAAHQWREDE
QY 121 EYVYNAKDDLDPEKNDSEPPSQRIKPVFIEDANFGRQISYOHAAVHIPTDIYEGST
DB 121 EYVYNAKDDLDPEKNDSEPPSQRIKPVFIEDANFGRQISYOHAAVHIPTDIYEGST
QY 181 NELNWTSDALDEVFKNRREDPSLLMQVSGSATGLARYYPASPWVNSRTPNKIDLYI
DB 181 NELNWTSDALDEVFKNRREDPSLLMQVSGSATGLARYYPASPWVNSRTPNKIDLYI
QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRITSVSEMLETSLDDDFVNVASFNSN
DB 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRITSVSEMLETSLDDDFVNVASFNSN
QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAGITDYKKGFSFAPFOLLNRYNSRANCNKI
DB 301 VSCFOHLVQANVRNKKVLKDAVNNITAGITDYKKGFSFAPFOLLNRYNSRANCNKI
QY 361 FTDGGEERAQELFNKYNKKVVRFRFSVGOHNYERGPIONMACENKGYIYIPISTIC
DB 361 FTDGGEERAQELFNKYNKKVVRFRFSVGOHNYERGPIONMACENKGYIYIPISTIC
QY 421 INTQBYLDVLGRPMVLADGAKQVQWTVNYLDALGLVITGTLPVFNITGQFNENKI
DB 421 INTQBYLDVLGRPMVLADGAKQVQWTVNYLDALGLVITGTLPVFNITGQFNENKI
QY 481 NQLILGVMGVDVLSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPNPKSQEI
DB 481 NQLILGVMGVDVLSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPNPKSQEI
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTRFTLVKSQDERYIDKGNRTYTWTPVNGTI
DB 541 DFLDAELENDIKVEIRNKMIDGESGKTRFTLVKSQDERYIDKGNRTYTWTPVNGTI
QY 601 ALVLPYTSFYIYIKAKLEETITQARY-----SETLKPONFESGYTFIAPRDYCNM
DB 601 ALVLPYTSFYIYIKAKLEETITQARY-----SETLKPONFESGYTFIAPRDYCNM
QY 661 SDNNTFEFLNPNFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGV
DB 661 SDNNTFEFLNPNFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGV
QY 721 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYE
DB 721 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYE
QY 781 MYSKAVEIYIQGLLKPAAVGIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVMC
DB 781 MYSKAVEIYIQGLLKPAAVGIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVMC
QY 841 LDDGGFLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAFNKSVDYOSVCEPGAP
DB 841 LDDGGFLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAFNKSVDYOSVCEPGAP

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FLMANHDDYTNQIGRFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 893
SAVPSVADILQIGWATAAAWSILQOFLSLTFPRLLLEAVEMEDDDFTASLSQ 960
SAVPSVADILQIGWATAAAWSILQOFLSLTFPRLLLEAVEMEDDDFTASLSQ 953
SAVPSVADILQIGWATAAAWSILQOFLSLTFPRLLLEAVEMEDDDFTASLSQ 953
2QYFFDNDKSGSVGLDCGNCNRI FHEKLMNTNLI FIMVSKGTGTCPCDTRLLI 1020
2QYFFDNDKSGSVGLDCGNCNRI FHEKLMNTNLI FIMVSKGTGTCPCDTRLLI 1013
3DGNPCDMVKQPRYKGPVCFDNNVLEDDYTDGCGVS 1063
3DGNPCDMVKQPRYKGPVCFDNNVLEDDYTDGCGVS 1056

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cation US/10090827
320030073132A1

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DN:

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c-Lambert

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DN: Method for the screening of alpha 2 delta-1 subunit

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```

DN: binding ligands

```

```

179

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```

ION NUMBER: US/10/090,827

```

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ATE: 2002-03-06

```

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NUMBER: US/09/397,549

```

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3: 1999-09-16

```

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NOS: 21

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In Ver. 2.1

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:rofa

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ity 98.8%; Score 5532; DB 15; Length 1063;

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iservative 6; Mismatches 8; Indels 0; Gaps 0;

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ALALTTLFQSLIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
ALALTTLFQSLIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
LYTVBPNNARQLVEAARDIEKLLNSRKALVSLALEAEKVAQAHHQWEDFASN 120
LYTVBPNNARQLVEAARDIEKLLNSRKALVSLALEAEKVAQAHHQWEDFASN 120
IAKDDLDPEKNDSEPGSRIKPVFIEDANFGROI SYQHAHVHPTDIYEGSTIVL 180
IAKDDLDPEKNDSEPGSRIKPVFIEDANFGROI SYQHAHVHPTDIYEGSTIVL 180
SALDVPKKNREEDPSLLWQVFGSATGLARYYPASPVWDSNRTPNKIDLYDVR 240
SALDVPKKNREEDPSLLWQVFGSATGLARYYPASPVWDSNRTPNKIDLYDVR 240
XGAASPKDMLILVDVSGVSLTKLIRTSVSEMLETLSDDDFVNVSFNSNAQD 300
XGAASPKDMLILVDVSGVSLTKLIRTSVSEMLETLSDDDFVNVSFNSNAQD 300
ILVQANVRNKKVLKDAVNNITAKITDYKKGFSFAPEQLLNYSRANCKIIML 360
ILVQANVRNKKVLKDAVNNITAKITDYKKGFSFAPEQLLNYSRANCKIIML 360
EIRAQIFNKYNKDKKVRFRSVGOHNYERGPIONMACENKGYIYSIGAIR 420
EIRAQIFNKYNKDKKVRFRSVGOHNYERGPIONMACENKGYIYSIGAIR 420
LDVLGRPMVLADGKAKQVQWNTNVLDALEGLVITGTLPVFNITGQFNKNLX 480
LDVLGRPMVLADGKAKQVQWNTNVLDALEGLVITGTLPVFNITGQFNKNLX 480
WGVNDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPLQPKNPKSQEPVTL 540

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481 NQLILGWGVDSLEDEIKLTPRFTLCPNGYFFAIDPNGYVLLHPLQPKNPKSQE
541 DFLDAELNDIKVEIRNMIDGESGEKTRTLVKSQDERYIDKGNRTYTTWTPVNGTI
541 DFLDAELNDIKVEIRNMIDGESGEKTRTLVKSQDERYIDKGNRTYTTWTPVNGTI
601 ALVLPTYSFYIKAKLEETITQARKSKGKMDSETLKPDNFEESGYTFAIPDYCNC
601 ALVLPTYSFYIKAKLEETITQARKSKGKMDSETLKPDNFEESGYTFAIPDYCNC
661 SDNNTFLLNFNEFIDRKTPNPNPCNTDLINRVLLDAGFTNVLQVYWSKQKNIKGV
661 SDNNTFLLNFNEFIDRKTPNPNPCNTDLINRVLLDAGFTNVLQVYWSKQKNIKGV
721 FVVTGGITRYVPKEAGENWOENPETTEDSYKRSNDNDNTVFTAPYFNKSGPGAYE
721 FVVTGGITRYVPKEAGENWOENPETTEDSYKRSNDNDNTVFTAPYFNKSGPGAYE
781 MVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACGVCDCCKNSDVM
781 MVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACGVCDCCKNSDVM
841 LDDGGFLLMANHDDYTNQIGRFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGA
841 LDDGGFLLMANHDDYTNQIGRFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGA
901 GAGHSAYVPSVADILQIGWATAAAWSILQOFLSLTFPRLLLEAVEMEDDDFTASL
901 GAGHSAYVPSVADILQIGWATAAAWSILQOFLSLTFPRLLLEAVEMEDDDFTASL
961 SCITEQTYQYFFDNDKSGSVGLDCGNCNRI FHEKLMNTNLI FIMVSKGTGTCPTR
961 SCITEQTYQYFFDNDKSGSVGLDCGNCNRI FHEKLMNTNLI FIMVSKGTGTCPTR
1021 QAEQTSQDPNPNCDMVKQPRYKGPVCFDNNVLEDDYTDGCGVS 1063
1021 QAEQTSQDPNPNCDMVKQPRYKGPVCFDNNVLEDDYTDGCGVS 1063

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RESULT 9

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US-10-090-827-9

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; Sequence 9, Application US/10090827

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; Publication No. US20030073132A1

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; GENERAL INFORMATION:

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; APPLICANT: Warner-Lambert

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; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 subu

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; FILE REFERENCE: 179

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; CURRENT APPLICATION NUMBER: US/10/090,827

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```

; CURRENT FILING DATE: 2002-03-06

```

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; PRIOR APPLICATION NUMBER: US/09/397,549

```

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; PRIOR FILING DATE: 1999-09-16

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```

; NUMBER OF SEQ ID NOS: 21

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; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 9

```

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; LENGTH: 1069

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; TYPE: PRT

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```

; ORGANISM: Sus scrofa

```

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US-10-090-827-9

```

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Query Match 98.8%; Score 5532; DB 15; Length 1069;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gai

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Qy 1 MAAGCLALTLTLFQSLIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQL
Db 1 MAAGCLALTLTLFQSLIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQL
Qy 61 YEKYQDLYTTPENNARQLVEAARDIEKLLNSRKALVSLALEAEKVAQAHHQWEDF
Db 61 YEKYQDLYTTPENNARQLVEAARDIEKLLNSRKALVSLALEAEKVAQAHHQWEDF

```

```

NAKDDLPKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEGSTIVL 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
NAKDDLPKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEGSTIVL 180
TSALDEVFKKREEDPSLLQWFGSGLTGLARYYPASPWVNSRTPNKIDLYDVR 240
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
TSALDEVFKKREEDPSLLQWFGSGLTGLARYYPASPWVNSRTPNKIDLYDVR 240
QGAASPKDMLILVDVSGVSGLTGLKRTSVSEMLETLSDDDFVNVAFSNAQD 300
QGAASPKDMLILVDVSGVSGLTGLKRTSVSEMLETLSDDDFVNVAFSNAQD 300
HLVQANVRNKKVLDVANNITAKGIDYKKGFSFAFEOLLNYSRANCNKIIML 360
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
HLVQANVRNKKVLDVANNITAKGIDYKKGFSFAFEOLLNYSRANCNKIIML 360
EERAEQEIFKNYKDKKVRVFRFSGVQHNYRGPQIOMACENKGYIYIPEISGAIR 420
EERAEQEIFAKYKDKKVRVFRFSGVQHNYRGPQIOMACENKGYIYIPEISGAIR 420
YLDVLGRPMVLADYKAKOVQWNTVYLDALGLVITGLTPVFNITGQENKTNLK 480
YLDVLGRPMVLADYKAKOVQWNTVYLDALGLVITGLTPVFNITGQENKTNLK 480
GVMGVDSLEDIKRLTPRFTLCPNGYYPALDPNGYVLLHPLNLOPKNPKSQBPVTL 540
GVMGVDSLEDIKRLTPRFTLCPNGYYPALDPNGYVLLHPLNLOPKNPKSQBPVTL 540
AELENDIKVEIRNKMIDGSGEKTFTLVKSGQDERYIDKGNRTYTWTPVNGTDYSL 600
AELENDIKVEIRNKMIDGSGEKTFTLVKSGQDERYIDKGNRTYTWTPVNGTDYSL 600
PYSFYIYKAKLETTQARSKKGMKDSKSETLKPDPNFESEGYTFIAPRYCNDLKI 660
PYSFYIYKAKLETTQARSKKGMKDSKSETLKPDPNFESEGYTFIAPRYCNDLKI 660
TEFLNPFNEIDRKTNNPNSCNADLINRVLLDAGFTNQLVQWSKQKNIKGVKAR 720
TEFLNPFNEIDRKTNNPNSCNADLINRVLLDAGFTNQLVQWSKQKNIKGVKAR 720
XGGITRYPKXAGENQWENPETYEDSGYKRSNDNDNYVFTAPYFNKSGPGAYESGI 780
XGGITRYPKXAGENQWENPETYEDSGYKRSNDNDNYVFTAPYFNKSGPGAYESGI 780
AVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840
AVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840
3FLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPGAAPKQ 900
3FLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPGAAPKQ 900
RSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
RSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
EOTQYFFDNDKSKSGVLDCCNCSRI FHGEKLMNTNLI FIVWESKGTCPDTRLLI 1020
EOTQYFFDNDKSKSGVLDCCNCSRI FHGEKLMNTNLI FIVWESKGTCPDTRLLI 1020
TSDGPNPCDMVKQPRYKGPVCFDNNVLEDYTDCCGVS 1063
TSDGPNPCDMVKQPRYKGPVCFDNNVLEDYTDCCGVS 1063

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ication US/10090827

US20030073132A1

ION:

er-Lambert

ION: Method for the screening of alpha 2 delta-1 subunit

ION: binding ligands

```

; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Sus scrofa
; US-10-090-827-5

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Query Match      98.8%; Score 5532; DB 15; Length 1091;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gc

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QY 1 MAAGCLLALTTLTFLQSLILIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGSVNQI
DB 1 MAAGCLLALTTLTFLQSLILIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGSVNQI
QY 61 YEKYQDLYTVVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHWRREDI
DB 61 YEKYQDLYTVVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHWRREDI
QY 121 EYVYNAKDDLPKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEGS'
DB 121 EYVYNAKDDLPKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEGS'
QY 181 NELNWTSALEDEVFKKREEDPSLLQWFGSGLTGLARYYPASPWVNSRTPNKIDLYI
DB 181 NELNWTSALEDEVFKKREEDPSLLQWFGSGLTGLARYYPASPWVNSRTPNKIDLYI
QY 241 RPYWIOGAASPKDMLILVDVSGVSGLTGLKRTSVSEMLETLSDDDFVNVAFSNSI
DB 241 RPYWIOGAASPKDMLILVDVSGVSGLTGLKRTSVSEMLETLSDDDFVNVAFSNSI
QY 301 VSCFOHLVQANVRNKKVLDVANNITAKGIDYKKGFSFAFEOLLNYSRANCNK
DB 301 VSCFOHLVQANVRNKKVLDVANNITAKGIDYKKGFSFAFEOLLNYSRANCNK
QY 361 FTDGGERAEQEIFAKYKDKKVRVFRFSGVQHNYRGPQIOMACENKGYIYIPEISPI
DB 361 FTDGGERAEQEIFAKYKDKKVRVFRFSGVQHNYRGPQIOMACENKGYIYIPEISPI
QY 421 INTQEYLDVLGRPMVLADYKAKOVQWNTVYLDALGLVITGLTPVFNITGQENK
DB 421 INTQEYLDVLGRPMVLADYKAKOVQWNTVYLDALGLVITGLTPVFNITGQENK
QY 481 NQILIGVMGVDSLEDIKRLTPRFTLCPNGYYPALDPNGYVLLHPLNLOPKNPKSQE
DB 481 NQILIGVMGVDSLEDIKRLTPRFTLCPNGYYPALDPNGYVLLHPLNLOPKNPKSQE
QY 541 DFLDAELENDIKVEIRNKMIDGSGEKTFTLVKSGQDERYIDKGNRTYTWTPVNGT
DB 541 DFLDAELENDIKVEIRNKMIDGSGEKTFTLVKSGQDERYIDKGNRTYTWTPVNGT
QY 601 ALVLPYSFYIYKAKLETTQARSKKGMKDSKSETLKPDPNFESEGYTFIAPRYCYN
DB 601 ALVLPYSFYIYKAKLETTQARSKKGMKDSKSETLKPDPNFESEGYTFIAPRYCYN
QY 661 SDNNTTEFLNPFNEIDRKTNNPNSCNADLINRVLLDAGFTNQLVQWSKQKNIK
DB 661 SDNNTTEFLNPFNEIDRKTNNPNSCNADLINRVLLDAGFTNQLVQWSKQKNIK
QY 721 FVVTDDGGITRYPKXAGENQWENPETYEDSGYKRSNDNDNYVFTAPYFNKSGPGAY
DB 721 FVVTDDGGITRYPKXAGENQWENPETYEDSGYKRSNDNDNYVFTAPYFNKSGPGAY
QY 781 MYSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVM
DB 781 MYSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVM

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FLMANHDDVTNOIGRFFGIDPSLMRHLVNIISVYAFNKSYDYQSVCEPGAAPKQ 900
 FLMANHDDVTNOIGRFFGIDPSLMRHLVNIISVYAFNKSYDYQSVCEPGAAPKQ 900
 SAYVPSVADILQIGWMTAAAWSTLQOFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960
 SAYVPSVADILQIGWMTAAAWSTLQOFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960
 QTOYFFNDKSGFSGVLDGNCBSIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020
 QTOYFFNDKSGFSGVLDGNCBSIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020
 SDGNPCDMVKQPRYKRGPDVCFDNNVLEDTYDCGGVS 1063
 SDGNPCDMVKQPRYKRGPDVCFDNNVLEDTYDCGGVS 1063

ication US/10375253
 S20040018510A1

ON: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ON: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

SD9813DA
 ION NUMBER: US/10/375,253

ATE: 2003-02-27

N NUMBER: 08/450,273

E: 1995-05-25

N NUMBER: 08/404,354

E: 1995-02-15

N NUMBER: 07/914,231

E: 1992-07-13

N NUMBER: 08/314,083

E: 1994-09-28

N NUMBER: 07/914,231

E: 1992-07-13

N NUMBER: 07/603,751

E: 1990-11-09

N NUMBER: 08/290,012

E: 1994-08-11

N NUMBER: 08/149,097

E: 1993-11-05

N NUMBER: 08/105,536

E: 1993-08-11

N NUMBER: 08/149,097

E: 1993-11-05

Application data removed - See File Wrapper or PALM.

NOS: 65

Q for Windows Version 4.0

98.6%; Score 5523; DB 12; Length 1103;
 97.5%; Pred. No. 0;
 0; Mismatches 1; Indels 26; Gaps 2;

LLALTLTLFQSLIGPSEPPPSAVTIKSWYDKMQEDLVTIAKTASGVNQLVDI 60

LLALTLTLFQSLIGPSEPPPSAVTIKSWYDKMQEDLVTIAKTASGVNQLVDI 60

DLTYTEPNNAQOLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120

DLTYTEPNNAQOLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120

ANAKDLDPKNDSEPGSQRIKPVFIEDANFGQISVQHAHVHIPTDIYEGSTIVL 180

ANAKDLDPKNDSEPGSQRIKPVFIEDANFGQISVQHAHVHIPTDIYEGSTIVL 180

ANAKDLDPKNDSEPGSQRIKPVFIEDANFGQISVQHAHVHIPTDIYEGSTIVL 180

ANAKDLDPKNDSEPGSQRIKPVFIEDANFGQISVQHAHVHIPTDIYEGSTIVL 180

ANAKDLDPKNDSEPGSQRIKPVFIEDANFGQISVQHAHVHIPTDIYEGSTIVL 180

ANAKDLDPKNDSEPGSQRIKPVFIEDANFGQISVQHAHVHIPTDIYEGSTIVL 180

ANAKDLDPKNDSEPGSQRIKPVFIEDANFGQISVQHAHVHIPTDIYEGSTIVL 180

181 NELNWTSLDVEFKKREEDPSLLMQVFGSATGLARYYPASPWVDSNRPKNKIDLYI
 181 NELNWTSLDVEFKKREEDPSLLMQVFGSATGLARYYPASPWVDSNRPKNKIDLYI
 241 RPWYTOGAASPKDMLILVDVSGSVSGLTLKLRTSVSEMLETSLDDDFVNVASFNS
 241 RPWYTOGAASPKDMLILVDVSGSVSGLTLKLRTSVSEMLETSLDDDFVNVASFNS
 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGIDYKKGFGFAFQQLLNYNVSRANCKI
 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGIDYKKGFGFAFQQLLNYNVSRANCKI
 361 FTDGGEERAQEIFNKYKNDKKVRVFRFVSGQNYRGPIONMACENKGYIYIPSI
 361 FTDGGEERAQEIFNKYKNDKKVRVFRFVSGQNYRGPIONMACENKGYIYIPSI
 421 INTQBYLDVLGRPMVLADGKAKOVMTNVLDALELGLVITGLPVFNITGQFENKI
 421 INTQBYLDVLGRPMVLADGKAKOVMTNVLDALELGLVITGLPVFNITGQFENKI
 481 NOLILGVMGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHPLNLPK-
 481 NOLILGVMGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHPLNLPK-
 531 -----NPKSQBPVTLDLDALENDIKVEIRNKMIDGESGKTFRTLKVSQDI
 541 LKRRPNIQNPKSQBPVTLDLDALENDIKVEIRNKMIDGESGKTFRTLKVSQDI
 582 DKGNRTYTWTPVNGTDYSLALVLPYFVYIKAKLEETITQARSKKGKMKDSETLKI
 601 DKGNRTYTWTPVNGTDYSLALVLPYFVYIKAKLEETITQARSKKGKMKDSETLKI
 642 BESGYTFIAPRDYCNLDKISDNNTEFLNFEFIDRKTNNPNSCNADLNRLVLLDA
 654 BESGYTFIAPRDYCNLDKISDNNTEFLNFEFIDRKTNNPNSCNADLNRLVLLDA
 702 ELVQNTWSKQKNIKGVKARFVVTDDGITRVYKPEAGENQENPETYEDSFYKRSLDI
 714 ELVQNTWSKQKNIKGVKARFVVTDDGITRVYKPEAGENQENPETYEDSFYKRSLDI
 762 VBTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTS
 774 VBTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTS
 822 CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGCEIDPSLMRHLVNI
 834 CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGCEIDPSLMRHLVNI
 882 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWMTAAAWSTLQOFLLSL
 894 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWMTAAAWSTLQOFLLSL
 942 LLEAVEMEDDDFTASLSKOSCTEOTQYFDFDNDKSGFSGVLDGNCBSIFHGEKLM
 954 LLEAVEMEDDDFTASLSKOSCTEOTQYFDFDNDKSGFSGVLDGNCBSIFHGEKLM
 1002 IFIMVESKGTCPDTRLLIQAESQTSQDPNCPDMVKQPRYKRGPDVCFDNNVLEDTYI
 1014 IFIMVESKGTCPDTRLLIQAESQTSQDPNCPDMVKQPRYKRGPDVCFDNNVLEDTYI
 1062 VS 1063
 1074 VS 1075

RESULT 12

US-10-375-253-51

; Sequence 51, Application US/10375253

; Publication No. US20040018510A1

; GENERAL INFORMATION:

; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; METHODS

SD9813DA
ION NUMBER: US/10/375,253
DATE: 2003-02-27

IN NUMBER: 08/450,273
E: 1995-05-25

IN NUMBER: 08/404,354
E: 1995-02-15

IN NUMBER: 07/914,231
E: 1992-07-13

IN NUMBER: 08/314,083
E: 1994-09-28

IN NUMBER: 07/914,231
E: 1992-07-13

IN NUMBER: 07/603,751
E: 1990-11-09

IN NUMBER: 08/290,012
E: 1994-08-11

IN NUMBER: 08/149,097
E: 1993-11-05

IN NUMBER: 08/105,536
E: 1993-08-11

IN NUMBER: 08/149,097
E: 1993-11-05

Application data removed - See File Wrapper or PALM.
NOS: 65

EQ for Windows Version 4.0

98.3%; Score 5503; DB 12; Length 1079;

arity 98.8%; Pred. No. 0;

onservative 0; Mismatches 1; Indels 12; Gaps 2;

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CLALATLTLFQSLIGSSSEPPSPSAVTKSWDKQEDLVTLAKTASGVNQLVDI 60
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QDLVTPNNARQVETAAEDIEKLSNRKALVSLAEKQVAAHQWEDFASN 120
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YNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROIYQHAHVHIPTDIYEGSTIVL 180
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WTSALDEVFKQREEDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240
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IQGAASPKDMLILVDVSGVSGLTCLKIRTSVSEMLETSLDDDFNVNVSFNSNAQD 300
QHLVQANVRNKKVLDKAVNNITAKGITYKKGFSFAFEQLLNYNVSRANCKNIIML 360
QHLVQANVRNKKVLDKAVNNITAKGITYKKGFSFAFEQLLNYNVSRANCKNIIML 360
GEERAQEIFNKNKKVRFPSVQGHYERGPQWACENKGYVEIPIGAI 420
GEERAQEIFNKNKKVRFPSVQGHYERGPQWACENKGYVEIPIGAI 420
EYLDVGLRPMVLADKAKQVQWNTVYLDALGLVITGLPVFNITGOFENKTNLK 480
EYLDVGLRPMVLADKAKQVQWNTVYLDALGLVITGLPVFNITGOFENKTNLK 480
LGVMGVDVSLIEDIKELTRFTLCFNGYYFAIDPNGYVLLHPNLPKPKSQEPVTL 540
LGVMGVDVSLIEDIKELTRFTLCFNGYYFAIDPNGYVLLHPNLPKPKSQEPVTL 540
AELENDIKVEIRNKMIDGESSEKTRTLVKSQDERYIDKGNRTYTWTPVNGT 600

Db 536 DELDALENDIKVEIRNKMIDGESSEKTRTLVKSQDERYIDKGNRTYTWTPVNGT
QY 601 ALVLPITYFYIKAKLEETITQARSKKGMKMDSETLKPONFESGYTFIAPRDYCN
Db 596 ALVLPITYFYIKAKLEETITQARY-----SETLKPONFESGYTFIAPRDYCN
QY 661 SDNNTFLLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQVWSKQKNIKG
Db 649 SDNNTFLLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQVWSKQKNIKG
QY 721 FVVTGGITRVYPKBAGENQENPETYEDSFYKRSILDNDNYVFTAFYFNKSGPGAY
Db 709 FVVTGGITRVYPKBAGENQENPETYEDSFYKRSILDNDNYVFTAFYFNKSGPGAY
QY 781 MYSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVM
Db 769 MYSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVM
QY 841 LDGGFLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAFNKS YDYQSVCEPGA
Db 829 LDGGFLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAFNKS YDYQSVCEPGA
QY 901 GAGHRSAVPSVADILQIGWATAAAWSILQOELLSTLTPRLLEAVEMEDDDFTAS
Db 889 GAGHRSAVPSVADILQIGWATAAAWSILQOELLSTLTPRLLEAVEMEDDDFTAS
QY 961 SCITEQTQYFPDNDKSFSGVLDCGNCRI FHGKELMNTNLIIFIMVESKGTCPCDT
Db 949 SCITEQTQYFPDNDKSFSGVLDCGNCRI FHGKELMNTNLIIFIMVESKGTCPCDT
QY 1021 QAEQTSQGNPCDMVKQPRYKGPDYCFDNNVLEDYTDCCGVS 1063
Db 1009 QAEQTSQGNPCDMVKQPRYKGPDYCFDNNVLEDYTDCCGVS 1051

RESULT 13

US-10-375-253-20
; Sequence 20, Application US/10375253
; Publication No. US20040018510A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: SD9813DA
; CURRENT APPLICATION NUMBER: US/10/375,253
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354
; PRIOR FILING DATE: 1995-02-15
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 08/314,083
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 07/603,751
; PRIOR FILING DATE: 1990-11-09
; PRIOR APPLICATION NUMBER: 08/290,012
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: 08/105,536
; PRIOR FILING DATE: 1993-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 1091
; TYPE: PRT


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ITEFLINFEFIDRKTNNPSCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
|||||
ITEFLINFEFIDRKTNNPSCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
|||||
'DGGITRVYVPEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGFGAYESGI 780
'DGGITRVYVPEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGFGAYESGI 780
|||||
'AVEIYIOGKLLKPAVVGIKIDVNSIENFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840
'AVEIYIOGKLLKPAVVGIKIDVNSIENFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840
|||||
'KGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
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'EQTOYFFDNDKSKSGVLDGCGNCSRI FHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020
|||||
'TSDGPNPCDMVK 1036
'TSDGPNPCDMVK 1036

ication US/10090827
US20030073132A1
ION:
er-lambert
ION: binding ligands
179
TION NUMBER: US/10/090,827
DATE: 2002-03-06
ON NUMBER: US/09/397,549
TE: 1999-09-16
D NOS: 21
tIn Ver. 2.1

scrofa
96.1%; Score 5380; DB 15; Length 1036;
arity 98.7%; Pred. No. 0;
onservative 6; Mismatches 7; Indels 0; Gaps 0;

CLLALTTLFQSLILIGPSSPPFPFSAVITKSWDKMQEDLVTLAKTASGVNQLVDI 60
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QDLVTVBNARQVLAARDIEKLLSNRSALVSLALEAEKVQAQAHQWRDPASN 120
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YNKXDDLDPKXNDSEPSQRIKPVFIEDANFGROI SYQHA AVHIPTDIYEGSTIVL 180
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361 FTDGGEERAQEI FNKYNKD KKVRFVFRFVSGQHNHYERGPIQMACENKGYIYFIPS
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361 FTDGGEERAQEI FAKYNKD KKVRFVFRFVSGQHNHYERGPIQMACENKGYIYFIPS
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421 INTQYILDLVGRPMVLADGKAKQVQWNTVYLDALGLVITGTLVPVFNITGPFENI
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481 NOLILGVNMGVDVSLIEDIKRLTPRFTLCPNGYVFAIDPNGYVLLHFNLOPKPKSQI
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|||||
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961 SCITEQTOYFFDNDKSKSGVLDGCGNCSRI FHGEKLMNTNLIFIMVESKGTCPD
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1021 QAEQTSQGNPCDMVK 1036
1021 QAEQTSQGNPCDMVK 1036

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Search completed: February 20, 2004, 17:12:08
Job time : 34.7161 secs


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GenCore version 5.1.6
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In search, using sw model

February 20, 2004, 16:51:31 ; Search time 38.1957 Seconds
(without alignments)
7181.696 Million cell updates/sec

10-090-827-15
19
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1op 10.0 , Gapext 0.5
1525 seqs, 258052604 residues
1s satisfying chosen parameters: 830525
1th: 0
1th: 2000000000
1imum Match 0%
1imum Match 100%
1ting first 45 summaries

TREMEL23:*
sp_archaea:*
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sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
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sp_virus:*
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sp_archaeap:*

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the number of results predicted by chance to have a
 . than or equal to the score of the result being printed,
 d by analysis of the total score distribution.

SUMMARIES

ID	Length	Description
4	1110	Q9UIU0 homo sapien
6	077773	Q77773 sus scrofa
3	1091	Q9ERS3
2	1084	Q8CFG7
1	1103	Q08532 mus musculus
6	1079	Q8VHS9
3	745	Q9UDQ3
4	1150	Q9NY47
9	1143	Q9NY48
9	1156	Q9EQG2
8	1157	Q8CFG6
8	1148	Q8CER8
7	1145	Q9Y268
5	1098	Q8CHE9
4	1084	Q920H6
3	1076	Q9UEW0

ID	Length	Description
17	2814	50.3
18	1124.5	20.1
19	1119.5	20.0
20	1114.5	19.9
21	1112	19.9
22	1045.5	18.7
23	1009	18.0
24	1000.5	17.9
25	937	16.7
26	891.5	15.9
27	882.5	15.8
28	875	15.6
29	738.5	13.2
30	658	11.8
31	580.5	10.4
32	541.5	9.7
33	526.5	9.4
34	514.5	9.2
35	506	9.0
36	498.5	8.9
37	482	8.6
38	465	8.3
39	462.5	8.3
40	459	8.2
41	402	7.2
42	344	6.1
43	237.5	4.2
44	227	4.1
45	223	4.0

ALIGNMENTS

RESULT 1

ID	Length	Description
Q9UIU0	1110	AA.
AC	Q9UIU0	PRELIMINARY;
DT	01-MAY-2000	(TREMELrel. 13, Created)
DT	01-MAY-2000	(TREMELrel. 13, Last sequence update)
DT	01-MAR-2002	(TREMELrel. 20, Last annotation update)
DE	Dihydropyridine receptor alpha 2 subunit.	
GN	CACNA2D1.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20005942; PubMed=10534405;	
RA	Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;	
RT	"Genomic structure and functional expression of a human alpha (2) /	
RL	calcium channel subunit gene (CACNA2).";	
DR	Genomics 61:201-209(1999).	
DR	EMBL; AF083854; AAF03259.1; JOINED.	
DR	EMBL; AF083817; AAF03259.1; JOINED.	
DR	EMBL; AF083818; AAF03259.1; JOINED.	
DR	EMBL; AF083819; AAF03259.1; JOINED.	
DR	EMBL; AF083820; AAF03259.1; JOINED.	
DR	EMBL; AF083821; AAF03259.1; JOINED.	
DR	EMBL; AF083822; AAF03259.1; JOINED.	
DR	EMBL; AF083823; AAF03259.1; JOINED.	
DR	EMBL; AF083824; AAF03259.1; JOINED.	
DR	EMBL; AF083825; AAF03259.1; JOINED.	
DR	EMBL; AF083826; AAF03259.1; JOINED.	
DR	EMBL; AF083827; AAF03259.1; JOINED.	
DR	EMBL; AF083828; AAF03259.1; JOINED.	
DR	EMBL; AF083829; AAF03259.1; JOINED.	
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DR	EMBL; AF083832; AAF03259.1; JOINED.	
DR	EMBL; AF083833; AAF03259.1; JOINED.	
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3; AAF03259.1; JOINED.
004010; Cache.
002035; VWF_A.
; Cache; 1.
; vwa; 1.
7; VWA; 1.
234; VWA; 1.
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arity 99.4%; Score 5565.5; DB 4; Length 1110;
conservative 1; Mismatches 2; Indels 19; Gaps 1;
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CLLALTLTFLQSLLIGSPSPSPSAVTKSWNDKQEDLVTLAKTAGSVNQLVDI 60
QDLVTVFPNNARQIVETAAARDIEKLLNSRKALVSLALEAEKVOAAHWRDFASN 120
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YNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROI SYOHAHVHIPTDIYEGSTIVL 180
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Db 601 DKGNRTYTWTPVNGTDSLALVLPYTFYFIKAKLEETITQARSKKGMKDSITL
QY 642 RESGYTFIAPRDYCNLDKISDNTTEFLNFEFDIRKTPNNPSCNADLINRVLLD
Db 661 RESGYTFIAPRDYCNLDKISDNTTEFLNFEFDIRKTPNNPSCNADLINRVLLD
QY 702 ELVQYMSKQNIKGVKARFVVTGGITRVYKESAGENWQENPETYEDSFYKRSIL
Db 721 ELVQYMSKQNIKGVKARFVVTGGITRVYKESAGENWQENPETYEDSFYKRSIL
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTE
Db 781 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTE
QY 822 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDVTNQTGRPFGEIDPSLMRHLVNI
Db 841 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDVTNQTGRPFGEIDPSLMRHLVNI
QY 882 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAAWSILOQFLLSI
Db 901 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAAWSILOQFLLSI
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDSKSPSGVLDGNCRSRI FHGEKLM
Db 961 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDSKSPSGVLDGNCRSRI FHGEKLM
QY 1002 IFIMVESKGTCTPCTRLLIQAEQTSQGNPCDMVKQPRYKRGPDVCFDNNVLEDT
Db 1021 IFIMVESKGTCTPCTRLLIQAEQTSQGNPCDMVKQPRYKRGPDVCFDNNVLEDT
QY 1062 VS 1063
Db 1081 VS 1082
RESULT 2
O77773 PRELIMINARY; PRT; 1091 AA.
ID O77773 AC O77773;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Voltage-dependent calcium channel alpha-2 delta subunit precursor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=98411353; PubMed=9738015;
RA Brown J.P., Gee N.S.;
RT "Cloning and deletion mutagenesis of the alpha2 delta calcium cha
subunit from porcine cerebral cortex. Expression of a soluble for
the protein that retains [3H]gabapentin binding activity.";
J. Biol. Chem. 273:25458-25465 (1998).
RL EMBL; AF077665; AAC36289.1; --
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWA; 1.
KW Signal.
FT SIGNAL 1 24
FT CHAIN 25 1091
FT CHAIN
SQ SEQUENCE 1091 AA; 123150 MW; 293DDC7EBE9EB60E CRC64;
Query Match 98.8%; Score 5532; DB 6; Length 1091;
Best Local Similarity 98.7%; Pred. No. 0;

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XLLALTLTQSLIGPSSPEPPSAVTIKSWDKMOEDLVTLAKTASGYNQVLVDI 60
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RESULT 3
Q9ERS3 PRELIMINARY; PRT; 1091 AA.
AC Q9ERS3;
DT 01-MAR-2001 (T-REMBLrel. 16, Created)
DT 01-MAR-2001 (T-REMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (T-REMBLrel. 21, Last annotation update)
DE Voltage-gated calcium channel alpha2/delta-1 subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rati
OC NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Superior cervical ganglion;
RA Lin Y., Lipscombe D.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP286488; AAG28164.1; -
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; WVF_A.
DR Pfam: PF02743; Cache; 1.
DR SMART: SM00327; VWA; 1.
DR PROSITE: P850234; VWEA; 1.
FT VARIANT 209 212 GSAT -> AADR.
FT VARIANT 338 338 S -> T.
FT VARIANT 599 600 SL -> RY.
FT VARIANT 869 869 S -> R.
SQ SEQUENCE 1091 AA; 123467 MW; C155088971628E19 CRC64;

Query Match 97.3%; Score 5447; DB 11; Length 1091;
Best Local Similarity 96.5%; Pred. NO. 0;
Matches 1026; Conservative 22; Mismatches 15; Indels 0; G

QY 1 MAAGCLLALTLTQSLIGPSSPEPPSAVTIKSWDKMOEDLVTLAKTASGYNQI
DB 1 MAAGCLLALTLTQSLIGPSSPEPPSAVTIKSWDKMOEDLVTLAKTASGYNQI
QY 61 YKYQDLYTPEPNARQALVEIARDIEKLSNRKALVSLALEAEKVQAAHQRREDI
DB 61 YKYQDLYTPEPNARQALVEIARDIEKLSNRKALVRLALEAEKVQAAHQRREDI
QY 121 EVYVYNAKDDLPEKNDSEPGSQRKIPKVFIEDANFGRIQISYQAAHVHIPTDIYEGS
DB 121 EVYVYNAKDDLPEKNDSEPGSQRKIPKVFIEDANFGRIQISYQAAHVHIPTDIYEGS
QY 181 NELNMTSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVNSRTENKIDLYI
DB 181 NELNMTSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVNSRTENKIDLYI
QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKLIIRTSVSEMLETLSDDDPFVNVASFNSI
DB 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKLIIRTSVSEMLETLSDDDPFVNVASFNSI
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQQLLNNVNSRANCKI
DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQQLLNNVNSRANCKI
QY 361 FTDGGEERAQEIENKYNKDKKVRFPSPVSGHNYVERGPIQWMACENKGYIYEPSIGI
DB 361 FTDGGEERAQEIENKYNKDKKVRFPSPVSGHNYVERGPIQWMACENKGYIYEPSIGI
QY 421 INTQEYLDVLRGPMVLADGKAKQVQNTNVLDALEGLVITGTLVPFNITQGFENKI
DB 421 INTQEYLDVLRGPMVLADGKAKQVQNTNVLDALEGLVITGTLVPFNITQGFENKI
QY 481 NQILIGVMGVDSLEDIKRLTPRFTLCPNGYYPADPNQVGVLLHPNLQPNKPSQEI
DB 481 NQILIGVMGVDSLEDIKRLTPRFTLCPNGYYPADPNQVGVLLHPNLQPNKPSQEI
QY 541 DFLLDAELENDIKVEIENKMDGSGEKTFTLVKSQDERYIDKGNRTYTWTPVNGTI

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[illegible]

azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
190;

N.A.

514; PubMed=8955374;

Hofmann F.;

7:331-337(1996).

CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
V-CONTRACTION COUPLING.

THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:

ALPHA-2, BETA AND GAMMA.

ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-

AR LOCATION: INTEGRAL MEMBRANE PROTEIN.

VE PRODUCTS: 5 ISOFORMS; 2A (SHOWN HERE), 2B, 2C, 2D AND

REDUCED BY ALTERNATIVE SPLICING.

SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AND

IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D IS

IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN

SCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE

JULAR SYSTEM.

1-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM

OR FORM.

(; TO OTHERS SPECIES ALPHA-2 SUBUNIT.

AAB50139.1; -

AAB50140.1; -

AAB50138.1; -

AAB50141.1; -

AAB50142.1; -

; Caccna2d1.

04010; Cache.

02035; VWF_A.

; Cache; 1.

; vwa; 1.

; VWA; 1.

234; VWF; 1.

al; Transmembrane; Ion transport; Voltage-gated channel;

al; Glycoprotein; Phosphorylation; signal;

licing.

POTENTIAL.

L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT.

L-TYPE CALCIUM CHANNEL DELTA SUBUNIT.

POTENTIAL.

POTENTIAL.

POTENTIAL.

PHOSPHORYLATION (BY CAPK) (POTENTIAL).

PHOSPHORYLATION (BY CAPK) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

QY 1 MAAGCLLALTLTLFOSLLIGPSEPPSPSVATTIKSWVDKMQEDLVTLAKTASGVNQ
DB 1 MAAGCLLALTLTLFOSLLIGPSEPPSPSVATTIKSWVDKMQEDLVTLAKTASGVNQ
QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLSNRSKALVSLALEAEKVOAAHQWRED
DB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLSNRSKALVSLALEAEKVOAAHQWRED
QY 121 EYVYTNKADLDPEKNDSEPSQRIKPVFIEDANFGROIYSHAAVHIPDIEVGS
DB 121 EYVYTNKADLDPEKNDSEPSQRIKPVFIEDANFGROIYSHAAVHIPDIEVGS
QY 181 NELNWTLSALDEVFKKREEDPSLLMQVFGSATGLARYYPASPMVDNSRTNPKIDLY
DB 181 NELNWTLSALDEVFKKREEDPSLLMQVFGSATGLARYYPASPMVDNSRTNPKIDLY
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETISDDDFVNVASFNS
DB 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETISDDDFVNVASFNS
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGSPAFQQLIYNNVSRANCNK
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGSPAFQQLIYNNVSRANCNK
QY 361 FTDGGERAQEIEFNKYNKDKKRVFRFVSQGHYVERGPIQWMACENKGYIYEIPSI
DB 361 FTDGGERAQEIEFNKYNKDKKRVFRFVSQGHYVERGPIQWMACENKGYIYEIPSI
QY 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVYLDLELGLVITGLPVNITGQFENK
DB 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVYLDLELGLVITGLPVNITGQFENK
QY 481 NQILGLVMGVDVSLIEDIKRLTPRFTLCPNGYVFAIDPBGVYLLHPNLOPK
DB 481 NQILGLVMGVDVSLIEDIKRLTPRFTLCPNGYVFAIDPBGVYLLHPNLOPK
QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKWIDGESGEKTRTLVKSQD
DB 541 LRKRRPNVQPKSQEPVTLDFDAELENDIKVEIRNKWIDGESGEKTRTLVKSQD
QY 582 DKGRTYTTWTPVNGTDYSLALVLTYSFYVYIKAKLETTITQARSKKGKMDSETLK
DB 601 DKGRTYTTWTPVNGTDYSLALVLTYSFYVYIKAKLETTITQARSKKGKMDSETLK
QY 642 EESGYTFIAPRDYCNLDKISDNNTEFLNPNFEDIRKTPNPNPCNADLINRVLDDA
DB 654 EESGYTFIAPRDYCNLDKISDNNTEFLNPNFEDIRKTPNPNPCNADLINRVLDDA
QY 702 ELVQNYWSKQKNIKGVKARFVVTDDGGITRVYPKEAGENWOENPETYEDSFYKRSLO
DB 714 ELVQNYWSKQKNIKGVKARFVVTDDGGITRVYPKEAGENWOENPETYEDSFYKRSLO
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVIYIQGKLLKPAVVGKIDVNSWIENFTKTS
DB 774 VFTAPYFNKSGPGAYESGIMVSKAVIYIQGKLLKPAVVGKIDVNSWIENFTKTS
QY 822 CAGPVCDCCKNSDVMDCVTLDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI
DB 834 CAGPVCDCCKNSDVMDCVTLDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI
QY 882 FNKSIDYQSVCEPGAAPKQAGHRSAYVFSVADILQIGWATAAAWSIIQOFLLSL
DB 894 FNKSIDYQSVCEPGAAPKQAGHRSAYVFSVADILQIGWATAAAWSIIQOFLLSL
QY 942 LLRAVEMBEDDFTASLSKQSCITEQYQYFFDNDKSKFSFGLVDCGNCRSRIPHGEKLM
DB 954 LLRAVEMBEDDFTASLSKQSCITEQYQYFFDNDKSKFSFGLVDCGNCRSRIPHGEKLM
QY 1002 IFTWVESKGTCPDTELLIQABOTSQGNPCDMVKQPRYRKGPVDCVCFDNNVLEDTYI
DB 1014 IFTWVESKGTCPDTELLIQABOTSQGNPCDMVKQPRYRKGPVDCVCFDNNVLEDTYI

[illegible][illegible]

1 AA; 84396 MW; BC07B53484B71EA4 CRC64;
 68.3%; Score 3823; DB 4; Length 745;
 99.7%; Pred. No. 9.3e-232;
 1; Mismatches 1; Indels 0; Gaps 0;
 ANCNKIIMLFTDGGGERAQEIFNKNYKDKKVRVFSVQGHNYRGPQIOMACEN 406
 ANCNKIIMLFTDGGGERAQEIFNKNYKDKKVRVFSVQGHNYRGPQIOMACEN 60
 EIPSGAIRINTQEVLDVLRPMVLGAKQVQWNTVYLDALGLVITGLPV 466
 EIPSGAIRINTQEVLDVLRPMVLGAKQVQWNTVYLDALGLVITGLPV 120
 QPENKTNLKNQILILGVMGVDSLEIDIKLTPTFTLCPNGYYPADIPNGVLLHPN 526
 QPENKTNLKNQILILGVMGVDSLEIDIKLTPTFTLCPNGYYPADIPNGVLLHPN 180
 PKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSDERYIDKGNR 586
 PKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSDERYIDKGNR 240
 PVNGTDSLALVLPYSFYIYKAKLEETITQARSKKGKMDSETLKPDPFESGY 646
 PVNGTDSLALVLPYSFYIYKAKLEETITQARSKKGKMDSETLKPDPFESGY 300
 RDYCNLDKISDNTEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVN 706
 RDYCNLDKISDNTEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVN 360
 KNIKGVKARFVTDGGITRVYPKEAGENQENPETYDSFYKRSLDNDNYFTAP 766
 KNIKGVKARFVTDGGITRVYPKEAGENQENPETYDSFYKRSLDNDNYFTAP 420
 GPAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENTFTKTSIRDCAGPV 826
 GPAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENTFTKTSIRDCAGPV 480
 NSDVMDCVILDDGGFLMANHDDYTNQIGRFEGEIDPSLMRHLNVIYAFNKS 886
 NSDVMDCVILDDGGFLMANHDDYTNQIGRFEGEIDPSLMRHLNVIYAFNKS 540
 CEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLSLTPRLEAV 946
 CEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLSLTPRLEAV 600
 DPTASLSKQSCITQTQYFFDNDSKSPGVLDGCGNCSRIFHGEKLMNTLIFIMV 1006
 DPTASLSKQSCITQTQYFFDNDSKSPGVLDGCGNCSRIFHGEKLMNTLIFIMV 660
 CPCTRLLIQAEQISDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063
 CPCTRLLIQAEQISDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 717

ELIMINARY; PRT; 1150 AA.

REMBLrel. 15, Created)

REMBLrel. 15, Last sequence update)

REMBLrel. 23, Last annotation update)

1, alpha 2/delta subunit 2.

Human).

azoa; Chordata; Craniata; Vertebrata; Euteleostomi;

eria; Primates; Catarrhini; Hominidae; Homo.

6;

N.A.

;

Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Thyroid;
 RA Hobom M., Dai S., Marais E., Lacinova L.;
 RT "Neuronal distribution and functional characterization of the cal.
 channel alpha2delta-2 subunit."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ251368; CAB86193.1; -
 DR InterPro; IPR004010; Cache.
 DR InterPro; IPR002035; WVF.A.
 DR Pfam; PF00743; Cache; 1.
 DR Pfam; PF00092; vwa; 1.
 DR SMART; SM00327; vwa; 1.
 DR PROSITE; PS00234; WVF.A; 1.
 SQ SEQUENCE 1150 AA; 129876 MW; 37B75F687AF5E73C CRC64;
 Query Match 54.4%; Score 3045; DB 4; Length 1150;
 Best Local Similarity 54.6%; Pred. No. 1.4e-182;
 Matches 588; Conservative 172; Mismatches 286; Indels 30; G;
 QY 7 LALTLTLFQSLIGPSSEPEPSAVTIKSWDKMQEDLVTAKTASGVNQLVDIYE
 DB 44 LMLLLPPLLALPAGASAYSFPOQHTMQHWARKLEQVGVGVRIFGVQOOLREIYK
 QY 67 LYTVEPNNAQLVETIAARDIEKLLSNRSKALVSLALEAEKQVAAHQRWEDFASNEV
 DB 104 LPRVQENEPQKLVEKVAGDIESLLDRKQALKLADAAENFQKAHRWQDNKEEDI
 QY 127 AKDDL--DPEKNDSPGSG--RIKPVFTEDANFGROIYQYHAAVHIPTDIYEGST
 DB 164 AKADAEELDPESDEVERGSKASTLRIDFTEDPNFKKNVSYAAVQIPTDIYKGST
 QY 182 ELNWTALDEVFKONREEDPSLLWVFGSATGLARYYPASPWVDNSRTNKNKIDLYD
 DB 224 ELNWTALENVFMEKRRQDPTLLWVFGSATGVTRYYPATPW----RAFKKIDLYD
 QY 242 PWYIOGAASPDKMLILVDVSGVSGLTLLKIRTSVSEMLETISDDDDFVNVASFNSN
 DB 280 PWYIOGASPKDMWIIVDVSGVSGLTLLKMKTSVCEMLDTLSDDDDVNVASFNEK
 QY 302 SCFQHLVQANRNKVKLVDAVNNITAKGTDYKKGSPFAFEQLNLYNVSRANCKI
 DB 340 SCFTHLVQANRNKVKVKEAVQWAKGTTGYKAGFEYAFDQIQNSNITRANCKM
 QY 362 TDGGERAQEIEKNY-KDKKVRVFRFSVQGHNYRGPQIOMACENKGYIYETPSI
 DB 400 TDGGERVQDVFEKTNPNRTVTVFVSQGHNYDVTPLQMACANGYIFELPSI
 QY 421 INTQEVLDVLRPMVLGAKQVQWNTVYLDALGLVITGLPVFNITGOFENK
 DB 460 INTQEVLDVLRPMVLGAKQVQWNTVYLDALGLVITGLPVFNITG--DGRK
 QY 481 NQILIGVMGVDSLEIDIKLTPTFTLCPNGYYPADIPNGVLLHPNLPQNPKNKQBI
 DB 518 NQILIGVMGIDVALNDIKLTPTFTILGANGYYPADIPNGVLLHPNLPKQPTNFRE
 QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSDERYIDKGNRTYTWTPNGTI
 DB 578 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSDERYIDKGNRTYTWTPNGTI
 QY 601 ALVLPYSFYIYKAKLEETITQARSKKGKMDSETLKPDPFESGYTFIAPDYCNI
 DB 638 GLVLPYSFYIYKAKLEETITQARSKKGKMDSETLKPDPFESGYTFIAPDYCNI
 QY 661 SDNTEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQK-NIKG
 DB 698 SDNTEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQK-NIKG
 QY 720 RFWVTDGGITRVYPKEAGENQENPETYDSFYKRSLDNDNYFTAPYFNK-SGFGP
 DB 758 VFAATDGGITRVYPKEAGENQENPETYDSFYKRSLDNDNYFTAPYFNK-SGFGP

Db	224	ELNWTAEALENVFMENRRQDFTLLNQVFSGATGVTTRYPATPW----	RAPKKDLIDLY
QY	242	PWYIQGAASPDKMILLVDVSGSVSGITLKLIRTSVSEMLLETLSDDDFVNVASFNSN	
Db	280	PWYIQGAASSPKDMVIIVDVSGSVSGITLKLIMKTSVCSEMLDTLSDDDFVNVASFNEK	
QY	302	SCFOHLQVANRNKKVLKDAVNNTAKGITYDKKGPSAPAEOLLNANVNVSRANCKNI	
Db	340	SCFTHLQVANRNKKVFKFAVQGVAKGTTGYKAGFEYAPDQLQNSNITRANCKNM	
QY	362	TDGGERAQEIPFNKYN-KDKKVRVFRFSGVQHNYERGPQMWACENKGYEYIETPSI	
Db	400	TDGGBDRYQDVFEXYNPNPRTVRFVFSVQGHNYDVTPLQMWACANKGYEYIETPSI	
QY	421	INTQBYLDVLRPMVLADGKAKQVQWNTVNLDALELGLVITGTLVPFNITQGFENK	
Db	460	INTQBYLDVLRPMVLTAGKAKQVQWNTVYEDALGVLVVTGTLVPFNLQ--DGP	
QY	481	NQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYFPAIDPNGYVILLHPLNLOPKMPKQOE	
Db	518	NQLILGVMGIDVALNDIKRLTPNYTLGANGYVPAIDNGYVLLHPLNKLPQITNPRE	
QY	541	DFLDAELENDIKVIRNKMIDGSGSEKTFRTLVKSQDERYIDKGNRTTWTVPVNGT	
Db	578	DFLDAELDENKERIRRSMTDGNKHKQRTLVKSLDERYIDDEVTRNTTWTVPIRST	
QY	601	ALVLPTFSFYVIKAKLBETITQARSKKGMKMDSETLKPDNFEESGYTPIAPROYCN	
Db	638	GLVLPPTSYTFVLQANLSDQLQ-----VKYFEFLPSSFESEGHVFIAPREYCK	
QY	661	SDNNTFLLINFEFIDRKTNNPSCNADLINRVLLDAGFTNELVOLQVYNSKOK-NIK	
Db	691	SDNNTFLLKNFIELMEKVTPDSKQCNFLHNLILDTGITQQLVERVWRDQDLNTY	
QY	720	REVTVTGGITRVYPKAEGENQWNPETYEDSFYKGSNDNDNVETAPYFNK-SGPG	
Db	751	VEAATDGGITRVFPNKAEDOWTENPFPNASFRRSELDNHGVFKPPHQDALLAPL	
QY	779	---GIMVSKAVEIYIOGKLKPAAVGIKIDVNSWIENF-----TKTSIRDP--CAG	
Db	811	DTVIGILVSTAVELSLGRRTLRPAVGVGLDLAAWAEKFKVLASNRTHQDQPKC-G	
QY	826	-VCDCKRNSVDWCVILDDCGFLLMANHHDDYTNQGRPFGEIDPSLMRHLNIVSY	
Db	870	CEMCEVNEVDLLCVLDDGGFLVLNSQNHQMDQVGRPFSEVDANLMALNLYNSFY	
QY	885	SYDYQSVCEPAAKPKQAGHRSAVPSVADIILQIHWATAAAWSLIQOFLLSLTFP	
Db	930	SYDYQAACAPQPPGNLGAAPRGVFVPTVADFNLAWTSAAAWSLFQQLLGLIVH	
QY	945	AVEMEDDDFTASLSKQSCITEQTYFFDNDSKSPSGVLDCGNCRSIRPGEKLMNTN	
Db	990	ADPAEAEAG-SPETRESSCVMKQTYTYFGSVNASYNAIIDCGNCSSLFHAQBLTNTN	
QY	1005	WYESKGTCPCDTRLIIQAEQTSIDGPNPCDMWQOPRVKRGPDVCFDNNVLEDYDTCG	
Db	1049	VAEKPLSCQEAQELLQKETHSDGPRQCELVQRPYRRGPHLCFDYNATEBTSQCG	
RESULT 10			
Q9BQG2			
ID	Q9BQG2	PRELIMINARY;	PRT; 1156 AA.
AC	Q9EGG2		
DT	01-MAR-2001	(TrEMBLrel. 16, Created)	
DT	01-MAR-2001	(TrEMBLrel. 16, last sequence update)	
DT	01-MAR-2003	(TrEMBLrel. 23, last annotation update)	
GN	Voltage-dependent calcium channel alpha-2-delta-2 subunit.		
DE	CACNA2D2.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
ON	NCBI_TaxId=10090;		
RX	[1]		

2P	N.A.	116; PubMed=11130987;
3C	ies M.;	ization of the mouse and human alpha2delta2 voltage-
3K	ium channel subunit genes.";	
3A	11:1142-1144 (2000).	
3T	9; AAG47846.1; -.	
3L	313; Cacca2d2.	
3R	104010; Cache.	
3D	102035; VWF_A.	
3E	: Cache; 1.	
3F	: vwa; 1.	
3G	234; VWA; 1.	
3H	36; A; 130611 MW; A732545A2B302A52 CRC64;	
3I	53.9%; Score 3015.5; DB 11; Length 1156;	
3J	urity 54.0%; Pred. No. 1e-180;	
3K	nservative 177; Mismatches 287; Indels 33; Gaps 15;	
3L	TLTFQSLIGP--SSREPPPSAVTIKSWDKMQEDLVTLAKTAGSGVNLVDIYEKY 64	
3M	?PELLLPILITAFGASAYSFQOCHTMQHARRLEQEDGVMRIFGGVQQLREIYKDN 104	
3N	TVPEPNARQLVETAAARDIEKLNSRKALVSLALEAKVQAQAHOMREDFASNEVVY 124	
3O	3VOENEPQKLVEKVAGDIESLLDRKVOALKRLADAAENFQKAHRWQDNIKEEDIMY 164	
3P	DDI----DPEKNDSEPSQ--RIKPVIEDANFGROIISYQAAVHIPTDIIYEGSTIV 179	
3Q	ADAELDDPSEDMERSGKTSALSRLDIEDENFNKNVNYSTAVQIPTDIIYKGSTVI 224	
3R	WTSALDVEFKKREDDPSLLWQVFGSATGLARYYPASPMVDNSRTNPKLIDLVDVR 239	
3S	WNTBALENVFIEENRQDPTILLWQVFGSATGVITYYPATPW---RAPKKLIDLVDVR 280	
3T	TIQGAASPDKMLILVDVSGSVSGLTLKIRTSVSEMLETLISDDDDFVNVSFNSNAQ 299	
3U	TIQGASSPKDVIIVDVGSVSGSLTLKMKTSVCEMLDTLSDDDDYVNVASFNEKAQ 340	
3V	FOHLVQANVRNKKVLQDANNITAKGLTDYKKGFSPAFEGQLLNNVNSRANCKLIM 359	
3W	FTHLVQANVRNKKVFEKAVQGVAKGTYGKAGFEYAFDQLQNSNITFRANCKRMIM 400	
3X	SGEERAQEIFNKN-KDKKVRVFRFSVQGNHYERGPLOMACENKGYIYFIPSLIGA 418	
3Y	3GEDRVQDVFKEKNWNFRVFRVTFFSVQGNHYDVTPLQWMACTNKGYYFIEPISLIGA 460	
3Z	IQEYLDVLGRPMVLADGKAKQVQWNTVYLDLDALELGLVITGLTPVFNITGOFENKTN 478	
3A	IQEYLDVLGRPMVLADGKAKQVQWNTVYEDALGLVVTGLTPVFNLTQ--DGPGE 518	
3B	LILGVNGVDVLEDDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPMLQPNKFSQBVPV 538	
3C	LILGVNGVIDVALNDIKRLTNYITLGGANGYYFAIDLNGYVLLHPNLKQPTTFNREP 578	
3D	LDLAELNDIKVEIRNKMIDGESGEKTPRTLVKSQDERYIDKGNRTYTWTPUNGTDY 598	
3E	LDLAELDENKEEIRRSMDIDGKGHKQIRTLVKSLDERYIDDEVIRNYTWVPIRSTNY 638	
3F	VLPTYGYIYKAKLEETITQARSKKGKMDSETLKPONFBSGYYFTIAPRDYCNLD 658	
3G	VLPPYSTYIYQANLRDQLQVLPISKLADQFEFLPPSSFSESGHVFTIAPREYCKDL 698	
3H	NNTFELINFNEFIDRKTNNPNNSCNADLINRVLLDAGFTNELVQNWYSKQK-NIKGV 717	
3I	NSTEFLLKDFIELMEKVTPDSKQCNFNFLHNLILDTGITQQLVERWRDQDLNTYSL 758	
3J	VVTDGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNTVFTTAPYFNK-SGPGAY 776	
3K	AATDGGITRVYFPNKAEDMTENPEPNFNASFYRRSLDNHGYIFKPPHQDSSLRLPUEL 818	

[illegible]

GenCore version 5.1.6
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in search, using sw model
bruary 20, 2004, 16:52:19 ; Search time 18.7568 Seconds
(without alignments)
5450.141 Million cell updates/sec

-10-090-827-15
39
AAGCLLALTLFQSLIG.....PVCFDNNVLEDYDCGGVS 1063
SUM62
pop 10.0 , Gapext 0.5
3308 seqs, 96168682 residues
s satisfying chosen parameters: 283308
fth: 0
fth: 2000000000
inimum Match 0%
ximum Match 100%
isting first 45 summaries
[R:76:*
pir1:*
pir2:*
pir3:*
pir4:*

the number of results predicted by chance to have a
than or equal to the score of the result being printed,
ad by analysis of the total score distribution.

SUMMARIES

Entry	Length	DB	ID	Description
1.0	1091	2	JH0565	calcium channel al
1.3	1091	2	A44147	calcium channel pr
1.1	1106	1	CHRB2	calcium channel pr
1.0	1091	2	T30256	calcium channel al
1.8	734	2	S44617	CS0C3.11 protein -
1.4	1148	2	T18770	probable calcium c
1.5	1450	2	C86880	hypothetical prote
1.5	886	2	S54355	inter-alpha-trypsi
1.3	885	2	S30350	inter-alpha-trypsi
1.1	1819	2	D97033	uncharacterized pr
1.9	889	2	JC5576	inter-alpha-trypsi
1.9	2706	2	T28155	variant-specific s
1.8	1984	2	A44396	P-type cation tran
1.8	575	2	D64998	hypothetical prote
1.8	918	2	E90542	lipoprotein [impor
1.8	680	2	A97331	membrane associate
1.8	1516	2	E71619	RAD2 endonuclease
1.8	2364	2	I40884	cytotoxin L - Clo
1.8	946	1	IYH2	inter-alpha-trypsi
1.8	1315	2	T28679	fibrinogen-binding
1.7	932	2	JC5953	inter-alpha-inhibi
1.7	1291	2	S46431	botulinum neurotox
1.7	1291	2	A49777	botulinum neurotox
1.7	420	2	S76691	hypothetical prote
1.7	1426	2	A99580	hypothetical prote
1.7	921	2	JC4625	inter-alpha-trypsi
1.7	1385	2	D89824	hypothetical prote
1.7	654	2	A69656	methyl-accepting c
1.7	1027	2	B90527	atp-binding protei

30	149	2.7	459	2	F64688	proteinase
31	149	2.7	930	2	JX0368	inter-alpha
32	148.5	2.7	2401	2	T28676	thoptry prc
33	148	2.6	964	2	S25855	DNA-directe
34	146.5	2.6	1285	2	B72420	hypothetica
35	146	2.6	688	2	D96930	methyl-acce
36	146	2.6	4688	2	F82885	hypothetica
37	145.5	2.6	676	2	T47637	hypothetica
38	145.5	2.6	689	2	F84811	probable re
39	145.5	2.6	1237	2	AC1583	internalin
40	145.5	2.6	2013	2	AD1129	probable pe
41	145.5	2.6	3216	2	C90538	hypothetica
42	145.5	2.6	5005	2	F82884	hypothetica
43	144	2.6	1087	1	S41797	cellulose 1
44	144	2.6	1091	2	S33850	fibronectin-
45	143.5	2.6	1252	2	H97178	ATP-depende

ALIGNMENTS

RESULT 1
JH0565
calcium channel alpha-2b chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug
C:Accession: JH0565
R:Williams, M.X.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi,
Neuron 8, 71-84, 1992
A:Title: Structure and functional expression of alphas, alpha2, and be
A:Reference number: JH0564; MUID:92110010; PMID:1309651
A:Accession: JH0565
A:Molecule type: mRNA
A:Residues: 1-1091 <WIL>
A:Cross-references: GB:M76559; NID:g179761; PIDN:AAA51903.1; PID:g1797
A:Experimental source: basal ganglia
A:Note: Several conflicts are found between GenBank submission, author
C:Comment: This protein is a subunit of the voltage dependent calcium
C:Superfamily: calcium channel alpha-2 chain
C:Keywords: glycoprotein; phosphoprotein
F:1-24/Domain: signal sequence #status predicted -SIG>
F:25-1067/Product: calcium channel alpha-2b chain #status predicted <C
F:32,268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by
F:91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by prot
F:92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/B
F:501/Binding site: phosphate (Thr) (covalent) #status predicted
F:833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kina

Query Match	100.0%	Score	5599;	DB	2;	Length	1091;
Best Local Similarity	100.0%	Pred. No.	0;				
Matches	1063;	Conservative	0;	Mismatches	0;	Indels	0;
Gy	1	MAAGCLLALTLTLFQSLIGSSSEPPSPS	AVTIKSWDKMQEDLVTLAKTASGVNQ				
Db	1	MAAGCLLALTLTLFQSLIGSSSEPPSPS	AVTIKSWDKMQEDLVTLAKTASGVNQ				
Gy	61	YEKYQDLYTVEPNARQVIAARDIEKLSNR	SKALVSLALAEKVQAAHQWRD				
Db	61	YEKYQDLYTVEPNARQVIAARDIEKLSNR	SKALVSLALAEKVQAAHQWRD				
Gy	121	EVVYNAKODLDEPKNDSEFGSRQIRKPV	FIEDANFGRIQISYQAAVHIPTDIYEGS				
Db	121	EVVYNAKODLDEPKNDSEFGSRQIRKPV	FIEDANFGRIQISYQAAVHIPTDIYEGS				
Gy	181	NELNWTSDALDEVKQKREDDPSLLQVFG	SATGLARYYPASPVWDSRTPNKIDLY				
Db	181	NELNWTSDALDEVKQKREDDPSLLQVFG	SATGLARYYPASPVWDSRTPNKIDLY				
Gy	241	RPWYIQGAASPKDMLILVDVSGSVGLTK	LRTSVSEMLETSSDDDFVNVASFNS				
Db	241	RPWYIQGAASPKDMLILVDVSGSVGLTK	LRTSVSEMLETSSDDDFVNVASFNS				
Gy	301	VSCFOHLVQANVRNKKVLDVANNITAKG	ITDYKKGFSFAPEQLLNVTNVRANCNK				

QHLVQAVNRKVKYLKDAVNNITAKGITDYKKGSFAPQLLNVNVRANCNKIML 360
 GERARQEI FNKYWNOKKVRVFRFSVGOHNYERGPLOMWACENKGYTTEISGAIR 420
 GERARQEI FNKYWNOKKVRVFRFSVGOHNYERGPLOMWACENKGYTTEISGAIR 420
 EYLDVLGRPMVLAGDKAKQOVMTNVYLDALIELGLVITGTLPVFNITQOFENKTNLK 480
 EYLDVLGRPMVLAGDKAKQOVMTNVYLDALIELGLVITGTLPVFNITQOFENKTNLK 480
 LGVMGVDSVLSLEDKRLTPRFTLCPNGYTFADPNCGYVLLHNLKPKPKSOEPTVL 540
 LGVMGVDSVLSLEDKRLTPRFTLCPNGYTFADPNCGYVLLHNLKPKPKSOEPTVL 540
 AELENDIKVEIRNKMIDGESSEKTFRTLKVSQDERYIDKGNRTYTWTVPNGTDYSL 600
 AELENDIKVEIRNKMIDGESSEKTFRTLKVSQDERYIDKGNRTYTWTVPNGTDYSL 600
 PTTSFYIYKAKLEBETITQARSKKGWKOSETLKPDPNFEESGYTPIAPRDYCNLDKI 660
 PTTSFYIYKAKLEBETITQARSKKGWKOSETLKPDPNFEESGYTPIAPRDYCNLDKI 660
 TEFLLMNFBEIDRKTPNNPSCNADLINRVLLDAGFTNELVQYWSKQNKIKGVKAR 720
 TEFLLMNFBEIDRKTPNNPSCNADLINRVLLDAGFTNELVQYWSKQNKIKGVKAR 720
 DGGITRVYPKEAGENWOENPETVYESFYKRSLDNDNVYFTAPYFNKSGPGAYSEGI 780
 DGGITRVYPKEAGENWOENPETVYESFYKRSLDNDNVYFTAPYFNKSGPGAYSEGI 780
 AVEIYLOGLKLPVAVGIIKIDVNSWIENTFTKTSIRDPCAGVCCOCKNSDVMDCVI 840
 AVEIYLOGLKLPVAVGIIKIDVNSWIENTFTKTSIRDPCAGVCCOCKNSDVMDCVI 840
 GFLLMANHDDYTNIQIGRFFGEIDPSLMRHLVNI SVYAFNKSYDYQSVCECPAAPKQ 900
 GFLLMANHDDYTNIQIGRFFGEIDPSLMRHLVNI SVYAFNKSYDYQSVCECPAAPKQ 900
 RSAYVPSVADILOIGHWATAAAWSILOQFLSLSTPPRLLEAVEMEDDDFTASLSKQ 960
 RSAYVPSVADILOIGHWATAAAWSILOQFLSLSTPPRLLEAVEMEDDDFTASLSKQ 960
 EQTYQYFPDNDKSFSGVLDCGNCRSIFHGEKLMNTNLI FIMVBSKGTCPCDTRLLI 1020
 EQTYQYFPDNDKSFSGVLDCGNCRSIFHGEKLMNTNLI FIMVBSKGTCPCDTRLLI 1020
 TSDGPNPCDMVKQPRYRKGPDYCFDNNVLEDYTDCCGVS 1063
 TSDGPNPCDMVKQPRYRKGPDYCFDNNVLEDYTDCCGVS 1063

otein alpha-2 chain precursor - rat

dihydropyridine-sensitive L-type

m channel alpha-2 chain

norvegicus (Norway rat)

4 #sequence_revision 27-Jun-1994 #text change 20-Aug-1999

7

H.; Lee, P.; King, R.G.; Chin, H.

Sci. U.S.A. 89, 3251-3255, 1992

expresses an alternatively spliced form of the dihydropyridine-sensitive

: A44147; MUID:92228762; PMID:1314383

7

ary

RNA
-RTM-

<KIM>

.. GB:M86621; NID:g203954; F
cium channel alpb3-3 chain

CLUM CHANNEL alpha-2 chain
E: glycosylated. ion channel. transmembrane protein

III; glycoprotein; ion channel; transmembrane protein

96.3%: score 5390: DB 2: Length 1091:

DATE RECEIVED: 06/07/2008

Best Local Similarity 95.8%; Pred. No. 7.1e-316; Matches 1019; Conservative 24; Mismatches 19; Indels 2;	
QY	1 MAAGCLLALTLTLPQSLLIGPSEBPPPSAVITKSWDKMQEDLVTLAKTASGVN
Db	1 MAAGCLLALTLTLPQSLLIGPSEBPPPSAVITKSWDKMQEDLVTLAKTASGVN
QY	61 YEKYQDLVYEPNNARQLVEIAARDIEKLLSNRSKALVSLAEAKVQAAHWEI
Db	61 YEKYQDLVYEPNNARQLVEIAARDIEKLLSNRSKALVRLAMEAKVQAAHWEI
QY	121 EYVYNKADLDLPEKNDSESGSQRIPVIEDANFGRQISYQAAVHPTDIYEGE
Db	121 EYVYNKADLDLPERNESESGSQRIPVIEDANFGRQISYQAAVHPTDIYEGE
QY	181 NELNWTLSALDEVFKKNEEEDPSLLWQVFGSATGLARYYPASPWVNSRTPNKIDL
Db	181 NELNWTLSALDEVFRNRDDEPTLLWQVF-AADELRARYYPASPWVNSRTPNKIDL
QY	241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDDFVNVSFNE
Db	240 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDDFVNVSFNE
QY	301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAPELLNLYNVSRACNF
Db	300 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFTFAPELLNLYNVSRACNF
QY	361 FTDGGEERAQBI FNKNYKDKKRVFRFVSQGHYERGPIONMACENKGYVEIIPS
Db	360 FTDGGEERAQBI FAKNYKDKKRVVFTFSQGHYDRGPIONMACENKGYVEIIPS
QY	421 INTQBYLDVLGRPMVLAGDAKQVQMTNVYLDALGLVITGTLFPVFNITQGFNI
Db	420 INTQBYLDVLGRPMVLAGDAKQVQMTNVYLDALGLVITGTLFPVFNITQGFNI
QY	481 NQLILGCVGVDSVEDIKRLTPFTLCPNGYFAIDPNGYVLLHNPLOPKPKSQI
Db	480 NQLILGCVGVDSVEDIKRLTPFTLCPNGYFAIDPNGYVLLHNPLOPKPKSQI
QY	541 DFLDAELNDIKVEIRNMKIDGSGEKTFTLVKSDQERYIDKGNRTYTWTPVNGT
Db	540 DFLDAELNDIKVEIRNMKIDGSGEKTFTLVKSDQERYIDKGNRTYTWTPVNGT
QY	600 LALVLPYTSFYIYKAKLEETITQARSKGKQKMDSETLPDNPESGYTFIAPRYC
Db	600 LALVLPYTSFYIYKAKLEETITQARSKGKQKMDSETLPDNPESGYTFIAPRYC
QY	660 TSDNTEPELLNFNFIIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSQKNIK
Db	660 PSDNNTPELLNFNFIIDRKTNNPNSCNTDLINRILLDAGFTNELVQNTWSQKNIK
QY	720 RPVVTGGITRVYPKEAGENQENPTYEDSFYKRSLNDNDNVFTAPYFNKSGPGF
Db	720 RPVVTGGITRVYPKEAGENQENPTYEDSFYKRSLNDNDNVFTAPYFNKSGPGF
QY	780 IWSKAVEIYIQGKLLKPAVVGKIDVNSWNIENFTKTSIRDPCAGPVCCKRNSDV
Db	780 IWSKAVEIYIQGKLLKPAVVGKIDVNSWNIENFTKTSIRDPCAGPVCCKRNSDV
QY	840 ILDDGGFLLMANHDDYTNQIGRPFGBIDSLMRHLVNIISVYAFNKSVDYQVCSBP
Db	840 ILDDGGFLLMANHDDYTNQIGRPFGBIDPRMRHLVNIISLAFNKSVDYQVCSBP
QY	900 OGAGHRSAYVPSVADILIQGWATAAANSILQOFLLSLTFPRLLLEAVEMEDDDFTA
Db	900 OGAGHRSAYVPSITDILIQGWATAAANSILQOFLLSLTFPRLLLEAVEMEDDDFTA
QY	960 QSCITEQTQVFFNDKSKFSGLVLDCCNCSRI FPHGEKLMNTNLIFIMVESKGTCPDI
Db	960 QSCITEQTQVFFNDKSKFSGLVLDCCNCSRI FPHVEKLMNTNLVFMVESKGTCPDI
QY	1020 IQABQTSXGNPNCMDMKQPRYKGPDPVCFDNNVLVDYTDCCGVS 1063

TSDGPDPCDMVKQPRYKRGPDVCFDNNVLEDYTDGGS 1063

tein alpha-2 chain precursor - rabbit
dihydropyridine-binding protein, 140K
guinea coniculus (domestic rabbit)
#sequence revision 31-Mar-1992 #text_change 22-Jun-1999
; A39518; A33409
Iams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell
664, 1988
and expression of mRNAs encoding the alpha (1) and alpha (2) subunits of
; S10579; MUID:88336904; PMID:2458626

UNA
<ELL>
EMBL:M21948; NID:g164762; PIDN:AAA81562.1; PID:g164763
-Lys, and deletion of 620-Ser were also found
A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P.
3287-3293, 1991
Characterization of the dihydropyridine-sensitive calcium channel al
; A39518; MUID:91131638; PMID:1847144

rotein
ice represents the amino end of a glycosylated peptide that appears ad
and identical molecular weights (17K) following deglycosylation
lawkes, M.J.; Brush, K.; Cook, R.
120-7828, 1989
position of the purified dihydropyridine binding protein from skelet
; A33409; MUID:90122765; PMID:2558713

ity
rotein
S', 46-47 <HAM>
ium channel alpha-2 chain
i; disulfide bond; glycoprotein; ion channel; membrane protein; phosph
al sequence #status predicted <SIG>
calcium channel alpha-2 chain #status predicted <MAT>
; 0,470,477,606,615,678,697,784,891,898,988,1001,1081/Binding site:

96.1%; Score 5380.5; DB 1; Length 1106;
arity 94.8%; Pred. No. 2.7e-315;
nservative 15; Mismatches 12; Indels 29; Gaps 4;
LLALTLTLQS--LLIGPSSEPPSPSAVTIKSWVDKQEDLVTLAKTAGVGNQV 58
PLAWTLTLQAWLILIGPSSEPPSPSAVTIKSWVDKQEDLVTLAKTAGVGNQV 60

CYDLYTVEPNNARQVIAARDIEKLSNRKALVSLALEAEKVQAAHQRDFA 118
CYDLYTVEPNNARQVIAARDIEKLSNRKALVSLALEAEKVQAAHQRDFA 120
YYNAKDDLDPEKNDSEPGSQRIKPFIEDANFRQISYQAAVHIPTDIYEGSTI 178
YYNAKDDLDPEKNDSEPGSQRIKPFIEDANFRQISYQAAVHIPTDIYEGSTI 180
NNTSALDVFVKQKREDDPSLLQVFGSAGLARYYPASPWVNSRTPNKIDLYDV 238
NNTSALDVFVKQKREDDPSLLQVFGSAGLARYYPASPWVNSRTPNKIDLYDV 240
NYLQGAASPKDMLILVDVSGVSLTLKLRITSVSEMLETLSDDDFVNVASFNSNA 298
NYLQGAASPKDMLILVDVSGVSLTLKLRITSVSEMLETLSDDDFVNVASFNSNA 300
CFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFQQLLNYSRANCKII 358
CFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFQQLLNYSRANCKII 360
OGGERAQEIIFKNYKDKKVRFRFSPVQGNHYERGPIQWACENKGYIIPISGA 418
OGGERAQEIIFKNYKDKKVRFRFSPVQGNHYERGPIQWACENKGYIIPISGA 420

419 IRINTQYILDVLRPMVLADGKAKAQVQWNTVYLDALGLVITGTLPVFNITQOFI
421 IRINTQYILDVLRPMVLADGKAKAQVQWNTVYLDALGLVITGTLPVFNITQOFI
479 LKNQLILGVGVDSLEDEIKLTPRFTLCPNGYFFAIDPNGYVLLHPNLOPK---
481 LKNQLILGVGVDSLEDEIKLTPRFTLCPNGYFFAIDPNGYVLLHPNLOPKIGV
531 -----NPKSQBPVTLDFDAELNDIKVEIRNMIMDGESEKTPRTLVKS
541 INURKRPNVQNPQSPVTLDFDAELNDIKVEIRNMIMDGESEKTPRTLVKS
580 YIDKGNRTTWTVPNGTDY-SLALVPTYSFYVYKAKLEETITQARSKKGKMDSE
601 YIDKGNRTTWTVPNGTDYSSALVPTYSFYVYKAKLEETITQARSKKGKMDSE
639 DNPESGYTFIAPRDYCNLDIKISDNTTEFLNNEFIDRKTNNPSCNADLINRVL
654 DNPESGYTFIAPRDYCNLDIKISDNTTEFLNNEFIDRKTNNPSCNADLINRVL
699 FTNELQVNTWSKKNIGVKARFVVTGGITRVYPKEAGENWQENPETYEDSFYKR
714 FTNELQVNTWSKKNIGVKARFVVTGGITRVYPKEAGENWQENPETYEDSFYKR
759 DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLLKPAVVGKIDVNSWIENFT
774 DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLLKPAVVGKIDVNSWIENFT
819 RDCAGPVCCKNSDVMDCVILDDGGFLMANHDDYTNOIGRFGCEIDPSLMRHL
834 RDCAGPVCCKNSDVMDCVILDDGGFLMANHDDYTNOIGRFGCEIDPSLMRHL
879 VYAFNKSIDYQSVCEPGAAPKQAGHRSATVPSVADILQIGWATAAAWSILOQFL
894 VYAFNKSIDYQSVCEPGAAPKQAGHRSATVPSVADILQIGWATAAAWSILOQFL
939 FPRLLRAVENEDDDFTASLSKQSCITEQTQYFFDNDNSKSFSGVLDGCGNCSRI FHGE
954 FPRLLRAVENEDDDFTASLSKQSCITEQTQYFFDNDNSKSFSGVLDGCGNCSRI FHGE
999 TNLIFMVESKGTCPDTRILLIQABQTSQDNPDCDMVKQPRYKRGPDVCFDNNVLE
1014 TNLIFMVESKGTCPDTRILLIQABQTSQDNPDCDMVKQPRYKRGPDVCFDNNVLE
1059 CGGS 1063
1074 CGGS 1078

RESULT 4

T30256
calcium channel alpha-2 delta-C chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun
R;Accession: T30256
R;Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.
J. Neurosci. 19, 648-691, 1999
A;Title: Molecular diversity of the calcium channel alpha2delta subuni
A;Reference number: Z20794
A;Accession: T30256
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1091 <KLU>
A;Cross-references: EMBL:AJ010949; PIDN:CAA09423.1
A;Experimental source: brain
C;Superfamily: calcium channel alpha-2 chain

Query Match 20.0%; Score 1119.5; DB 2; Length 1091;
Best Local Similarity 28.5%; Pred. No. 4.3e-59;
Matches 321; Conservative 230; Mismatches 443; Indels 131; G

Qy 3 ACCLALTLTLFOSLLIGPSEBPPSPSAVTIKSWVDKQEDLVTLAKTAGVGNQV

LA-TALLYAALGDVVRSEOOIPLSV-VKLWASAFQGEIKSAAYKSGQLLKQYK 71
LYTVENPNARQLVEJAARDIEKLLNSRKALVSLALEAKVQAAHOWREDPASNEV 122
DVAIEHIDGLOLVKLAKIWEEMPHKKSBAVRULVEAAEHAHLKHEFDADU---QY 128
AK--DDLDPKNDSEPGSORIKPVFIEDANFOR-QISYCHAAVHIPTDIYEGSTIV 179
AVLINERXDKGNFLELKGKEFI--LAPNDHFNNLVPNISLSDVQVPTMYNKOPAI 185
NWTISALDEVKPKNREEDPSLLHQVFGSATGLARYYPASPWVDNGBRTNKIDLYDVR 239
TWSESUNKVYFVDFNDPDSLIIWQYFGSAKGPFRQYFGIKWEPDE---NGVIAPDOR 242
TQGAASPKDMLILVDVSGVSGSLTKLIRTSVSMLRTLSDDDFVNVASPNNAQ 299
TQAASTPKDVLILVDVSGSMKGLRLTAKQTVSSILDTLGDGDFNIIITNEELH 302
TQ--HLVQAVNRKKVLKDAVNNITAKGITDYKKGFSFAPELLNINYSRAN--CN 355
LNGTLVQADRTNKEHREHLDKLPAGLIGMLDIALNEAFNILSDFNHTQGSICS 362
TJFDGSEERAAQILFNKYN-KDKKRVYFPFSGVQHNYERGPTQWACENKGYEYIEP 414
TJTDGAVDTYDTIFAKYNNWPKDRKRIPTYLIGREAAFPADNLKWWACANKGFFTOIS 422
IRINTQBYLDVLRPMVLADGKAKOVMTNVYLD-----ALEGLVI--TGT 463
JOENVMEYLHVLSRPKVI--DOEHVWVTEAYIISTLPQAOKLADDOGLVMTTVA 480
JITGOFENKTNILKNQILIGVMGVDSLEDIKRLTPRFTLCPNGYFPAIDPNGVYLL 523
J--KONETRSKG-ILLGWCTDVPVKELLTIPKYGLIHGYAFATNNGYILT 535
JP---KNPKSQBP--VTLDPLDAELENDIKVEIRNKNIDGSSGKTRFRTLKVSODE 578
JPLYEYGKRRKPNPNTSSVDLSVEWEDRDDV-LRANMVNRKTGK--FSMEVK---588
JGNRT-----JTWTPVNGTDSYLAALVPT--YSFYIYKALEETITQARSKGNMK 631
JGRVLVMTNDYYTIDIKGTPSLGVALSRGHGKYFP-----RGNVT 634
JPDNPFESGYTFIAPRDYCN-DLKISDNNTFELFLNPFNEFIDRKTPNPNSCADLI 690
J--HDLHPDVSADWESYCNLDLHPHRRHLSQLAEIKLYLKGKEP-LLQCDKELI 691
JAGFTNELVQNYWS-----KQKNIKGVKARFVVTDGGITRVYP-----733
JDA-VVSAPIEAWTYSALANKSENSDKGVAVFGLTGTLSRLNFLVGAESQLTNQD 750
JENWQENPETYRSDSPKVSRLDN--DNVYFTAPY---PNKSGPGAYESGIMVSKAV 786
JDKENIFNADHPFLVYRRAAQIAGSFVISIPFTGTGKN-----NVYTAFTSI 804
JOKLLKPAVVGIKIDVNSMIENFTKTSIRDPGCPVCDCKNSDWMDCVILDDGFF 846
JRKSPVAAVGIQWKLEFFORKEFTWTSRQCSASLDGKCSISCDDETVCYLIDNNGF 864
JHDDYTNQIGRFGELDPSLMRHLVNI SVYAFNKSYDYQSVCEPGAAPKQAGHRS 906
J--EDYT-QTGDFPFGVEGAVMNKLLTMGSFKRITLYDYQAMCR---ANKSSSDSAH 918
JYADJLQIGMWATAWSITLQOFLSLSTFRPLLEAVEMEDDFTASLSK-----QS 961
JYKAFI-----SAAKWIMTELVLVFLVEF-----NLCSGWHMSDMTAKAQLKOTLEP 968
JYQYFFDNDSKSGFSGVLDCGNCRSRIFHGEKLMNTNLIFIMVESKGTCPCDTRLLIQ 1021
JYAFVSERTIKETTGNACEDCSKSFVJQOIPSSNLMFWVDS--SCLCESVAPIT 1026
JDPN---PCDMVKOPRYRKGDVCFDNNVLEDYTDCCGVS 1063

Db 1027 WAPIRIYNESLKCRLEKQAKRRRPPESCHGFHPENARECGGAS 1071

RESULT 5
S44617

C50C3.l1 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 30-Jun
C;Accession: S44617
R;Favello, A.D.

submitted to the EMBL Data Library, May 1993
A;Description: Sequence of the C. elegans cosmid C50C3.
A;Reference number: S44627
A;Accession: S44617
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-734 <P>
A;Cross-references: EMBL:L14433; NID:g289649; PID:g289650
C;Genetics:
A;Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

Query Match 10.8%; Score 607; DB 2; Length 734;
Best Local Similarity 26.6%; Pred. No. 1.5e-28;
Matches 180; Conservative 127; Mismatches 258; Indels 112; G

QY 47 LAKTAGVNOVLDIYEKYODLYTVPENNAOLUEIJAARDIEKLGNRS----KALV.
:
Db 36 MKETFSKISHETILKONYEKLVEEEQFDPAELKKSKHRIEDYLKVRSQAYKAKI.
:
QY 103 EAEKVQAHQWREDFASNWVYYNADLDLPK-NDSEPGSQRIKP-----VFIE.
|| || :
Db 94 EARSVNDSTVNPDQSQRIFRMFAKSQGDGTIIYESNHLGKRLLKLVNETKSFNLTO.
:
QY 156 -GROISYQAAVHIPDIDYEGSTIVLINELMTSALDEYFKKNREDEPSLLWQVFGS.
:
Db 154 YLTPTSSVSSAVHIPTPLYDRNEDLLRKIDW-SDIDAVYTRNRRETQDLAFQLFCSI.
:
QY 215 ARYPASPWW- DNSRTFNKIDLVDVRRRPWYTGGASPKOMLLILDVSGSVSGGLTL.
||||| :
Db 213 MRYTPAASWFWDNQ--DEHLDLDFCDRTNTEWTYSATNSKNVLIMLMSGSMLGORY.
:
QY 274 TSVSEMLETISDDDFNVVASFNSNA---QDVSCFOHLVOANVRNKVKYLKDVAUNIT.
:
Db 271 QTETAILETISHNDYFNIMTFKNTFLDGCCMGTNGLLOATRNNKALKRRMDTYTO.
:
QY 331 TDYXKGFSFAPEOLLNYY-----VSRLCNKIIMLFTDGGEEARAEIFNKYNKDKKC.
:
Db 331 AEYEKALPLAFSLVDLNNGGGDNNGRGACENVIMLITDGAPNAYKKIFDMYNADKK.
:
QY 386 RFSVGQHNYERGIOWMACENKGYIYEPSIGAIRINTQEYL-----DYLRGPWLVA.
:
Db 391 TFLVGDRAIDFNVREMCCRNGYGVHVHANMADVDEKIHYYIRMSRVVGRHYKESI.
:
QY 442 KQOVNTNWVLDALELGL--VITCTLPVENITQGPNKTN-----
:
Db 451 ---NWTVGERLYLPRPIFAEPVPIINQSPAVNVMASRRKIRLOKSEARGEMF.
:
QY 479 ----LNQOLILGVMGVDVLSIEDIKLTRFTLCPCNGYFAIDPNGYLLHPNLPQPK.
:
Db 508 SYPVIVNETPMGAAVNIPLTEVAOKSHPANITGSKFYFMLDQNGFWTHPQLRPII.
:
QY 533 --KSQEPVTLDLDEL-----AELENDIKVEIRNI.
:
Db 568 KYHKQNTNMDDLIELVGQNQVNRSSQSAVSDLVCESGANVABCDDLLRKAVRK.
:
QY 562 GESGEKFRTLVKSQDERY----IDK---GNRTYTWTPVNGTDYSLALVPTYTSFYI.
:
Db 628 CDNSD-----VOOLDVLATALLDRVVPTQNTYYAACINHANFVLGLAVAKGDDYI.
:
QY 615 KLEFITTQARKSGKGMK 631
:
Db 682 K-----QKKYPDGRVK 692
: :

[illegible]

```

24 DPEKNDSEPGSQRKIP---VFIEDANFGROIYQHAHVH----- 167
25 : : : : : : : : : : : : : : : : : : : : : : : : : :
26 NNESSQRETVSOLKQDSQLAFSPNFGIKASFNDLAQNYENISPEYRQDETGLSP 240
27 IPTDIYEGSTIVLHNLWTSALDEVFKKQREDDPSLLMQVFGSATGLARYYPASFW 223
28 : : : : : : : : : : : : : : : : : : : : : : : : : :
29 IPT-----GNTTVVHQGNNSF-----SSQMDGVNSWN--GEATNLNLSVIEYAG 287
30 : : : : : : : : : : : : : : : : : : : : : : : : : :
31 -----SRTPNKIDLY-DVRRRWYIQGAASPKMDLILVDVSGSVSGLTLK 270
32 : : : : : : : : : : : : : : : : : : : : : : : : : :
33 VDFALRYKAKETETFGLYDVLYNRGN---VQNPVKPVDIVLIDMSGMOGAKET 344
34 : : : : : : : : : : : : : : : : : : : : : : : : : :
35 SVSEMLETSLDD---DFNVV--ASFNSNAQDVSCFQHLVQANRNKKVLKD----A 321
36 : : : : : : : : : : : : : : : : : : : : : : : : : :
37 GVSDFLSTIQNTAYADYVNVGIVGYSSPGNTVGTASGYITVPI--DKVSSSHVKS 402
38 : : : : : : : : : : : : : : : : : : : : : : : : : :
39 TA---KGTIDYKGFSAFAPFOLLNYSRANCKIIMLFTDGGHRAQEIFKNYK 378
40 : : : : : : : : : : : : : : : : : : : : : : : : : :
41 LAQFSGTFTQLGLRKGTML---EQSSNQKQMLMTDG---VPTFSYKYN 455
42 : : : : : : : : : : : : : : : : : : : : : : : : : :
43 R--VRFPSVGQHNTERG---PIQ---WMACENKGYIYEI-----PSIGAIRINTQE 425
44 : : : : : : : : : : : : : : : : : : : : : : : : : :
45 DNVIYQGSFAESRDEPGNTSKIQSPYVYKDGSGNSIEIRDTWAATLGEABISQBE 515
46 : : : : : : : : : : : : : : : : : : : : : : : : : :
47 LGRPMVLADG-----KAKQVQWNTVYLDALGLVITGTLPLVFNITGQFE 474
48 : : : : : : : : : : : : : : : : : : : : : : : : : :
49 HTLGIQLGNDGYSLSQBEVKSRTSLIATGLYQDANSAN-----DITDYLK 565
50 : : : : : : : : : : : : : : : : : : : : : : : : : :
51 -----LKNQILGVMDVSLIEDIKLTPRTLCFNGYYPALDPNGYVLLHPN 526
52 : : : : : : : : : : : : : : : : : : : : : : : : : :
53 VLSRFNTITNGLIDPLGAQFEYKOTK-----FEITSVG----- 604
54 : : : : : : : : : : : : : : : : : : : : : : : : : :
55 NPKSQEPVTLDFLDAELNDIKVIRKMKIDGESCKETFTLVKSQDERYIDKGNR 586
56 : : : : : : : : : : : : : : : : : : : : : : : : : :
57 -----EDSIDNLPKINEKGLSISNLNI--GKQEQVQIHVQVRLNFTETDDPKNY 653
58 : : : : : : : : : : : : : : : : : : : : : : : : : :
59 -----TWTPVNGT--DYSIALVLPYSPFYIKAKLE-----ETITQARSKK 627
60 : : : : : : : : : : : : : : : : : : : : : : : : : :
61 NGETTLTP--NGSNPDKNVNFQVPSAKSGSINGLTLEKQWLANSENIPEENVELLIGRR 712
62 : : : : : : : : : : : : : : : : : : : : : : : : : :
63 DSE-----TLKPDNFESGYTFIAPRDYCNLDKISDNNTEFLNFEIDRKTPNN 682
64 : : : : : : : : : : : : : : : : : : : : : : : : : :
65 SSWTKVTTLKEDDEWTSOLENLPKYSILGEEFYIEIKDELVLN--SELYDWITIGE 771
66 : : : : : : : : : : : : : : : : : : : : : : : : : :
67 ADLNRVLLD---AGFTNELVQWYKQKNIKGVKARFVVTDGGITRVYPKEAGE 738
68 : : : : : : : : : : : : : : : : : : : : : : : : : :
69 IANIEKPLQLIKTSNHDNEPLSEVEFVLKNSQGEIDKAVTN-----EKGE 822
70 : : : : : : : : : : : : : : : : : : : : : : : : : :
71 ENPTYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGIMVSK-----AVEIYIQ 791
72 : : : : : : : : : : : : : : : : : : : : : : : : : :
73 KTRILNYGEEYQLHEIKSPGHSLEGPWKIKT---EFENGQPIIKYDGEQIALDEHYN 879
74 : : : : : : : : : : : : : : : : : : : : : : : : : :
75 KPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVMDCVILD-----DG-- 844
76 : : : : : : : : : : : : : : : : : : : : : : : : : :
77 S---LNTINDIN--VEEF-----RNSVTIDKRAVDSEKLDGAV 917
78 : : : : : : : : : : : : : : : : : : : : : : : : : :
79 LMANHDYTNQIGRFFGEIDPSLMRHLNIVSYAFNKSVDYQSVCEPAAAPKQAG 903
80 : : : : : : : : : : : : : : : : : : : : : : : : : :
81 QIESVDDELTLQKPL--EITNNLLPGL-----YALQESVSPNGYVRDDEV 964
82 : : : : : : : : : : : : : : : : : : : : : : : : : :
83 SAYVPSVADILQIGWATAAWSILQOFL-----LSLTF- 939
84 : : : : : : : : : : : : : : : : : : : : : : : : : :
85 VKFNGSIVAIGSEG-----IDIPLDENESGKGLVINEENGDLHLTLIFY 1015
86 : : : : : : : : : : : : : : : : : : : : : : : : : :
87 PRLLAEVEMEDDDFTASLSKQSC-ITEQTOYFFDNDN-----KSPSGVLDCCNCSRI 990
88 : : : : : : : : : : : : : : : : : : : : : : : : : :
89 PPLQLEVDKIDDDFTSLAGVSPFLTRLGKASTSDSVKRLNSFDRLIKTFN--NE 1073
90 : : : : : : : : : : : : : : : : : : : : : : : : : :
91 KL--MNTNL 1001
92 : : : : : : : : : : : : : : : : : : : : : : : : : :
93 TALKSNL 1085

```

```

RESULT 8
S54355
inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 04-Feb
C:Accession: S54355
R:Chan, P.; Rialler, J.L.; Raguenes, G.; Salier, J.P.
Biochem. J. 306, 505-512, 1995
A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor
A:Reference number: S54353; MUID:95194326; PMID:7534067
A:Accession: S54355
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-886 <CRA>
A:Cross-references: EMBL:X70393; NID:G95635; PIDN:CAA49843.1; PID:G69
C:Superfamily: inter-alpha-trypsin inhibitor complex component II

Query Match 3.5%; Score 194.5; DB 2; Length 886;
Best Local Similarity 19.9%; Pred. No. 0.0013;
Matches 185; Conservative 138; Mismatches 347; Indels 261; G

QY 27 FPSAVTIKSWVDKMQEDLVTLAKTAGVNLQVDIYEVKYQDLYTVPPNNARQLVEIF
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 98 YPGNVKEVAQKQYKAVSQKTAG---LVKASGRKLEKFTVSVNVVAAGSKVTF
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 EKLISNRSKALVSLALEAEKQVAAQHWREDPASNEVVYVYNAKDDLDPEKNDSEPG
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 154 EELL-KRNGKGYEMLKVQPKQLVRHFEID-----AHIFEP--
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 PVFIEDANFGROIYQHAHVHPTDIYEGSTIVLHNLWTSALDEVFKKQREDDPS
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 GISMLDAB-----ASFITNDL-LGSALTQSF-----
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 207 VFGSATGLARYYPASPMVDNSRT--PNKID-----LYDVRRRP-----
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 215 -----SGKKGHVSFKPSLDQORSCTCTDLSLLGDFTVIVDVNRESQGVQVINGY
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 246 ---QG--AASPKMDLILVDVSGSVSGLTLKIRTSVSEMLETSLDDDFVNVASFNSN
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 270 PAPQGLPVVPKNIVFVIDVSGSGMSGRKIQTQREALLKILDDVDKEDDYLNFILFST-
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 SCFO-HLVQAVNRKKVLKQAVNNITAKGTYDKKGFSAFPEQLLNYNVSRAN---
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 327 TTWKDHLVQATPANLKBKAKTFVKNIHQSMTNINDGLLKGIEML---NKAREHTV
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 355 NKIIMLFTDG---GEBAQEIFPNKYK--DKKVRVFRFSVGOHNYERGPQIOWMAC
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 384 TSIILMLTDGANTGESRPEKIQENVRNAIGGKFPYLNLFGLG--NNLNYNFIETLAL
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 409 YYPEISGAIIRINTQBYLDVLRPMVLGAKQVQWNTVYLDALBLGL--VITG
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 443 LARRIYEDSDANLQOGFYEEVANPLL-----TNVEVEYPENAILDLTRN
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 467 FNITGQFENKTNLKNQILILGVMDVSLIEDIKLTPRTLCFNGYYPALDPNGYVL
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 492 F-----YDG-----SEIVAGRLVDRNMDN-----FKADYKGHGA
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 527 LQPNKPSQBPVTLDFLDAELNDIKVIRKMKIDGESGEK--TFRTLKVSQDERY
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 524 ----DLTFTFEVDMEEMDAALK-----EGYIFGDIYIERLMAYLTIEQLLEKRR
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 585 NRTYTWTPVNGTDSYLA--LVLPITYSPYIKAKLEETITQARSKKQKWKDSET---
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 573 DEKENIT-AEALDLSLKVHFVTPLTSMVVTKPEDNEDQTSIADNAGEAEAFETTM
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 638 PDNFEESGYTFIAPRDYCNLDKISDNNTEFLNFEIDRKTPNNPSCNADLNIRV
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 632 TQSSSQSPFYV-----DGDPHFIIQI-----PGKNDISICFNI
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 698 GFTNELVQWYKQKNIKGVKARFVVTDGGITRVYPKEAGENWQENPETYEDSFYK
Db : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 669 GTVLRLLIQD-----PVT--GIT-VTGIIIGD-----K

```

[illegible]

inhibitor heavy chain 3 precursor - human
HC3; inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor heavy
chain 3 precursor - human
#sequence_revision 20-Feb-1995 #text_change 04-Feb-2000
#S4123; S02141; D34245; A39079; S50133; B53642; A59167
Diarra-Mehrputz, M.; Thiberville, L.; Bost, F.; Seabouee, R.; Martin,
D. 771-776, 1993
alpha-trypsin inhibitor-precursor heavy chain cDNA and deduced amino-
acid sequence. PMID:93215656; PMID:7681778

NA
BOU1>
EMBL:X67055; NID:g288562
BL Data Library, June 1999
S34123

NA
K', 312-343, R', 345-885 <BOU2>
EWELX670055; NID:9288562; PIDN:CAA47439.1; PID:9288563
M.; Bourguignon, J.; Sesboues, R.; Mattei, M.G.; Passage, E.; Salier,
9, 147-154, 1989
ma inter-alpha-trypsin inhibitor is encoded by four genes on three ch
S02141; MUID:89137072; PMID:2465147

red with conceptual translation

'G', 358-845, 'H', 847-885 <DIAL>
EMBL:X14650; NID:G35464; PIDN:CAA32821.1; PID:G35465
ogersen, I.B.; Pizzo, S.V.; Salvessen, G.
15975-15981. 1989

of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-A92736; MUID:89380192; PMID:2476436

otin

ENGL>
Ivessen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V.
747-751, 1991
n 4-sulfate covalently cross-links the chains of the human blood prot
A39079; PMID:91093267; PMID:1898736

tein

M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesboue, R.; Muschio-Bon
cta 1219, 551-554, 1994
entation of the inter-alpha-trypsin inhibitor heavy chain H1 and H3 g
SS0132; MUID:95002176; PMID:7522574

27

A
IA2>
EMBL:X75318
Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.

arthritis-associated hyaluronan binding protein, forms a stable complex with hyaluronan. **PMID:7516184**

otin

A;Residues: 30-34,'X' <WIS>
R;Jessen, T.E.; Paarvang, K.L.; Ploug, M.
FEBS Lett. 230, 195-200, 1988
A;Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin:
A;Reference number: S02431; MUID:88167187; PMID:2450785

A;Accession: A59167

A;Molecule type: protein

A:Residues: 30-32,'GEKEQAVDT', <JES>
C:Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked with alpha-1-antitrypsin.
C:Genetics:

A;Gene: GDB: ITIH3

A;Cross-references: GDB:120109; OMIM:146650

A;Map position: 3p13-3p12
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; heterodimer
F;1-19/domain: signal sequence #status predicted <SIG>

F;20-25/Domain: propeptide #status predicted <PRO>
F;30-487/Product: inter-alpha-trypsin inhibitor heavy chain 3 #status
F;640-885/Domain: carboxy-terminal propeptide #status predicted <CTP>
F;87,576/Binding site: carbonylhydrate (Aen) (covalent) #status predicted
F;647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (lin

Query Match 3.3%; Score 185; DB 2; Length 885;
Best Local Similarity 20.4%; Pred. No. 0.0048;
Matches 133; Conservative 106; Mismatches 243; Indels 170; G

Qy : | | | | | | | | | |
27 FPSAVTIKSWVDKQEDLVLTAKTAGSVNQVLDIYEKYQDLYTVEPNNARQLVEIAF
D6 : YPGNVKEKEVAKTGYEKAVSOGKTAG-----LTKASG

```

QY      87  EKLLSNRSKAL---VSLALEAEKQAAHQAOWREDFASNEVVYNAKODLDPEKNDSEI
      ||  ::  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Dp     132  EKFTSVNVAAGSKYFRI.TYFEL.LKRHEGK-----YRMYLKVQOPY-----

```

```

QY      144 RIKPVIEDANFGROISYQHAAVHIPTDIYEGSTIVLNLNWT$ALDEVFKNREEI
          : || || || || || || || || || || || || || || || || || || || ||
Dh      174 IYKHEEIT-----VQTEEOGICMTDAPASCTNDY-----

```

Qy 204 LMQVFGSATGLARYYPASPWTNRS-T-PNKID-----LYDVRRRP
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dh 209 IATVSSGCVGVGVSVSG--TADPSGPRMTNSTVNGDPTITVVIVNDGGSDNVVITA
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

```

Qy 245 I-----QG-AASPKDMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFVNVASF
      :      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Dh 246 VHEFAA DGGI DINDVNVA EVINISGSMAGCEET EOTVETAI IDTI ENMOCEENVN DDTI ES

```

```

Qy      299 QDVSCP-QHLVQANVRNKGVLKDAVNNTAKGITDYKKGFSFAFEQLLNYSR---
           ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : :
Db      324 -NVSMTFVTVQAMTENT QEAETMDVSGMRYQVMTNDCY I DAT GMI NVADDEI

```

QY 352 ANCNKIIMLFTDG-----GEERAQEIFNKYNK--DKKVRFVRFSSVQGHNVYRGP IQM

```

QY
-----
406  NKGYYPEISGAIRINTQEYLDVLGRPMVLGDKAKQVQWTVVYLDALB
      ||| : | : | : | : | : | : | : | : | : | : | : | : | :
407  NKGYYPEISGAIRINTQEYLDVLGRPMVLGDKAKQVQWTVVYLDALB
      ||| : | : | : | : | : | : | : | : | : | : | : | : | :

```

QY 457 GLVITGTLPVFNITQFENKTNLK-----NQILILGVMGVDVSLDIKRLTRPFTLCI
: : | | | | | : : | | | : : : : : |

Qy 512 YPAIDPN-----GYVLLHPNLQPK--NPKSQEPVTLDFLDAELENDIKVEIRNKN

QY 563 ESGETFRLVKSQDERYI-DKGNRTYTWTPVN-GTDYSLALVLPYTSFYI 612

RESULT 10

RESULT 10
D97033

otein, probably surface-located [imported] - Clostridium acetobutylicum acetobutylicum

1 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

3

ton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, net, G.N.; Koonin, E.V.; Smith, D.R.

4823-4838, 2001

quence and Comparative Analysis of the Solvent-Producing Bacterium Clo

9 A96900; MUID:21359325; PMID:21359325

3

ary

NA

<KUR>

GB:AB001437; PIDN:AAK79055.1; PID:gl5023996; GSPDB:GN00168

rice: Clostridium acetobutylicum ATCC824

3.11; Score 175.5; DB 2; Length 1819;

arity 18.84; Pred. No. 0.055;

nservative 154; Mismatches 342; Indels 335; Gaps 51;

PSAVTIKSWDXMQEDL-VTLAKTAGVGNQVLD-----IYEKYQDLYTVEPNA 75

KNARTSG-ADLTKEIGTGTANTSDSIKGIFDMRTGTAVSDYQFLITQVNSN 191

SIAARDIEKLSNRSKALVSLALE-----AEKVQAHQWREDFASNEVYNA 127

---LQDINSWLTGKRYALISKILSTVDKITTAVSNINNANDHESDFALQI--YNV 243

DPBKND-----SEPGSQRKPVF-----IEDANFR-QISYQH--A 164

VPFLNENISAANKGSDLSSEINTVVKDLSKLQDALERINLQGTLDYHFIG 303

PTDIYEGSTVLNELNWSALDEVFKNR--EDPSSLWQV--FGSATGLARYPA 220

QENLEDVNGWANGKW-----FERNAAIEINSIVEPLSRINSGDSTAADYDA 356

VDNSRTPN-----KIDLYDVRPRRYTQGA 248

EVDNNIDNKSIVAEKKQKLGKRNLAETAKSAVEEYKTVLDFDLIK-----GT 411

MLILVDVS-GSVSGL-----TLKLRTSVSEMLTISD-----DD 287

DYNAIGLTGVTEDNVTDNELLKNRDIKTLNKLQDNINSIISKLKNINAGTDTPDD 471

AFNSNAQDVSCP-----QHLVQANVR--NKVLKDAVNNITAK-----328

NISSVTQDNISFIRDIDIKAKQANGSDLNKGKIQDSVNSLKLRSAMDRINAGSA 530

YK----KGFSAFEQLLNYSRANCNKIIMLFTDGEERAQEIFENKYNK-----378

ALLGIEGTSNLTFFVNNQVKSNGKTIIDELTKVSD--ALKLIDSYNKVNGNDA 588

QVRV-FRFSVQGHNYERGPIQWACENKGYI-YEIPSIG--AIRIN-----422

YKIGIVIKIEEVTYNG-----VFKGKNTFLEELKVGINIAVRVISTENIKNG 643

-----TQEYLDVGRPMVLADGKAKQV-----OWTNVYL 451

EDFTIAGYTGVTENIKYINKVIEGGDASPEAISNIITEVNVVEIOSLKEWSSQV 703

ALELGL-VITGTLVPVNIQFQENKTNLKNQLILGVNGVDVSLIEDIKLTPRTLIC 507

VKSLGLSIVTEENISYIMDRVVRNTYYSKVELIEAVEAIKKEIYERINLQATV 763

YFAI-----DPNGYVLLHPNLQPKNPQSQEPVTLDFLDAELENKIVK-----554

YIKVTGTVSNITSINDYV-----KSGNLTITREELQAKI--DVVIEQTQS 810

--IRNMIDGESSEKTPR-----TLVKSQDBRYIDKGNRTYVTPVNGTDSLALVL 604

DYVIGRVNLGEANISDFEPMGITVWNSFNTQYVDDHLKDDKYTTTIDAIAKAATVVFV 870

Qy 605 PTYSFYIKAKLBETITQARSKKMKDSETLKPDNFEESGYTFIAPRDYCNDLKI

Db 871 GQYSIY-----EIN-----KGTATL-----DIYNSLGI

Qy 665 TEFLNFNEFTDRKTPNNPSCNADLINRVLLDAGFTNELVQNYWSKOKNIKGVKAR

Db 899 TENITYINLNKSSYFNAS---DIQTKV-----NALISVYGYEEINKGEATV

Qy 725 DGGITRVYPKEAGENWOENPETVEDSFYKRSNDNDNVFTAPYFNKSGPGAYESGI

Db 949 SLGITGV-----TKENIIFINTYIKE---GQYFDLT

Qy 785 AVEI-----YIQ---GKLLKPAVGIKIDVNSWIENFTKTSIRDPCAGPVCDCCK

Db 981 SVEVLEEKYEAAYKITSGK---AVWG-----DYTKVGIKQVTEENIAYIN

Qy 835 VMDC 838

Db 1027 LQNC 1030

RESULT 11

JC5576

inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C>Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar

C:Accession: JC5576; PC4486

R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.

J. Biochem. 122, 71-82, 1997

A:Title: Molecular cloning and sequencing of cDNAs encoding three heav

sin inhibitor heavy chain family.

A:Reference number: JC5574; MUID:97420688; PMID:9276673

A:Accession: JC5576

A:Molecule type: mRNA

A:Residues: 1-889 <NAK>

A:Cross-references: DDBJ:D89287

A:Experimental source: liver

A:Accession: PC4486

A:Molecule type: protein

A:Residues: 34-53;449-475;509-526 <NA2>

C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy cha

that the complexes play important role for pancreatic cancer.

C:Superfamily: inter-alpha-trypsin inhibitor complex component II

F:236-239,664-865/Disulfide bonds: #status predicted

Query Match 2.94; Score 164.5; DB 2; Length 889;

Best Local Similarity 23.24; Pred. No. 0.082;

Matches 66; Conservative 56; Mismatches 112; Indels 51; G

Qy 202 SLLWQVFGSATGLARYYPASPWVDSNRT-PNKID-----LYDVRRR-PWYIQ

Db 211 SALTSPSGKKGHVSKFPS---LDQQRSCPTCTDSLNGDFTIYDVNRESPGNVQ

Qy 249 -----ASPKMLILVDVSGSVGLTKLIRTSVSEMLTISDDDFVNA

Db 268 YVHFPAQGLPVVPKNIVFVIDISSMAGRKIQQTFVALLKILDDMKQDYLNFI

Qy 297 NAQDVSCFQHLVQANVRNKVLKDAVNNITAKITDYKKGFSFAFQLLN-----YN

Db 328 GV--TTWKDSLQVQATPANLEEARTFVRSISDQGMNTINDGLLRIMLTDAREQHT

Qy 353 NCNKIMLFTDG---GEERAQEIFENKYNKDKKVRVFRFSVG-QHNVERGPQIOWMA

Db 386 STSIILML-TDGDANTGESRPEKIQENVRKAIEGRFPLYNLGFNNLNYNFLETMA

Qy 408 GYTYEIPSGIAIRINTQEYLDVGRPMVLADGKAKQVQWNTNVYLD 452

Db 445 GVARRIYEDSDANLQGGFYEEVANPLL-----TNVEVE 478

RESULT 12

T28155

IAISRLKKKFSISCLCPHKINAGINTWVFDKGT-TLTENNLOFIGHTQKKNK 547
LDLDAELENDIKVEIRNKMIDGESGKFTFLVKSODERYIDKGNRTYTTPVNG 595
-DFHIK-----EMNTSYTHSKDDNHNKN----- 577
LALVLPYFYIYKAKLBETTQAKSKKGMKD-----SETLKPDPFESSG 645
-----SIISYYIKDNMKNLHTSSK-KKSITKRSNPLVQTIKSCLLKDHVYKCK 627
APRYCNDLKISDNN-TEFLN-----FNEF--IDRKTNNPNSCADLINRVLLD 696
TNNYCNLHINDTSCSYLLNSETKDAYCEYNIH-----LCD-----INKNMD 678
NELQNYMSKOKNKGKAVFVVDGGITRVYKPEAGENQENPETVDSFYKESL 756
NELMGYSKNELMGKTIKNELM-----GKYSKNEL 712
YVFTAPYKSGPGAYESGIMVSKAVEIYIOGKLLKPAVW-----IKIDVNSWI 810
---MGKYSKNELMGKYSKNELMGKYSKNELMGKTIKNQVGVDTNIYH 765
KTSIRD-PCAGPVCDCRRNSDVMDCV---ILDDGGFLMANHDDYTNQIGRF--- 862
NDYNDYPCD---YNCNNDYTHRLEVHNKONSFNIPERKNSYNNISEHIKI 822
LFEALACCHTLKSVNNKMGVBLFMFTNCDMLNNSNFIIEKKKNSYDFQ 882
PGAPKOGAGHRSAYSVADILQIGWATAAANSILOQFLLSLTFPRLLBAVEME 949
-DGNKTGANDERCHLNN-----NLVSYNLIKRF----- 912
TASLSKOSCIETEOTQYFPDNDKS 977
QSRLQMSVIVKST-YGNNDNN 937
in b2270 - Escherichia coli (strain K-12)
7 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
8
Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co-
au, B.; Shao, Y.
1462, 1997
ate genome sequence of Escherichia coli K-12.
: A64720; MUID:97426617; PMID:9278503
3
ary; nucleic acid sequence not shown; translation not shown
NA
<BLAT>
: GB:AE000317; GB:U00096; MID:g1788605; PIDN:AC75330.1; PID:g1788606;
cce: strain K-12, substrain MG1655
Q 2.8%; Score 157.5; DB 2; Length 575;
arity 21.6%; Pred. No. 0.11;
onservative 93; Mismatches 206; Indels 105; Gaps 25;
ARQLVETARDIEKLSNRKALVSLAEKVAQAHQWREDFASNEVYVYNAKD 130
KESQOQOPSTPTEQVLAQQAIAK---EAEQSA---AKALAQEQVQYSDKQA 75
KND-----SPGSRKIPVFIEDANFGROISYQHA---VHIPTDI 172
QCAPTARAARAKATHIANPGTARYQOF---DNPVKQAQNPATFSLDVTGS 132
TIVLNE-----LNWTSALDVEFKKNEEDPSLLMQVFGSATGLARY 218
RFLNQLGLPPDPAVRVEIVNVPSPDWDI--KDKQSIPASKPIPFAMRYELA--- 187

QY 219 PASPWVDSRTPNKIDLYDVRRRPWIYIOGAASPKDMLILVDVSGS-VSGLTKLH
Db 188 PA-PW-NQORTLLKVLIDKDKSELPAS-----NLVFLIDTSGSMISDERPLIK
QY 278 EMLETLSDDDFNVASFNSNAQDVSCFOHLVQANVRNKKVLKDAVNNITAKGITD
Db 242 LLVLELRQDNIAIYVYAGDSRIA-----LPSISGSHKAEINAATDSLDAGSTNC
QY 338 SPAPOLLNVNVRANCNKIIMLFTDG-----GBERAQEIFNKYNKDKKVRVRE
Db 297 ELAVQATK-GFIKGINR-ILLATDGFNVGIDDPKSIEMVKKQRESGVTLSTE
QY 332 HNYRGPQIOMACENKGYEIPISGAIRINTQBYLDVLRPMVL--AGDKAKQVC
Db 355 SNYNEAMVRIADVGNNGNSYIDTLS---EAQKVLNSEMQLITVAKQVKAQIE
QY 446 WTVNYLDALGLVITGLPVFNITGQFENKTNLKNQILGVMDV-VSLEDI---
Db 411 WTEY---RQIG-----YE-----KQLRVEHFHNDVNDVADGIGAC
QY 502 PRFTLCPNGYVFAIDPNGYVLLHPLNLPKNPKSOE 536
Db 448 LIFELTNGQKASIDKLRYA--PDKLAKSDKTKE 480
RESULT 15
E90542
lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug
C:Accession: E90542
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissc
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathog
A:Reference number: A99512; MUID:21267165; PMID:111353084
A:Accession: E90542
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-918 <KUR>
A:Cross-references: GB:AL445566; PID:g14089658; PIDN:CAC13418.1; GSPDB
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU_2450
A:Genetic code: GSC3
Query Match 2.8%; Score 156.5; DB 2; Length 918;
Best Local Similarity 20.0%; Pred. No. 0.26; Mismatches 122; Indels 161; G
Matches 122; Conservative 99;
QY 305 QHLVQANVRNKKV---LKDAVNNITAKGITDYKGFSAFQQLNLYNVRANCNK
Db 91 KRILPSNVNENLDFNSLKLITKNTLIGKNTPKNYTVAFSIDPN-SVENASADN
QY 361 FTGGBERAQEIFNKYNKDKV---RVFRFSVGOHNYRGPQIOMACENKGYE
Db 146 -TDG-----SNIIIVSLKDKNGVLEKVKFIT-----GLLSEL
QY 418 AIRINTQBYLDVLRPMVLADGKAKQVQWNTNVYLDALGLVITGTIP-----
Db 182 DQMLK-----VDVPKNENILASSIVEVEQITNE-----KISLTQKQVPSTFDITKY
QY 468 NITQGFENKTNLKNQILGVMG-----VDVSLEDIKR--LTPRFTL-CPNGYVFA
Db 233 HVLSHDDKGLKIRVSLSAKSTKSKDPDYTTIEGFKQSFLEDRISLAKAQVYNT
QY 519 GYVLLHPLNLPKNPKSOEPVTLDFLDAELENDIKVEIRNKMIDGESGKFTFLVK
Db 292 --TIKSLQLLPSSASSED--KLVLSAYDISVPDGLKFNFSFEAKQGT-----
QY 579 RYTDKGNRTYTTPVNGTDSLALVLPYFYIYKAKLBETTITQAKSKKGMKQDE
Db 339 ---DKGVLYTFLTQINGTRTRTEEVKLDIOTFNTIKRYLDETILKIDSV--VLKENS!

